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(54) Title: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE AGENT, COMPOSITION, KIT AND TREATMENTS

## (57) Abstract

A composition comprises a nucleic acid comprising an oligo anti-sense to a target such as polypeptide(s) associated with an ailment afflicting lung airways, genes and mRNAs encoding them, genomic and mRNA flanking regions, intron and exon borders and all regulatory and functionally related segments of the genes and mRNAs encoding the polypeptides, their salts and mixtures. Various formulations contain a requisite carrier, and optionally other additives and biologically active agents. The agent of the invention may be prepared by selecting a target gene(s), genomic flanking region(s), RNA(s) and/or polypeptide(s) associated with a disease(s) or condition(s) afflicting lung airways, obtaining the sequence of the mRNA(s) corresponding to the target gene(s) and/or genomic flanking region(s), and/or RNAs encoding the target polypeptide(s), selecting at least one segment of the mRNA which may be up to 60 % free of thymidine (T) and synthesizing one or more anti-sense oligonucleotide(s) to the mRNA segments which are free of adenosine (A) by substituting a universal base for A when present in the oligonucleotide. The agent may be prepared by selection of target nucleic acid sequences with GC running stretches, which have low T content, and by optionally replacing A in the anti-sense oligonucleotides with a AUniversal base@. The agent, composition and formulations are used for prophylactic, preventive and therapeutic treatment of ailments associated with impaired respiration, allergy(ies) and/or inflammation, such as pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, lung pain, cystic fibrosis, bronchoconstriction, pulmonary hypertension and bronchoconstriction, chronic bronchitis, emphysema, chronic obstructive pulmonary disease (COPD), acute respiratory distress syndrome (ARDS), ischemic conditions including ischemia itself, and cancers such as leukemias, lymphomas, carcinomas, and the like, e.g. colon cancer, breast cancer, pancreatic cancer, lung cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastasis, etc., as well as all types of cancers with may metastasize or have metastasized to the lung(s), including breast and prostate cancer. The present treatment is suitable for administration in combination with other treatments, e.g. before, during and after other treatments, including radiation, chemotherapy, antibody therapy and surgery, among others. The present agent is effectively administered preventatively, prophylactically or therapeutically by itself for conditions without known therapies, or as a substitute for, or in conjunction with, other therapies exhibiting undesirable side effects. The treatment of this invention may be administered directly into the respiratory system of a subject, so that the agent has direct access to the airways and the lungs.

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## LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE AGENT, COMPOSITION, KIT & TREATMENTS

### BACKGROUND OF THE INVENTION

#### Field of the Invention

This application relates to an agent comprising anti-sense oligonucleotides of low or no adenosine content. These agents are suitable for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. Examples of these diseases are allergies, asthma, impeded respiration, pain, cystic fibrosis, and cancers such as leukemias, e.g. colon cancer, and the like. The present agent may be administered prophylactically or therapeutically in conjunction with other therapies, or may be utilized as a substitute for therapies that have significant, negative side effects.

#### Background of the Invention

Respiratory ailments, associated with a variety of diseases and conditions, are extremely common in the general population, and more so in certain ethnic groups, such as African Americans. In some cases they are accompanied by inflammation, which aggravates the condition of the lungs. Asthma, for example, is one of the most common diseases in industrialized countries. In the United States it accounts for about 1% of all health care costs. An alarming increase in both the prevalence and mortality of asthma over the past decade has been reported, and asthma is predicted to be the preeminent occupational lung disease in the next decade. While the increasing mortality of asthma in industrialized countries could be attributable to the increased reliance upon beta agonists in the treatment of this disease, the underlying causes of asthma remain poorly understood.

Anti-sense oligonucleotides have received considerable theoretical consideration as potential useful pharmacological agents in human disease. Their practical application in actual models of human disease, however, has been somewhat elusive. One important impediment to their effective application has been a difficulty in finding an appropriate route of administration to deliver them to their site of action. Many in vivo experiments were conducted by administering anti-sense oligonucleotides directly to specific regions of the brain. These applications, however, necessarily have limited clinical utility due to their invasive nature.

The systemic administration of anti-sense oligonucleotides also presents significant problems, not the least being an inherent difficulty in targeting disease-involved tissues. In contrast, the lung is an excellent target for the direct administration of anti-sense oligonucleotides, and provides a non-invasive and a tissue-specific route. The delivery of anti-sense agents to the lung has been relatively undeveloped.

Adenosine may constitute an important mediator in the lung for various diseases, including bronchial asthma. Its potential role was suggested by the finding that asthmatics respond favorably to aerosolized adenosine with marked bronchoconstriction whereas normal individuals do not. An asthmatic rabbit animal model, the dust mite allergic rabbit model for human asthma, responded in a similar fashion to aerosolized adenosine with marked bronchoconstriction whereas non-asthmatic rabbits showed no response. More recent work with this animal model suggested that adenosine-induced bronchoconstriction and bronchial hyperresponsiveness in asthma may be mediated primarily through the stimulation of adenosine receptors. Adenosine has also been shown to cause adverse effects, including death, when administered therapeutically for other diseases and conditions in subjects with previously undiagnosed hyper reactive airways.

A handful of medicaments have been available for the treatment of respiratory diseases and conditions, although in general they all have limitations. Theophylline, an important drug in the treatment of asthma, is a known adenosine receptor antagonist which was reported to eliminate adenosine-mediated bronchoconstriction in asthmatic rabbits. A selective adenosine A<sub>1</sub> receptor antagonist, 8-cyclopentyl-1, 3-dipropylxanthine (DPCPX) was also reported to inhibit adenosine-mediated bronchoconstriction and bronchial hyperresponsiveness in allergic rabbits. The therapeutic and preventative applications of currently available adenosine A<sub>1</sub> receptor-specific antagonists are, nevertheless, limited by their toxicity. Theophylline, for example, has been widely used in the treatment of asthma, but is associated with frequent, significant toxicity resulting from its narrow therapeutic dose range. DPCPX is far too toxic to be useful clinically. The fact that, despite decades of extensive research, no specific adenosine receptor antagonist is available for clinical use attests to the general toxicity of these agents.

Anti-sense oligonucleotides have received considerable theoretical consideration for their potential use as

pharmacological agents in human disease. Finding practical and effective applications of these agents in actual models of human disease, however, have been few and far between, particularly because they had to be administered in large doses. Another important consideration in the pharmacologic application of these molecules is their route of administration. Many in vivo applications have involved the direct administration of anti-sense oligonucleotides to limited regions of the brain. Such applications, however, have limited clinical utility due to their invasive nature.

The systemic administration of anti-sense oligonucleotides as pharmacological agents has been found to have also significant problems, not the least of which being a difficulty in targeting disease-involved tissues. That is, the necessary dilution of the anti-sense oligonucleotide in the circulatory system makes extremely difficult to attain a therapeutic dose at the target tissue by intravenous or oral administration. The bioavailability of orally administered anti-sense oligonucleotides is very low, of the order of less than about 5%.

There are presently no effective therapies for treating these ailments, or at least no therapies which are effective and devoid of significant detrimental side effects. Accordingly, there is still a need for an agent for the treatment of ailments afflicting the lung airways, including respiratory problems and inflammation, which is highly effective and producing minimal, or entirely devoid of, side effects.

### SUMMARY OF THE INVENTION

This invention relates to an agent which comprises an oligonucleotide (oligo) consisting essentially of less than about 15% adenosine (A), which is selected from the group consisting of anti-sense oligonucleotides to mRNAs corresponding to target genes, to genomic flanking regions selected from the group consisting of intron and exon borders, such as the 5' end, the 3' end and the juxta-section between coding and non-coding regions, and to all segments of mRNAs encoding polypeptides associated with ailments afflicting lung airways, combinations thereof, pharmaceutically acceptable salts thereof, and mixtures thereof. The mRNA(s), for example, encode polypeptide(s) such as transcription factors, stimulating and activating factors, interleukins, interleukin receptors, chemokines, chemokine receptors, endogenously produced specific and non-specific enzymes, immunoglobulins, antibody receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, adhesion molecules, defensins, growth factors, vasoactive peptides and receptors, and binding proteins; or those mRNA which correspond to an oncogene. The agents are provided in the form of specific compositions and formulations, with a carrier, and optionally with other therapeutic agents and additives which are typically used for administration by a specific route, e.g. into the respiratory system. The agent is also provided as a capsule or cartridge, and in the form of a kit.

This agent is suitable for the treatment of diseases and conditions associated with impaired respiration and inflammation, including lung diseases, ailments and conditions that have a negative effect on the lungs of a subject. Examples of diseases and conditions, which may be treated preventively, prophylactically and therapeutically with the agent of this invention, are pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas, and the like, e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, etc., as well as all types of cancers which may metastasize or have metastasized to the lung(s), including breast and prostate cancer. The present agent(s) is (are) also suitable for administration before, during and after other treatments, including radiation, chemotherapy, antibody therapy, phototherapy and cancer, and other types of surgery. Alternatively, the present agent may be effectively administered preventively, prophylactically or therapeutically, and in conjunction with other therapies, or by itself for conditions without known therapies or as a substitute for therapies that have significant negative side effects.

The composition of this invention may be administered by transdermal or systemic routes, including by, but not exclusively, oral, intracavitary, intranasal, intraanal, intravaginal, transdermal, intradermal, intrabuccal, intravenous, subcutaneous, intramuscular, intratumor, intraglandular, by inhalation, intraarterial, intravascular in general, into the ear, intracranial, intrathecal, intraorgan including via a shunt to, for example, the liver or other organs, by implantation and intraocular administration to a human or any other animal, including vertebrates, such as mammals. In a preferred embodiment, the present agents are administered directly into the respiratory

system of a subject, so that the agent has direct access to the lungs, in an amount effective to reduce or inhibit the effect in the lung of the targeted diseases or conditions.

Also part of this invention is a method of producing an anti-sense oligonucleotide consisting essentially of less than about 15% adenosine (A), by selecting a target including genes, genomic flanking regions, RNAs and polypeptide associated with an ailment afflicting the lung airways, obtaining the sequence of a mRNA(s) corresponding to the target gene(s) and/or their genomic flanking region(s) and/or the juxta-membrane regions thereof, and mRNA(s) encoding the target polypeptide(s), selecting at least one segment of the mRNA(s), and synthesizing one or more anti-sense oligonucleotide(s) to the selected mRNA segment(s), and substituting, if necessary, a universal base(s) for one or more A to reduce the proportion of A present in the oligonucleotide to less than 15%.

#### DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

This invention arose from a desire by the inventor to improve on his own prior discovery that anti-sense oligonucleotides (oligos) may be utilized therapeutically in the treatment of diseases or conditions which impair respiration, cause inflammation, constrict bronchial tissue or the lung airways, or otherwise impede normal breathing. The inventor reasoned that he could improve on his prior discovery that anti-sense oligos targeted to genes associated with such ailments could effectively treat and prevent the effects and symptomatology of such disease(s) or condition(s). The present invention is premised on the recent discovery by the inventor that oligonucleotides are metabolized in vivo to their deoxynucleotides. In the case of adenosine (A)-containing oligonucleotides, there is break down with release of deoxyadenosine which, in turn, activates adenosine receptors causing bronchoconstriction, inflammation and the like.

The present technology relies on the design of anti-sense oligos targeted to mRNAs associated with ailments involving lung airway pathology(ies), and on their modification to reduce the occurrence of undesirable side effects caused by their release of adenosine upon breakdown, while preserving their activity and efficacy for their intended purpose. In this manner, the inventor targets a specific gene to design one or more anti-sense oligonucleotide(s) (oligos) that selectively bind(s) to the corresponding mRNA, and then reduces, if necessary, their content of adenosine via substitution with universal base or an adenosine analog incapable of activating adenosine A<sub>1</sub>, A<sub>2a</sub>, or A<sub>3</sub> receptors. Based on his prior experience in the field, the inventor reasoned that in addition to Adownregulating@ specific genes, he could increase the effect of the agent(s) administered by either selecting segments of RNA that are devoid, or have a low content, of thymidine (T) or, alternatively, substitute one or more adenosine(s) present in the designed oligonucleotide(s) with other nucleotide bases, so called universal bases, which bind to thymidine but lack the ability to activate adenosine receptors and otherwise exercise the constricting effect of adenosine in the lungs, etc. Given that adenosine (A) is a nucleotide base complementary to thymidine (T), when a T appears in the RNA, the anti-sense oligo will have an A at the same position. For consistency's sake, all RNAs and oligonucleotides are represented in this patent by a single strand in the 5' to 3' direction, when read from left to right, although their complementary sequence(s) is (are) also encompassed within the four corners of the invention. In addition, all nucleotide bases and amino acids are represented utilizing the recommendations of the IUPAC-IUB Biochemical Nomenclature Commission, or by the known 3-letter code (for amino acids).

The method of the present invention may be used to treat ailments associated with reduced airway function in a subject, whatever its cause. The adenosine content of the anti-sense agent(s) of the invention have a reduced A content to prevent its liberation upon in vivo degradation of the agent(s). Examples of airway diseases that may be treated by the method of the present invention include cystic fibrosis, asthma, pulmonary hypertension and vasoconstriction, chronic obstructive pulmonary disease (COPD), chronic bronchitis, respiratory distress syndrome, lung cancer and lung metastatic cancers and other airway diseases, including those with inflammatory response.

Anti-sense oligos to the adenosine A<sub>1</sub>, A<sub>2a</sub>, A<sub>2b</sub>, and A<sub>3</sub> receptors, CCR3 (chemokine receptors), bradykinin 2B, CAM (vascular cell adhesion molecule), and eosinophil receptors, among others, have been shown to be effective in down-regulating the expression of their genes. Some of these act to alleviate the symptoms or reduce respiratory ailments and/or inflammation, for example, by Adown regulation@ of the adenosine A<sub>1</sub>, A<sub>2a</sub>, A<sub>2b</sub>, and/or A<sub>3</sub> receptors and CCR3, bradykinin 2B, VCAM (vascular cell adhesion molecule) and eosinophil receptors. These agents are preferably administered directly into the respiratory system, e.g., by

inhalation or other means, so that they may reach the lungs without widespread systemic dissemination. This permits the use of substantially lower doses of the agent of the invention as compared with those administered by the prior art, systemically or by other generalized routes and, consequently, reduce undesirable side effects resulting from the agent's widespread distribution in the body. The agent(s) of this invention has (have) been shown to reduce the amount of receptor protein expressed by the tissue. These agents, thus, rather than merely interacting with their targets, e.g. a receptor, lower the number of target proteins that other drugs may interact with. In this manner, the present agent(s) afford(s) extremely high efficacy with low toxicity.

The adenosine receptors discussed above are mere examples of the high power of the inventor's technology. In fact, a large number of genes may be targeted in a similar manner by the present agent(s), to reduce or down-regulate protein expression. By means of example, if the target disease or condition is ne associated with impeded or reduced breathing, bronchoconstriction, chronic bronchitis, pulmonary bronchoconstriction and/or hypertension, chronic obstructive pulmonary disease (COPD), allergy, asthma, cystic fibrosis, respiratory distress syndrome, cancers, which either directly or by metastasis afflict the lung, the present method may be applied to a list of potential target mRNAs, which includes the targets listed in Table 1 below, among others.

**Table 1: Pulmonary Disease or Condition (Asthma/Inflammation) Targets**

Nf6B Transcription Factor	Interleukin-8 Receptor (IL-8 R)
Interleukin-5 Receptor (IL-5R)	Interleukin-4 Receptor (IL-4R)
Interleukin-3 Receptor (IL-3R)	Interleukin-1beta (IL-1beta)
Interleukin-1 $\beta$ Receptor (IL-1beta R)	Eotaxin
Tryptase	Major Basic Protein
$\beta$ 2-adrenergic Receptor Kinase	Endothelin Receptor A
Endothelin Receptor B	Preproendothelin
Bradykinin B2 Receptor (B2BR)	IgE (High Affinity Receptor)
Interleukin-1 (IL-1)	Interleukin 1 Receptor (IL-1 R)
Interleukin-9 (IL-9)	Interleukin-9 Receptor (IL-9 R)
Interleukin-11 (IL-11)	Interleukin-11 Receptor (IL-11 R)
Inducible Nitric Oxide Synthase	Cyclooxygenase (COX)
Intracellular Adhesion Molecule 1 (ICAM-1)	Vascular Cellular Adhesion Molecule (VCAM)
Rantes	Endothelial Leukocyte Adhesion Molecule (ELAM-1)
Cyclooxygenase-2 (COX-2)	GM-CSF, Endothelin-1
Monocyte Activating Factor	Neutrophil Chemotactic Factor
Neutrophil Elastase	Defensin 1,2,3
Muscarinic Acetylcholine Receptors	Platelet Activating Factor
Tumor Necrosis Factor $\alpha$	5-lipoxygenase
Phosphodiesterase IV	Substance P
Substance P Receptor	Histamine Receptor
Chymase	CCR-1 CC Chemokine Receptor
Interleukin-2 (IL-2)	Interleukin-4 (IL-4)
Interleukin-12 (IL-12)	Interleukin-5 (IL-5)
Interleukin-6 (IL-6)	Interleukin-7 (IL-7)
Interleukin-8 (IL-8)	Interleukin-12 Receptor (IL-12R)
Interleukin-7 Receptor (IL-7R)	Interleukin-1 (IL-1)
Interleukin-14 Receptor (IL-14R)	Interleukin-14
CCR-2 CC Chemokine Receptor	CCR-3 CC Chemokine Receptor
CCR-4 CC Chemokine Receptor	CCR-5 CC Chemokine Receptor
Prostanoid Receptors	GATA-3 Transcription Factor
Neutrophil Adherence Receptor	MAP Kinase
Interleukin-15 (IL-15)	Interleukin-15 Receptor (IL-15R)
Interleukin-11 (IL-11)	Interleukin-11 Receptor (IL-11R)
NFAT Transcription Factors	STAT 4
MIP-1 $\alpha$	MCP-2
MCP-3	MCP-4
Cyclophilin (A, B, etc.)	Phospholipase A2
Basic Fibroblast Growth Factor	Metalloproteinase

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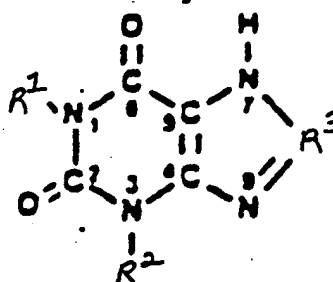
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CSBP/p38 MAP Kinase	Tryptase Receptor
PDG2	Interleukin-3 (IL-3)
Interleukin-10 (IL-10)	Cyclosporin A - Binding Protein
FK506-Binding Protein	$\alpha 4\beta 1$ Selectin
Fibronectin	$\alpha 4\beta 7$ Selectin
cMad CAM-1	LFA-1 (CD11a/CD18)
PECAM-1	LFA-1 Selectin
C3bi	PSGL-1
E-Selectin	P-Selectin
CD-34	L-Selectin
p150,95	Mac-1 (CD11b/CD18)
Fucosyl transferase	VLA-4
CD-18/CD11a	CD11b/CD18
ICAM2 and ICAM3	C5a
CCR3 (Eotaxin Receptor)	CCR1, CCR2, CCR4, CCR5
LTB-4	AP-1 Transcription Factor
Protein kinase C	Cysteinyl Leukotriene Receptor
Tachykinin Receptors (tach R)	I $\kappa$ B Kinase 1 & 2
Interleukin-2 Receptor (IL-2R)	(e.g., Substance P, NK-1 & NK-3 Receptors)
STAT 6	c-mas
NF-Interleukin-6 (NF-IL-6)	Interleukin-10 Receptor (IL-10R)
Interleukin-3 (IL-3)	Interleukin-2 Receptor (IL-2R)
Interleukin-13 (IL-13)	Interleukin-12 Receptor (IL-12R)
Interleukin-14 (IL-14)	Interleukin-6 Receptor (IL-6R)
Interleukin-16 (IL-16)	Interleukin-13 Receptor (IL-13R)
Medullasin	Interleukin-16 Receptor (IL-16R)
Adenosine A <sub>1</sub> Receptor (A <sub>1</sub> R)	Tryptase-I
Adenosine A <sub>2b</sub> Receptor (A <sub>2b</sub> R)	Adenosine A <sub>3</sub> Receptor (A <sub>3</sub> R)
$\beta$ Tryptase	
Adenosine A <sub>2a</sub> Receptor (A <sub>2a</sub> R)	IgE Receptor $\beta$ Subunit (IgE R $\beta$ )
Fc-epsilon receptor CD23 antigen	IgE Receptor $\alpha$ Subunit (IgE R $\alpha$ )
IgE Receptor Fc Epsilon Receptor (IgE R Fc $\epsilon$ R)	Substance P Receptor
Histidine decarboxylase	Tryptase-1
Prostaglandin D Synthase	Eosinophil Cationic Protein
Eosinophil Derived Neurotoxin	Eosinophil Peroxidase
Endothelial Nitric Oxide Synthase	Endothelial Monocyte Activating Factor
Neutrophil Oxidase Factor	Cathepsin G
Macrophage Inflammatory Protein-1-	Interleukin-8 Receptor $\alpha$ Subunit (IL-8 R $\alpha$ )
Alpha/Rantes Receptor	Substance P
Endothelin Receptor ET-B	Endothelin ETA Receptor

Examples of other targets are 5-lipoxygenase,  $\alpha$ -Rantes receptor, Cathepsin G, CCR-1 CC Chemokine receptor, CCR-1 CC Chemokine receptor, CCR-5 CC Chemokine receptor, CD-11-CD11a, c-Mas, Endothelial Nitric Oxide Synthase, Endothelial receptor ET-B, Endothelin 1, Eosinophil Cationic Protein, Eosinophil Derived Neurotoxin, Fc-epsilon receptor II (CD 23 Antigen), Histidine Decarboxylase, Interleukin 10 (IL-10), IL-10 receptor, IL-11 receptor, IL-12, IL-12 receptor, IL-13, IL-13 receptor, IL-14 and its receptor, IL-15 and its receptor, IL-16 and its receptor, IL-6 and its receptor, IL-7 and its receptor, Intracellular Adhesion Molecule -2 (ICAM-2), ICAM-3, Medullasin, Neurokinin-3 receptor (NK-3 R), Neutrophil Oxidase Factor, Platelet Activating Factor receptor, Prostaglandin D Synthase, Protein Kinase c, P-Selectin Glycoprotein Ligand 1 (PSGL-1), Tryptase Activated receptor, IL-2 and its receptor, IL-3 and its receptor, IL-4 and its receptor, IL-5 and its receptor, IL-8 and its receptor, IL-9 and its receptor, Intracellular adhesion Molecule-1, Leukocyte Adhesion Glycoprotein, Leukotriene C-4 Synthase, Major Basic Protein, MCP-3, Monocyte Activating Factor, Muscarinic Acetylcholine receptors, Neurokinin-1 Receptor, Neutrophil Chemotactic Factor, Neutrophil Elastase, NF $\kappa$ B, Phosphodiesterase IV, Prostaglandin Receptor, P-selectin, Rantes, Stat-1, Stat-2, Stat-3, Substance P and its receptor, Tryptase, Tumor Necrosis Factor A, Vascular Cellular Adhesion Molecule, AP-1 Transcription Factor, Basic Fibroblast Growth Factor, C5a, CCR-2 CC Chemokine Receptor, CSBP-p38 MAP Kinase,

Cyclooxygenase-2 (COX-2), Cyclophilin (A, B, C, and the rest), Cyclosporin A Binding Protein, Cysteinyl Leukotriene Receptor, E-Selectin, Fibronectin, Fusosyl Transferase, GATAS-3 Transcription Factor, Granulocyte-Macrophage Stimulating Factor (GM-CSF), Histamine Receptor, IKB Kinase 1 and 2, interleukin 7, L-Selectin, Mac-1 (CD11b and CD18), Mad CAM-1, Map Kinase, MCP-4, Metalloproteinase, MIP-1a, Neutrophil Adherence Receptors, NFAT Transcription Factors, NF-Interleukin-6 (NF-IL-6), Pecam-1, Phospholipase A2, Prostanoid Receptors, Stat-4, Stat-6, VLA-4, and others.

The oligos of this invention may be obtained by first selecting fragments of a target nucleic acid having at least 4 contiguous nucleic acids selected from the group consisting of G and C, and then obtaining a first oligonucleotide 4 to 60 nucleotides long which comprises the selected fragment and has a C and G nucleic acid content of up to and including about 15%. The latter step may be conducted by obtaining a second oligonucleotide 4 to 60 nucleotides long comprising a sequence which is anti-sense to the selected fragment, the second oligonucleotide having an adenosine base content of up to and including about 15%. This method may also comprise, when the selected fragment comprises at least one thymidine base, substituting an adenosine base in the corresponding nucleotide of the anti-sense fragment with a universal base selected from the group consisting of heteroaromatic bases which bind to a thymidine base but have antagonist activity and less than about 0.3 of the adenosine base agonist activity at the adenosine A<sub>1</sub>, A<sub>2b</sub> and A<sub>3</sub> receptors, and heteroaromatic bases which have no activity or have an agonist activity at the adenosine A<sub>2a</sub> receptor. The analogue heteroaromatic bases may be selected from all pyrimidines and purines, which may be substituted by O, halo, NH<sub>2</sub>, SH, SO, SO<sub>2</sub>, SO<sub>3</sub>, COOH and branched and fused primary and secondary amino, alkyl, alkenyl, alkynyl, cycloalkyl, heterocycloalkyl, aryl, heteroaryl, alkoxy, alkenoxy, acyl, cycloacyl, arylacyl, alkynoxy, cycloalkoxy, aroyl, arylthio, arylsulfoxyl, halocycloalkyl, alkylcycloalkyl, alkenylcycloalkyl, alkynylcycloalkyl, haloaryl, alkylaryl, alkenylaryl, alkynylaryl, arylalkyl, arylalkenyl, arylalkynyl, arylcycloalkyl, which may be further substituted by O, halo, NH<sub>2</sub>, primary, secondary and tertiary amine, SH, SO, SO<sub>2</sub>, SO<sub>3</sub>, cycloalkyl, heterocycloalkyl and heteroaryl. The pyrimidines and purines may be substituted at all positions as is known in the art, but preferred are those which are substituted at positions 1, 2, 3, 4, 7 and/or 8. More preferred are pyrimidines and purines such as theophylline, caffeine, dyphylline, etophylline, acephylline piperazine, bamifylline, enprofylline and xantine having the chemical formula



wherein R<sup>1</sup> and R<sup>2</sup> are independently H, alkyl, alkenyl or alkynyl and R<sup>3</sup> is H, aryl, dicycloalkyl, dicycloalkenyl, dicycloalkynyl, cycloalkyl, cycloalkenyl, cycloalkynyl, O-cycloalkyl, O-cycloalkenyl, O-cycloalkynyl, NH<sub>2</sub>, alkylamino-ketoxyalkyloxy-aryl, mono and dialkylaminoalkyl-N-alkylamino-SO<sub>2</sub> aryl, among others.

The inventor reduced the adenosine content of the anti-sense oligos corresponding to the thymidines (T) present in the target RNA to less than about 15%, or fully eliminated A from the oligonucleotide sequence as a means for preventing their breakdown products from freeing adenosine into the lung tissue environment and, thereby, aggravating the subject's ailment and/or countering the beneficial effect of the administered agent.

By means of example, the NF6B transcription factor may be selected as a target, and its mRNA or DNA searched for low thymidine (T) or desthymidine (desT) fragments. Only desT segments of the mRNA or DNA are selected which, in turn, will produce desA anti-sense as their complementary strand. When a number of RNA desT segments are found, the sequence of the anti-sense segments may be deduced. Typically, about 10 to 30 and even larger numbers of desA anti-sense sequences may be obtained. These anti-sense sequences may include some or all desA anti-sense oligonucleotide sequences corresponding to desT segments of the mRNA of the target, such as anyone of those shown in Table 1 above or Table 2 below. When this occurs, the anti-sense oligonucleotides found are said to be 100% A-free. For each of the original desA anti-sense oligonucleotide sequences corresponding to the target gene, e.g. the NF6B transcription factor, typically about 10 to 30 sequences

may be found within the target gene or RNA which have a low content of thymidine (RNA). In accordance with this invention, the selected fragment sequences may also contain a small number of thymidine (RNA) nucleotides within the secondary or tertiary or quaternary sequences. In some cases, a large adenosine content may suffice to render the anti-sense oligonucleotide less active or even inactive against the target. In accordance with this invention, these so called A non-fully desA sequences may preferably have a content of adenosine of less than about 15%, more preferably less than about 10%, and still more preferably less than 5%, and some even less than 2% adenosine. In some instances a higher content of adenosine is acceptable and the oligonucleotides are still active, particularly where the adenosine nucleotide may be Afixed@ or replaced with a AUniversal@ base that may base-pair with similar or equal affinity to two or more of the four nucleotide present in natural DNA: A, G, C, and T. A universal base is defined in this patent as any compound, more commonly an adenosine analogue, having the capacity to hybridize to thymidine, preferably having substantially reduced, or substantially lacking, ability to bind adenosine receptors. Alternatively, adenosine analogs which do not activate adenosine receptors, such as the adenosine A<sub>1</sub>, A<sub>2b</sub> and/or A<sub>3</sub> receptors, most preferably A<sub>1</sub> receptors, may be used. One example of a universal base is  $\alpha$ -deoxyribofuranosyl-(5-nitroindole), and an artisan will know how to select others. This Afixing@ step generates a further novel sequence, different from the one found in nature, that permits the anti-sense oligonucleotide to bind, preferably equally well, with the target RNA. An example of a universal base is 2-deoxyribosyl-(5-nitroindole). Other examples of universal bases are 3-nitropyrrole-2'-deoxynucleoside, 5-nitroindole, 2-deoxyribosyl-(5-nitroindole), 2-deoxyribofuranosyl-(5-nitroindole), 2'-deoxyinosine, 2'-deoxynebularine, 6H, 8H-3,4-dihydropyrimido [4,5-c] oxazine-7-one and 2-amino-6-methoxyaminopurine. In addition to the above, Universal bases which may be substituted for any other base although with somewhat reduced hybridization potential, include 3-nitropyrrole 2'-deoxynucleoside 2-deoxyribofuranosyl-(5-nitroindole), 2'-deoxyinosine and 2'-deoxynebularine (Glen Research, Sterling, VA). More specific mismatch repairs may be made using "P" nucleotide, 6H, 8H-3, 4-dihydropyrimido[4,5-c] [1,2] oxazin-7-one, which base pairs with either guanine (G) or adenine (A) and "K" nucleotide, 2-amino-6-methoxyaminopurine, which base pairs with either cytidine (C) or thymidine (T), among others. Others which are known in the art are also suitable. See, for example, Loakes, D. and Brown, D. M., Nucl. Acids Res. 22:4039-4043 (1994); Ohtsuka, E. et al., J. Biol. Chem. 260(5):2605-2608 (1985); Lin, P.K.T. and Brown, D. M., Nucleic Acids Res. 20(19):5149-5152 (1992); Nichols, R. et al., Nature 369(6480): 492-493 (1994); Rahmon, M. S. and Humayun, N. Z., Mutation Research 377 (2): 263-8 (1997); Amosova, O., et al., Nucleic Acids Res. 25 (10): 1930-1934 (1997); Loakes D. & Brown, D. M., Nucleic Acids Res. 22 (20): 4039-4043 (1994), the entire sections relating to universal bases and their preparation and use in nucleic acid binding is incorporated herein by reference.

When non-fully desT sequences are found in the naturally occurring target, they typically are selected so that about 1 to 3 universal base substitutions will suffice to obtain a 100% AdesA@ anti-sense oligonucleotide. Thus, the present method provides either anti-sense oligonucleotides to different targets which are low in, or devoid of, A content, as well as anti-sense oligonucleotides where one or more adenosine nucleotides, e. g. about 1 to 3, or more, may be Afixed@ by replacement with a AUniversal@ base. Universal bases are known in the art and need not be listed herein. An artisan will know which bases may act as universal bases, and replace them for A.

The present approach to the design of anti-sense oligonucleotide approach is also applicable to a variety of other diseases or conditions, including other inflammatory diseases, such as cystic fibrosis, chronic obstructive pulmonary disease, chronic bronchitis, pulmonary hypertension, cancers, including those which metastasize to the lung, such as breast cancer, colon cancer, respiratory distress syndrome, prostate cancer, pancreatic cancer, kidney cancer, lymphomas, melanomas, hepatocellular carcinomas, etc.

As used herein, the term "treat" or "treating" asthma or other respiratory and inflammatory conditions or diseases refers to a treatment which decreases the likelihood that the subject administered such treatment will manifest symptoms of a respiratory or inflammatory lung disease or other lung conditions. The term "down-regulate" refers to inducing a decrease in production, secretion or availability (and thus a decrease in concentration) of the targeted intracellular protein.

The present invention is concerned primarily with the treatment of vertebrates, and within this group, of mammals, including human and non-human simians, wild and domesticated animals, marine and land animals, household pets, and zoo animals, for example, felines, canines, equines, pachiderms, cetaceans, and still more preferably to human subjects. One particularly suitable application of this technology is for veterinary purposes,

and includes all types of small and large animals in the care of a veterinarian, including wild animals, marine animals, household animals, zoo animals, and the like. Targeted genes and proteins are preferably mammalian, and the sequences targeted are preferably of the same species as the subject being treated. Although in many instances, targets of a different species are also suitable, particularly those segments of the target RNA or gene that display greater than about 45% homology, preferably greater than about 85% homology, still more preferably greater than about 95% homology, with the recipient's sequence. A preferable group of agents is composed of des-A anti-sense oligos. Another preferred group is composed of non-fully desA oligonucleotides, where one or more adenosine bases are replaced with universal bases.

The terms "anti-sense" oligonucleotides generally refers to small, synthetic oligonucleotides, resembling single-stranded DNA, which in this patent are applied to the inhibition of gene expression by inhibition of a target messenger RNA (mRNA). See, Milligan, J. F. et al., *J. Med. Chem.* 36(14), 1923-1937 (1993), the relevant portion of which is hereby incorporated in its entirety by reference. The present agents inhibit gene expression of target genes, such as those of the adenosine A<sub>1</sub>, A<sub>2a</sub>, A<sub>2b</sub>, or A<sub>3</sub> receptors, CCR3 (chemical receptor 320, also known as the eotaxin receptor), VCAM (vascular cell adhesion molecule), eosinophil receptor, bradykinin 2B receptor, and many others listed in Table 1 above. This is generally attained by hybridization of the anti-sense oligonucleotides to coding (sense) sequences of a targeted messenger RNA (mRNA), as is known in the art. The exogenously administered agents of the invention decrease the levels of mRNA and protein encoded by the target gene and/or cause changes in the growth characteristics or shapes of the thus treated cells. See, Milligan et al. (1993); Helene, C. and Toulme, J. *Biochim. Biophys. Acta* 1049, 99-125 (1990); Cohen, J. S. D., Ed., *Oligodeoxynucleotides as Anti-sense Inhibitors of Gene Expression*; CRC Press: Boca Raton, FL (1987), the relevant portion of which is hereby incorporated in its entirety by reference. As used herein, "anti-sense oligonucleotide" is generally a short sequence of synthetic nucleotide that (1) hybridizes to any segment of a mRNA encoding a targeted protein under appropriate hybridization conditions, and which (2) upon hybridization causes a decrease in gene expression of the targeted protein.

The terms Ades-adenosine@ (desA) and Ades-thymidine@ (desT) refer to oligonucleotides substantially lacking either adenosine (desA) or thymidine (desT). In some instances, the des T sequences are naturally occurring, and in others they may result from substitution of an undesirable nucleotide (A) by another one lacking its undesirable activity. In the present context, the substitution is generally accomplished by substitution of A with a Auniversal base@, as is known in the art.

The mRNA sequence of the targeted protein may be derived from the nucleotide sequence of the gene expressing the protein. For example, the sequence of the genomic human adenosine A<sub>1</sub> receptor and that of the rat and human adenosine A<sub>3</sub> receptors are known. See, US Pat. No. 5,320,962; Zhou, F., et al., *Proc. Nat'l Acad. Sci. (USA)* 89 :7432 (1992); Jacobson, M.A., et al., U.K. Pat. Appl. No. 9304582.1. The sequence of the adenosine A<sub>2b</sub> receptor gene is also known. See, Salvatore, C. A., Luneau, C. J., Johnson, R. G. and Jacobson, M., *Genomics* (1995), the relevant portion of which is hereby incorporated in its entirety by reference. The sequences of many of the exemplary target genes are also known. See, GenBank, NIH. The sequences of those genes whose sequences are not yet available may be obtained by isolating the target segments applying technology known in the art. Once the sequence of the gene, its RNA and/or the protein are known, an anti-sense oligonucleotides may be produced according to this invention as described above to reduce the production of the targeted protein in accordance with standard techniques.

In one aspect of this invention, the anti-sense oligonucleotide has a sequence which specifically binds to a portion or segment of an mRNA molecule which encodes a protein associated with a disease or condition associated with impeded breathing, lung inflammation, airway obstruction, bronchitis, and the like. One effect of this binding is to reduce or even prevent the translation of the corresponding mRNA and, thereby, reduce the available amount of target protein in the subject's lung.

In one preferred embodiment of this invention, the phosphodiester residues of the anti-sense oligonucleotide are modified or substituted. Chemical analogs of oligonucleotides with modified or substituted phosphodiester residues, e.g., to the methylphosphonate, the phosphotriester, the phosphorothioate, the phosphorodithioate, or the phosphoramidate, which increase the in vivo stability of the oligonucleotide are particularly preferred. The naturally occurring phosphodiester linkages of oligonucleotides are susceptible to some degree of degradation by cellular nucleases. Many of the residues proposed herein, on the contrary, are highly resistant to nuclease degradation. See Milligan et al., and Cohen, J. S. D., *supra*. In another preferred



embodiment of the invention, the oligonucleotides may be protected from degradation by adding a "3'-end cap" by which nuclease-resistant linkages are substituted for phosphodiester linkages at the 3' end of the oligonucleotide. See, Tidd, D. M. and Wahrenius, H.M., *Be. J. Cancer* 60: 343-350 (1989); Shaw, J.P. et al., *Nucleic Acids Res.* 19: 747-750 (1991), the relevant section of which are incorporated in their entireties herein by reference. Phosphoramidates, phosphorothioates, and methylphosphonate linkages all function adequately in this manner for the purposes of this invention. The more extensive the modification of the phosphodiester backbone the more stable the resulting agent, and in many instances the higher their RNA affinity and cellular permeation. See Milligan, et al., *supra*. Thus, the number of residues which may be modified or substituted will vary depending on the need, target, and route of administration, and may be from 1 to all the residues, to any number in between. Many different methods for replacing the entire phosphodiester backbone with novel linkages are known. See, Millikan et al, *supra*. Preferred backbone analogue residues include phosphorothioate, methylphosphonate, phosphotriester, thioformacetal, phosphorodithioate, phosphoramidate, formacetal boranophosphate, 3'-thioformacetal, 5'-thioether, carbonate, 5'-N-carbamate, sulfate, sulfonate, sulfamate, sulfonamide, sulfone, sulfite., 2'-O methyl, sulfoxide, sulfide, hydroxylamine, methylene(methylimino) (MMI), and methyleneoxy(methylimino) (MOMI) residues. Phosphorothioate and methylphosphonate-modified oligonucleotides are particularly preferred due to their availability through automated oligonucleotide synthesis. See, Millikan et al, *supra*. Where appropriate, the agent of this invention may be administered in the form of their pharmaceutically acceptable salts, or as a mixture of the anti-sense oligonucleotide and its salt. In another embodiment of this invention, a mixture of different anti-sense oligonucleotides or their pharmaceutically acceptable salts is administered.

The agents of this invention have the capacity to attenuate the expression of one target mRNA and/or to enhance or attenuate the activity of one pathway. By means of example, the present method may be practiced by identifying all possible deoxyribonucleotide segments which are low in thymidine (T) or deoxynucleotide segments low in adenosine (A) of about 7 or more mononucleotides, preferably up to about 60 mononucleotides, more preferably about 10 to about 36 mononucleotides, and still more preferably about 12 to about 21 mononucleotides, in a target mRNA or a gene, respectively. This may be attained by searching for mononucleotide segments within a target sequence which are low in, or lack thymidine (RNA), a nucleotide which is complementary to adenosine, or that are low in adenosine (gene), that are 7 or more nucleotides long. In most cases, this search typically results in about 10 to 30 such sequences, i. e. naturally lacking or having less than about 40% adenosine, anti-sense oligonucleotides of varying lengths for a typical target mRNA of average length, i. e., about 1800 nucleotides long. Those with high content of T or A, respectively, may be fixed by substitution of a universal base for one or more As.

The agent(s) of this invention may be of any suitable length, including but not limited to, about 7 to about 60 nucleotides long, preferably about 12 to about 45, more preferably up to about 30 nucleotides long, and still more preferably up to about 21, although they may be of other lengths as well, depending on the particular target and the mode of delivery. The agent(s) of the invention may be directed to any and all segments of a target RNA. One preferred group of agent(s) includes those directed to an mRNA region containing a junction between an intron and an exon. Where the agent is directed to an intron/exon junction, it may either entirely overlie the junction or it may be sufficiently close to the junction to inhibit the splicing-out of the intervening exon during processing of precursor mRNA to mature mRNA, e.g. with the 3' or 5' terminus of the anti-sense oligonucleotide being positioned within about, for example, within about 2 to 10, preferably about 3 to 5, nucleotide of the intron/exon junction. Also preferred are anti-sense oligonucleotides which overlap the initiation codon, and those near the 5' and 3' termini of the coding region.

Table 2 below provides a selected number of targets to which the agents of the invention are effectively applied. Others, however, may also be targeted.

**Table 2: Cancer Targets**

Transforming Oncogenes	Therapy Targets
ras	thymidylate synthetase
src	thymidylate synthetase
myc	dihydrofolate reductase
bcl-2	thymidine kinase
	deoxycytidine kinase
	ribonucleotide reductase

A group of preferred targets for the treatment of cancer are genes associated with any of different types of cancers, or those generally known to be associated with malignancies, whether they are regulatory or involved in the production of RNA and/or proteins. Examples are transforming oncogenes, including, but not limited to, ras, src, myc, and bcl-2, among others. Other targets are those to which present cancer chemotherapeutic agents are directed to, such as various enzymes, primarily, although not exclusively, thymidylate synthetase, dihydrofolate reductase, thymidine kinase, deoxycytidine kinase, ribonucleotide reductase, and the like.

The present technology is particularly useful in the treatment of cancer ailments given that traditional cancer therapies are fraught with the unresolved problem of selectively killing cancer cells while preserving normal living cells from the devastating effects of treatments such as chemotherapy, radiotherapy, and the like. The present technology provides the ability of selectively attenuating or enhancing a desired pathway or target. This approach provides a significant advantage over standard treatments of cancer because it permits the selection of a pathway, including primary, secondary and possibly tertiary targets, which are not generally expressed simultaneously in normal cells. Thus, the present agent may be administered to a subject to cause a selective increase in toxicity within tumor cells that, for instance, express all three targets while normal cells that may express only one or two of the targets will be significantly less affected or even spared.

A group of preferred targets for the treatment of cancers are genes associated with different types of cancers, or those generally known to be associated with malignancies, whether they are regulatory or involved in the production of RNA and/or proteins. Examples are transforming oncogenes, including, but not limited to, ras, src, myc, and bcl-2, among others. Other targets are those to which present cancer chemotherapeutic agents are directed to, such as various enzymes, primarily, although not exclusively, thymidylate synthetase, dihydrofolate reductase, thymidine kinase, deoxycytidine kinase, ribonucleotide reductase, and the like.

In one embodiment, at least one of the mRNAs to which the MTA oligo of the invention is targeted encodes a protein such as transcription factors, stimulating and activating factors, intracellular and extracellular receptors and peptide transmitters in general, interleukins, interleukin receptors, chemokines, chemokine receptors, endogenously produced specific and non-specific enzymes, immunoglobulins, antibody receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, adhesion molecules, defensins, growth factors, vasoactive peptides and receptors, and binding proteins, among others; or the mRNA is corresponding to an oncogene and other genes associated with various diseases or conditions.

Examples of target proteins are eotaxin, major basic protein, preproendothelin, eosinophil cationic protein, P-selectin, STAT 4, MIP-1 $\alpha$ , MCP-2, MCP-3, MCP-4, STAT 6, c-mas, NF-IL-6, cyclophilins, PDG2, cyclosporin A-binding protein, FK5-binding protein, fibronectin, LFA-1 (CD11a/CD18), PECAM-1, C3bi, PSGL-1, CD-34, substance P, p150,95, Mac-1 (CD11b/CD18), VLA-4, CD-18/CD11a, CD11b/CD18, C5a, CCR1, CCR2, CCR4, CCR5, and LTB-4, among others. Others are, however, suitable, as well.

In another embodiment, at least one of the mRNAs to which the MTA oligo is targeted encodes intracellular and extracellular receptors and peptide transmitters such as sympathomimetic receptors, parasympathetic receptors, GABA receptors, adenosine receptors, bradykinin receptors, insulin receptors, glucagon receptors, prostaglandin receptors, thyroid receptors, androgen receptors, anabolic receptors, estrogen receptors, progesterone receptors, receptors associated with the coagulation cascade, adenohypophyseal receptors,

adenohypophyseal peptide transmitters, and histamine receptors (HisR), among others. However others are also contemplated.

The encoded sympathomimetic receptors and parasympathomimetic receptors include acetylcholinesterase receptors (AcChaseR) acetylcholine receptors (AcChR), atropine receptors, muscarinic receptors, epinephrine receptors (EpiR), dopamine receptors (DOPAR), and norepinephrine receptors (NEpiR), among others. Further examples of encoded receptors are adenosine A<sub>1</sub> receptor, adenosine A<sub>2B</sub> receptor, adenosine A<sub>3</sub> receptor, endothelin receptor A, endothelin receptor B, IgE high affinity receptor, muscarinic acetylcholine receptors, substance P receptor, histamine receptor, CCR-1 CC chemokine receptor, CCR-2 CC chemokine receptor, CCR-3 CC chemokine receptor (Eotaxin Receptor), interleukin-1 $\beta$  receptor (IL-1 $\beta$ R), interleukin-1 receptor (IL-1R), interleukin-1 $\beta$  receptor (IL-1 $\beta$ R), interleukin-3 receptor (IL-3R), CCR-4 CC chemokine receptor, cysteinyl leukotriene receptors, prostanoid receptors, GATA-3 transcription factor receptor, interleukin-1 receptor (IL-1R), interleukin-4 receptor (IL-4R), interleukin-5 receptor (IL-5R), interleukin-8 receptor (IL-8R), interleukin-9 receptor (IL-9R), interleukin-11 receptor (IL-11R), bradykinin B2 receptor, sympathomimetic receptors, parasympathomimetic receptors, GABA receptors, adenosine receptors, bradykinin receptors, insulin receptors, glucagon receptors, prostaglandin receptors, thyroid receptors, androgen receptors, anabolic receptors, estrogen receptors, progesterone receptors, receptors associated with the coagulation cascade, adenohypophyseal receptors, and histamine receptors (HisR). Others are also contemplated even though not listed herein.

The encoded enzymes for development of the MTA oligos of the invention include synthetases, kinases, oxidases, phosphatases, reductases, polysaccharide, triglyceride, and protein hydrolases, esterases, elastases, and polysaccharide, triglyceride, lipid, and protein synthases, among others. Examples of target enzymes are tryptase, inducible nitric oxide synthase, cyclooxygenase (Cox), MAP kinase, eosinophil peroxidase,  $\beta$ 2-adrenergic receptor kinase, leukotriene c-4 synthase, 5-lipoxygenase, phosphodiesterase IV, metalloproteinase, tryptase, CSBP/p38 MAP kinase, neutrophil elastase, phospholipase A2, cyclooxygenase 2 (Cox-2), fucosyl transferase, chymase, protein kinase C, thymidylate synthetase, dihydrofolate reductase, thymidine kinase, deoxycytidine kinase, and ribonucleotide reductase, among others. Any enzyme associated with a disease or condition, however, is suitable as a target for this invention.

Suitable encoded factors for application of this invention are, among others, NF $\kappa$ B transcription factor, granulocyte macrophage colony stimulating factor (GM-CSF), AP-1 transcription factor, GATA-3 transcription factor, monocyte activating factor, neutrophil chemotactic factor, granulocyte/macrophage colony-stimulating-factor (G-CSF), NFAT transcription factors, platelet activating factor, tumor necrosis factor  $\alpha$  (TNF  $\alpha$ ), and basic fibroblast growth factor (BFGF). Additional factors are also within the invention even though not specifically mentioned.

Suitable adhesion molecules for use with this invention include intracellular adhesion molecules 1 (ICAM-1), 2 (ICAM-2) and 3 (ICAM-3), vascular cellular adhesion molecule (VCAM), endothelial leukocyte adhesion molecule-1 (ELAM-1), neutrophil adherence receptor, mad CAM-1, and the like. Other known and unknown factors (at this time) may also be targeted herein.

Among the cytokines, lymphokines and chemokines preferred are interleukin-1 (IL-1), interleukin-1 $\beta$  (IL-1 $\beta$ ), interleukin-3 (IL-3), interleukin-4 (IL-4), interleukin-5 (IL-5), interleukin-8 (IL-8), interleukin-9 (IL-9), interleukin-11 (IL-11), CCR-5 CC chemokine, and Rantes. Others, however, may also be targeted, as they are known to be involved in specific diseases or conditions to be treated, or for their generic activities, such as inflammation.

Examples of defensins for the practice of this invention are defensin 1, defensin 2, and defensin 3, and of selectins are  $\alpha$ 4 $\beta$ 1 selectin,  $\alpha$ 4 $\beta$ 7 selectin, LFA-1 selectin, E-selectin, P-selectin, and L-selectin. Examples of oncogenes, although not an all inclusive list, are ras, src, myc, and bcl-2. Others, however, are also suitable for use with this invention.

In another preferred embodiment, the composition and formulations further comprise one or more surfactants. Suitable surfactants include, for example, polysorbates, polyoxyethylenes, and polyoxyethyleneglycols.

ubiquinones, lysophosphatidylethanolamine, lysophosphatidylcholine, palmitoyl-lysophosphatidylcholine, dehydroepiandrosterone, dolichols, sulfatidic acid, glycerol-3-phosphate, dihydroxyacetone phosphate, glycerol, glycerol-3-phosphocholine, dihydroxyacetone, palmitate, cytidine diphosphate (CDP) diacylglycerol, CDP choline, choline, choline phosphate; as well as natural and artificial lamellar bodies which are the natural carrier vehicles for the components of surfactant, omega-3 fatty acids, polyenic acid, polyenoic acid, lecithin, palmitic acid, non-ionic block copolymers of ethylene or propylene oxides, polyoxypropylene, monomeric and polymeric, polyoxyethylene, monomeric and polymeric, poly (vinyl amine) with dextran and/or alkanoyl side chains, Brij 35, Triton X-100 and synthetic surfactants ALEC, Exosurf, Survan and Atovaquone, among others. However, others may also be employed. These surfactants may be used either as single or part of a multiple component surfactant in a formulation, or as covalently bound additions to the 5' and/or 3' ends of the anti-sense oligonucleotides (oligos).

The agents administered in accordance with this invention are preferably designed to be anti-sense to target genes and/or mRNAs related in origin to the species to which it is to be administered. When treating humans, the agents are preferably designed to be anti-sense to a human gene or RNA. The agents of the invention encompass oligonucleotides which are anti-sense to naturally occurring DNA and/or RNA sequences, fragments thereof of up to a length of one (1) base less than the targeted sequence, preferably at least about 7 nucleotides long, oligos having only over about 0.02%, more preferably over about 0.1%, still more preferably over about 1%, and even more preferably over about 4% adenosine nucleotides, and up to about 30%, more preferably up to about 15%, still more preferably up to about 10% and even more preferably up to about 5%, adenosine nucleotide, or lacking adenosine altogether, and oligos in which one or more of the adenosine nucleotides have been replaced with so-called universal bases, which may pair up with thymidine nucleotides but fail to substantially trigger adenosine receptor activity. Examples of human sequences and fragments, which are not limiting, of anti-sense oligonucleotide of the invention are the following fragments as well as shorter segments of the fragments and of the full gene or mRNA coding sequences, exons and intron-exon junctions encompassing preferably 7, 10, 15, 18 to 21, 24, 27, 30, n-1 nucleotides for each sequence, where n is the sequence's total number of nucleotides. These fragments may be selected from any portion of the longer oligo, for example, from the middle, 5'-end, 3'-end or starting at any other site of the original sequence. Of particular importance are fragments of low adenosine nucleotide content, that is, those fragments containing less than or about 30%, preferably less than or about 15%, more preferably less than or about 10%, and even more preferably less than or about 5%, and most preferably those devoid of adenosine nucleotide, either by choice or by replacement with a universal base in accordance with this invention. The agent of the invention includes as a most preferred group sequences and their fragments where one or more adenines present in the sequence have been replaced by a universal base (B), as exemplified here. Similarly, also encompassed are all shorter fragments of the B-containing fragments designed by substitution of B(s) for adenosine(s) (A(s)) contained in the sequences, fragments thereof or segments thereof, as described above. A limited list of sequences and fragments is provided below.

Some of the examples of anti-sense oligonucleotide sequence fragments target the initiation codon of the respective gene, and in some cases adenosine is substituted with a universal base adenosine analogue denoted as "B", which lacks ability to bind to the adenosine A<sub>1</sub> and/or A<sub>3</sub> receptors. In fact, such replacement nucleotide acts as a "spacer". In fact, in all examples provided, whether it is an A or a B written in, either one of these may be substituted. In fact, what this means is that if an A is present A denotes adenosine or any universal base which may substitute for it, and if B is written in it also signifies adenosine or any universal base. Many of the examples shown below provide one such sequence and many fragments overlapping the initiation codon, preferably wherein the number of nucleotides n is about 7, about 10, about 12, about 15, about 18, about 21 and up to about 28, about 35, about 40, about 50, about 60. It may also be generally said that for the exemplary sequences B is adenosine or a universal base as well as an adenosine A<sub>2a</sub> receptor agonist, or adenosine A<sub>1</sub>, A<sub>2b</sub> or A<sub>3</sub> receptor antagonist.

#### **Human Receptor-related Antisense Polynucleotide**

5'-GGCGGCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCTGGG C TGCTTTTCT TTTCTGGGCC  
TCTGTGGTCT GTTTTTTCT GGCCTGCTG GGGCGCTCTC CGCCGCCCGC CTGGCTCCCG GBGCCBTGB TGGGCBTGCC  
GTGGTTCTTG CCTCCTTTG GCTGCCGTGC CCGCTCCCG GCCTCTGGC GGGTGGCCGT TGGGCCGTG TTCCCTGGG  
GCTGGGGCT CCTTCTCTC GCCCTTCTG CTGGGCTCT GCTGCTGCTG GTGCTGTGGC CCCCCTACA CCGAGGAGCC  
CATGATGGG ATGCCACAGA CGACAGGCGT BCBCCBGBB GCCBTGBTG GGCBTGCCB BGCBCBGBG C GGC GCC GTG  
CCG CGT CTT GGT GGC GGC GG GTT CGC GCC CGC GCG GGG CCC CTC CGG TCC GTT CGC GCC CGC GCG GGG CCC

CTC CGG TCC CGG GTC GGG GCC CCC CGC GGC C GCC TCG GGG CTG GGG CGC TGG TGG CCG GG CCG CGC CTC CGC  
CTG CCG CTT CTG GCT GGG CCC CGG GCG CCC CCT CCC CTC TTG CTC GGG TCC CCG TG ACA GCG CGT CCT GTG TCT  
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### Human Enzyme-related Antisense Polynucleotide

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### Human Factor Related Anti-sense Oligonucleotide

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#### Human Adenosine A<sub>1</sub> Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

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GACGGATGGA AGGAGAGAGG TTGAGGATGC ACTGGCTGT TCTGTAGGAG AGACTGGCCA GA GAT GGA GGG CGG CAT  
GGC GGG G CGG GTC GCC GG GGC GGG CBC BGG C GGC GGG CBC GC GGC CTG G GGB GGG CGG C GBT GGB GGG  
GG CTG GGC GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC ATGCCGCCCT  
CCATCTCAGC TTTCCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC CTGGTCTCTG TGCCGGGAA CGTGTGGT  
ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG CCGGATGCCA CTTCTGCTT CATGCTCTG CTGGCGGTGG CTGATGTGGC  
CGTGGGTGCC CTGGTCATCC CCTCGCCAT CCTCATCAAC ATTGGGCCAC AGACCTACTT CCACACTGC CTCATGGTTG  
CCTGTCGGT CCTCATCTC ACCCAGAGCT CCATCTAGC CTGCTGGCA ATTGCTGTG ACCGTACCT CCGGGTCAAG  
ATCCCTCTCC GGTACAAGAT GGTGGTGACC CCCCGGAGG CGGCGGTGGC CATAGCCGGC TGCTGGATCC TCTCTCTGT  
GGTGGGACTG ACCCTATGT TTGGCTGGAA CAATCTGAGT GCGGTGGAGC GGGCCTGGG AGCCAACGGC AGCATGGGG  
AGCCCGTAT CAAGTGGGAG TTCGAGAAGG TCATCAGCAT GGAGTACATG GTCTACTTCA ACTTCTTTGT GTGGGTGCTG  
CCCCGCTTCT TCTCATGGT CCTCATCTAC CTGGAGGTCT TCTACCTAAT CCGCAAGCAG CTCAACAAGA AGGTGTGGC  
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CACCTTCTT AAGATTTGGA ATGACCATT CCGCTGCCAG CTGCACCTC CCATTGACGA GGATCTCCCA GAAGAGAGGC  
CTGATGACTA G ATGAGTGTCA GAAGTGTGAA GGTGCTGT TCTGAATCCC AGAGCCTCT CTCCCTCTGT GAGGCTGGCA  
GGTGAGGAAG GTTTAACT CACTGGAAGG AATCCCTGGA GCTAGCGGT GCTGAAGGCG TCGAGGTGTG GGGCACTTG  
GACAGAACAG TCAGGCAGCC GGGAGCTCTG CCAGCTTTGG TGACCTTGG CCGGGCTGGG AGCGTGGG CCGGAGCCGG  
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 TCCCATGAGC AGTCCAGCGC TTCAGGGCTG GGCAGGTCTT GGGGAGCTG AGACTGCAGA GGAGCCACC GGGCTGGGAG  
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 GCCAGAGGCA GCTAAGGGGC AGGAATCAAG GAGCCTCCGT TCCCACCTCT GAGGACTCTG GACCCAGGC CATACAGGT  
 GCTAGGGTGC CTGCTCTCT TGCCTGGGC CAGCCAGGA TTGTACGTGG GAGAGGCAGA AAGGGTAGGT TCAGTAATCA  
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 AGGAGAGAGG TTGAGGATGC ACTGGCCTGT TCTGAGGAG AGACTGGCA GA -3'(FRAG.NO: )(SEQ.NO:2423)  
 5'-CGCATTTGTG TTTAATAAA AGAATCTGGA AGATAAATG TCTGAAGAG AGACAAAGGA AGGAAAATT  
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 CATCTACCTG GAGGTCTTCT ACCTAATCCG CAAGCAGCTC AACAAGAAGG TGTGGGCTC CTCGGCGAC CCGCAGAAGT  
 ACTATGGGAA GGAGCTGAAG ATCGCCAAGT CGCTGGCCCT CATCTCTTC CTCTTGCCC TCAGCTGGCT GCCTTGCAC  
 ATCTCAACT GCATCACCT CTTCTGCCG TCTGCCACA AGCCAGCAT CTTACCTAC ATTGCCATCT TCTCACGCA  
 CGGCAACTCG GGCATGAACC CCATTGTCTA TGCTTCCG ATCCAGAAGT TCCGCTAC CTTCTTAAG ATTGGAATG  
 ACCATTTCCG TCGCCAGCT GCACCTCCA TTGACGAGGA TCTCCAGAA GAGAGGCTG ATGACTAGAC CCGCCTTCC

GCTCCACCG CCCACCA CA GTGGGGTCTC AGTCCAGTCC TCACATGCCC GCTCCAG GGGTCTCCCT GAGCCTGCCC  
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TACCCTACAC CTCTGGGCCC TGCAGGAGGC CTGGGAGGGC AAGGGTCTA CGGAGGGACC AGGTGTCTAG AGGCAACAGT  
GTTCTGAGCC CCCACCTGCC TGACCATCCC ATGAGCAGTC CAGAGCTTCA GGGCTGGGCA GGTCTGGGG AGGCTGAGAC  
TGCAGAGGAG CCACCTGGGC TGGGAGAAGG TGCTTGGGCT TCTGCGGTGA GGCAGGGGAG TCTGCTTGTG TTAGATGTTG  
GTGGTGCAGC CCCAGGACCA AGCTTAAGGA GAGGAGAGCA TCTGCTCTGA GACGGATGGA AGGAGAGAGG TTGAGGATGC  
ACTGGCCTGT TCTGTAGGAG AGACTGGCCA GA -3' (FRAG. NO: ) (SEQ. ID NO: 2434)

5'- ATGAGTGTC GAAGTGTGAA GGGTGCTGT TCTGAATCCC AGAGCCTCCT CTCCCTCTGT GAGGCTGGCA  
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GACAGAACAG TCAGGCAGCC GGGAGCTCTG CCAGCTTTGG TGACCTTGGG CCGGGCTGGG AGCGCTGCGG CGGGAGCCGG  
AGGACTATGA GCTGCCGCGC GTTGTCCAGA GCGGAGCCCA GGCCTACGCG CGCGGCCCGG AGCTCTGTTT CCTGGAACCT  
TGGGCACTGC CTCTGGGACC CCGGCCGGCC AGCAGGCAGG ATGGTGCTTG CCTCGTGCCC CTGTGTGCC GTCTGTGAT  
GTGCCAGCC TGTCCCCGCC ATGCCGCCCT CCATCTCAGC TTCCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC  
CTGCTCTCTG TGCCCGGGA CGTGCTGGTG ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG CGGGATGCCA CCTTCTGCTT  
CATCGTGTG CTGGCGGTGG CTGATGTGGC CGTGGGTGCC CTGGTCATCC CCTCGCCAT CCTCATCAAC ATTGGGCCAC  
AGACCTACTT CCACACCTGC CTCATGGTTG CCTGTCCGGT CCTCATCTC ACCCAGAGCT CCATCCTGGC CTGCTGGCA  
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CATAGCCGGC TGCTGGATCC TCTCTTCGT GGTGGGACTG ACCCCTATGT TTGGCTGGAA CAATCTGAGT GCGGTGGAGC  
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GTCTACTTCA ACTTCTTTGT GTGGGTGCTG CCCCCGCTC TCCTCATGGT CCTCATCTAC CTGGAGGTCT TCTACCTAAT  
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AGTCGCTGGC CCTCATCTC TTCTCTTTG CCTCAGCTG GTCGCTTTG CACATCCTCA ACTGCATCAC CCTCTCTGC  
CCGTCTGCC ACAAGCCCAG CATCCTTACC TACATTGCCA TCTCCTCAC GCACGGCAAC TCGGCCATGA ACCCATTTGT  
CTATGCCTTC CGCATCCAGA AGTTCGCGT CACCTTCTT AAGATTGGA ATGACCATTT CCGCTGCCAG CCTGCACCTC  
CCATTGACGA GGATCTCCA GAAGAGAGGC CTGATGACTA GACCCCGCT TCCGCTCCA CCAGCCACA TCCAGTGGGG  
TCTCAGTCCA GTCCTACAT GCGCGCTGC CCAGGGGTCT CCTGAGCCT GCGCCAGCTG GGCTGTTGGC TGGGGGCATG  
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TGGGGGAAG CCTGCTGTC ATGTGAATCC CTCAATACC CTAGTATCTG GCTGGGTTT CAGGGGCTT GGAAGCTCTG  
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GGGAGGGCGA GCGGGGGAT CCTGGAGCCC CTGTGTCGGG GGGCGAGGGA GGGGAGGTGG CCGTCCGTTG ACCTTCTGAA  
CATGAGTGT AACTCCAGGA CTGCTTCCA AGCCCTTCCC TCTGTTGGA ATTGGGTGTG CCCTGGCTCC CAAGGAGGC  
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5'- ATGCCGCCCT CCATCTCAGC TTCCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC CTGGTCTCTG TGCCCGGGA  
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CTGATGTGGC CGTGGGTGCC CTGGTCATCC CCTCGCCAT CCTCATCAAC ATTGGGCCAC AGACCTACTT CCACACCTGC  
CTCATGGTTG CCTGTCCGGT CCTCATCTC ACCAGAGGT CCATCTGGC CTGCTGGCA ATTGCTGTGG ACCGCTACCT  
CCGGGTCAAG ATCCCTCTCC GGTACAAGAT GGTGTGACC CCGCGAGGG CGGCGGTGGC CATAGCCGGC TGCTGGATCC  
TCTCCTTCGT GGTGGGACTG ACCCTATGT TTGGCTGGAA CAATCTGAGT GCGGTGGAGC GGGCTGGGC AGCCAACGGC  
AGCATGGGGG AGCCCGTGAT CAAGTGCAG TTCGAGAAGG TCATCAGCAT GGAGTACATG GTCTACTTCA ACTTCTTTGT  
GTGGGTGCTG CCCCCGCTT TCCTCATGGT CCTCATCTAC CTGGAGGTCT TCTACCTAAT CCGCAAGCAG CTCAACAAGA  
AGGTGTCCGC CCTCTCCGC GACCCGAGA AGTACTATGG GAAGGAGCTG AAGATCGCCA AGTCGCTGGC CCTCATCTC  
TTCTCTTTG CCTCAGCTG GTCGCTTTG CACATCCTCA ACTGCATCAC CCTTCTCTGC CCGTCTGCC ACAAGCCCAG  
CATCCTTACC TACATTGCCA TCTCCTCAC GCACGGCAAC TCGGCCATGA ACCCATTTGT CTATGCCTTC CGCATCCAGA  
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GAAGAGAGGC CTGATGACTA G -3' (FRAG. NO: ) (SEQ. ID NO: 2432)

5'-CGCATTTGTG TTTAATAAA AGAATCTGGA AGATAAATAG TCTGAAGAG AGACAAAGGA AGGAAATTT  
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TTTGTGTTTT TGTTTTTTTT TGAGATGGAG TCTCGCTGTG TTACCGGGAG CGACAGAGCC GCACGGCCGA GTCGAGTCCC  
AGCCAGCTAC CATCCCTCTG GAGCTTACCG GCGGCCCTTG GTTCCCCAG GAATCCCTGG AGCTAGCGGC TGCTGAAGGC  
GTCGAGGTGT GGGGGCACTT GGACAGAACA GTCAGGCAGC CGGGAGCTCT GCCAGCTTTG GTGACCTTGG GTGCTTGCTT  
CGTGCCCTT GGTGCCCGTC TGCTGATGTG CCCAGCCTGT GCGGCCATG CCGCCCTCA TCTAGCTTT CCAGGCCGCC  
TACATCGGCA TCGAGGTGCT CATCGCCTG GTCTGTGTC CCGGGAACGT GCTGGTGATC TGGGCGGTGA AGGTGAACCA



GAGAAGGTCA TCAGCATGGA GTACATGGTC TACTTCAACT TCTTTGTGTG GGTGCTGCCC CCGCTTCTCC TCATGGTCTC  
CATCTACCTG GAGGTCTTCT ACCTAATCCG CAAGCAGCTC AACAAGAAGG TGTCGGCCTC CTCGGGCGAC CCGCAGAAGT  
ACTATGGGAA GGAGCTGAAG ATCGCCAAGT CGCTGGCCCT CATCTCTTC CTCTTTGCCC TCAGCTGGCT GCCTTTGCAC  
ATCCTCAACT GCATCACCCT CTCTGCCCCG TCCTGCCACA AGCCAGCAT CTTACCTAC ATTGCCATCT TCCTCACGCA  
CGGCAACTCG GCCATGAACC CCATTGTCTA TGCTTCCCG ATCCAGAAGT TCCGCGTCAC CTTCCTTAAG ATTTGGAATG  
ACCATTTCCG TCGCCAGCCT GCACCTCCCA TTGACGAGGA TCTCCAGAA GAGAGGCCTG ATGACTAGAC CCGCCTTCC  
GCTCCACCG CCCACATCCA GTGGGGTCTC AGTCCAGTCC TCACATGCCC GCTGTCCCAG GGGTCTCCCT GAGCCTGCCC  
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TACCCTACAC CTCTGGGCCC TGCAGGAGGC CTGGGAGGGC AAGGTCCTA CGGAGGGACC AGGTGTCTAG AGGCAACAGT  
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TGCAGAGGAG CCACCTGGGC TGGGAGAAGG TGCTTGGGCT TCTGCGGTGA GGCAGGGGAG TCTGCTGTG TTAGATGTTG  
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ACTGGCTGT TCTGTAGGAG AGACTGGCCA GA -3' (FRAG. NO: ) (SEQ. ID NO: 2422)

5'-ATGAGTGTCA GAAGTGTGAA GGGTGCCTGT TCTGAATCCC AGAGCCTCT CTCCCTCTGT GAGGCTGGCA  
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GACAGAACAG TCAGGCAGCC GGGAGCTCTG CCAGCTTTGG TGACCTTGG CCGGGCTGGG AGCCTGCGG CCGGAGCCGG  
AGGACTATGA GGTGCCGCGC GTTGTCAGA GCCAGCCCA GCCCTACGCG CGCGGCCCGG AGCTCTGTC CCTGGAACCT  
TGGGCACTGC CTCTGGGACC CTGCCCCGCC AGCAGGCAGG ATGGTGTCTG CCTCGTCCC CTGGTGCCC GTCTGTGAT  
GTGCCAGCC TGTGCCGCC ATGCCGCCCT CCATCTCAG TTCCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC  
CTGGTCTCTG TGCCCGGGA CGTGCTGGTG ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG CCGGATGCCA CTTCTGCTT  
CATCGTGTG CTGGCGGTGG CTGATGTGGC CGTGGGTGCC CTGGTCATCC CCTCGCCAT CCTCATCAAC ATTTGGCCAC  
AGACCTACTT CCACACCTGC CTCATGTTG CCTGTCCGT CTCATCCTC ACCCAGAGCT CCATCTGGC CTGCTGGCA  
ATTGCTGTG ACCGCTACCT CCGGTCAAG ATCCCTCTCC GGTACAAGAT GGTGGTGACC CCGGAGGG CCGCGGTGGC  
CATAGCCGGC TGCTGGATCC TCTCTTCGT GGTGGGACTG ACCCTATGT TTGGCTGGAA CAATCTGAGT GCGGTGGAGC  
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AGTCGTGGC CCTCATCTC TTCCTTTG CCTCAGCTG GTCGCTTTG CACATCTCA ACTGCATCAC CCTCTTCTGC  
CCGTCTGCC ACAAGCCCAG CATCCTTACC TACATTGCCA TCTCTCAC GCACGGCAAC TCGGCATGA ACCCATTTGT  
CTATGCTTC CGCATCCAGA AGTCCCGCT CACCTTCCT AAGATTGGA ATGACCATT CCGTGCCAG CCTGCACCTC  
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AGGAGAGGAG AGCATCTGCT CTGAGACGGA TGAAGGAGA GAGGTTGAGG ATGCACTGGC CTGTTCTGTA GGAGAGACTG  
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CCACAGCTC CACTGGCCCC CGTTGCCGG CCTGAGCTG CTAGGTGAC CCCATCTCTG CTGCTTCTG GCCTGATGGA  
GAGGAGACA CTAGACATGC CAACTCGGGA GCATTCTGCC TGCTGGGAA CCGGGTGGAC GAGGGAGTGT CTGTAAGGAC  
TCAGTGTGA CTGAGGCGC CCTGGGGTG GGTTAGCAG GCTGCAGCAG GCAGAGGAG AGTACCCCC TGAGAGCATG  
TGGGGGAAG CCTGTCTGT ATGTGAATCC CTCAATACC CTAGTATCTG GCTGGGTTT CAGGGGCTT GGAAGCTCTG  
TTGAGGTGT CCGGGGTCT AGGACTTAG GATCTGGGA TGTGGGAA GACCAACCA TGCCTGCCA AGCCTGGAGC  
CCCTGTGTT GGGGGCAAG TGGGGAGCC TGGAGCCCT GTGTGGAGG GCGAGGCGG GGAGCTGGA GCCCTGTGT  
GGGAGGGCA GCGGGGGAT CCTGGAGCCC CTGTGTCGG GGGGAGGGA GGGGAGGTG CCGTGGTTG ACCTTCTGAA  
CATGAGTGT AACTCCAGGA CTGCTTCCA AGCCCTCCC TGTGTGGA ATTGGGTGT CCCTGGCTCC CAAGGAGGC  
CCATGTGACT AATAAAAAAC TGTGAACCCT -3' (FRAG. NO: ) (SEQ. ID NO: 2421)

5'-ATGCCGCCCT CCATCTCAGC TTCCAGGCC GCCTACATCG GCATCGAGGT GTCATCGCC CTGGTCTCTG TGCCCGGAA  
CGTGCTGGT ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG CCGGATGCCA CTTCTGCTT CATGCTCTG CTGGCGGTGG  
CTGATGTGGC CTGGGTGCC CTGGTCATCC CCTCGCCAT CCTCATCAAC ATTGGGCCAC AGACCTACTT CCACACCTGC  
CTCATGTTG CTGTCCGT CCTCATCTC ACCCAGAGCT CCATCTGGC CTGCTGGCA ATTGCTGTG ACCGCTACCT  
CCGGTCAAG ATCCCTCTCC GGTACAAGAT GGTGGTGACC CCGGAGGG CCGCGGTGGC CATAGCCGGC TGCTGGATCC  
TCTCTTCGT GGTGGGACTG CCCCTATGT TTGGCTGGA CAATCTGAGT GCGGTGGAGC GGGCTGGG AGCCAACGGC  
AGCATGGGG AGCCGTGAT CAAGTGCAG TTCGAGAAGG TCATCAGCAT GGAGTACATG GTCTACTTCA ACTTCTTGT  
GTGGGTGCTG CCCCCGCTC TCCTCATGGT CCTCATCTAC CTGGAGGTCT TACTACCTAAT CCGCAAGCAG CTCAACAAGA  
AGGTGTCCG CTCTCCGGC GACCCGAGA AGTACTAGG GAAGGAGCTG AAGATCGCCA AGTCTGTGC CCTCATCTC  
TTCCTTTG CCCTCAGCTG GCTGCTTTG CACATCTCA ACTGCATCAC CCTCTTCTG CCGTCTGCC ACAAGCCAG  
CATCCTTACC TACATTGCCA TCTCTCAC GCACGGCAAC TCGGCATGA ACCCATTTGT CTATGCTTC CGCATCCAGA  
AGTCCCGCT CACCTTCCTT AAGATTGGA ATGACCATT CCGTGCCAG CTGCACCTC CCATTGACGA GGATCTCCA  
GAAGAGAGGC CTGATGACTA G (FRAG. NO: ) (SEQ. ID NO: 2420)

5'-GAT GGA GGG CGG CAT GGC GGG-3' (FRAG. NO: 1657) (SEQ ID NO: 1670)

5'-G CGG GTC GCC GG-3' (FRAG. NO: 1658) (SEQ ID NO: 1671)

5'-GGC GGG CBC BGG C-3' (FRAG. NO: 1659) (SEQ ID NO: 1672)

5'-GGC GGG CBC-3' (FRAG. NO: 1660) (SEQ ID NO: 1673)

5'-GC GGC CTG G-3' (FRAG. NO: 1661) (SEQ ID NO: 1674)

5'-GGB GGG CGG C-3' (FRAG. NO: 1662) (SEQ ID NO: 1675)



5'-GBT GGB GGG-3' (SEQ. NO: 1663) (SEQ. ID NO: 1676)  
5'-GG CTG GGC-3' (FRAG. NO: 1664) (SEQ. ID NO: 1677)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 1) (SEQ. ID NO: 11)  
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 2) (SEQ. ID NO: 12)  
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 3) (SEQ. ID NO: 13)  
5'-GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 4) (SEQ. ID NO: 14)  
5'-C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 5) (SEQ. ID NO: 15)  
5'-CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 6) (SEQ. ID NO: 16)  
5'-TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 7) (SEQ. ID NO: 17)  
5'-G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 8) (SEQ. ID NO: 18)  
5'-GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 9) (SEQ. ID NO: 19)  
5'-AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 10) (SEQ. ID NO: 20)  
5'-A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 11) (SEQ. ID NO: 21)  
5'-AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 12) (SEQ. ID NO: 22)  
5'-GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 13) (SEQ. ID NO: 23)  
5'-C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 14) (SEQ. ID NO: 24)  
5'-TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 15) (SEQ. ID NO: 25)  
5'-GA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 16) (SEQ. ID NO: 26)  
5'-A GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 17) (SEQ. ID NO: 27)  
5'-GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 18) (SEQ. ID NO: 28)  
5'-AT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 19) (SEQ. ID NO: 29)  
5'-T GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 20) (SEQ. ID NO: 30)  
5'-GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 21) (SEQ. ID NO: 31)  
5'-GA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 22) (SEQ. ID NO: 32)  
5'-A GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 23) (SEQ. ID NO: 33)  
5'-GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 24) (SEQ. ID NO: 34)  
5'-GG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 25) (SEQ. ID NO: 35)  
5'-G CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 26) (SEQ. ID NO: 36)  
5'-CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 27) (SEQ. ID NO: 37)  
5'-GG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 28) (SEQ. ID NO: 38)  
5'-G CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 29) (SEQ. ID NO: 39)  
5'-CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 30) (SEQ. ID NO: 40)  
5'-AT GGC GGG CAC AGG CTG GGC-3' (FRAG. 31) (SEQ. ID NO: 41)  
5'-T GGC GGG CAC AGG CTG GGC-3' (FRAG. 32) (SEQ. ID NO: 42)  
5'-GGC GGG CAC AGG CTG GGC-3' (FRAG. 33) (SEQ. ID NO: 43)  
5'-GC GGG CAC AGG CTG GGC-3' (FRAG. 34) (SEQ. ID NO: 44)  
5'-C GGG CAC AGG CTG GGC-3' (FRAG. 35) (SEQ. ID NO: 45)  
5'-GGG CAC AGG CTG GGC-3' (FRAG. 36) (SEQ. ID NO: 46)  
5'-GG CAC AGG CTG GGC-3' (FRAG. 37) (SEQ. ID NO: 47)  
5'-G CAC AGG CTG GGC-3' (FRAG. 38) (SEQ. ID NO: 48)  
5'-CAC AGG CTG GGC-3' (FRAG. 39) (SEQ. ID NO: 49)  
5'-AC AGG CTG GGC-3' (FRAG. 40) (SEQ. ID NO: 50)  
5'-C AGG CTG GGC-3' (FRAG. 41) (SEQ. ID NO: 51)  
5'-AGG CTG GGC-3' (FRAG. 42) (SEQ. ID NO: 52)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 43) (SEQ. ID NO: 53)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG. 44) (SEQ. ID NO: 54)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG. 45) (SEQ. ID NO: 55)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG. 46) (SEQ. ID NO: 56)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG CAC AGG CT-3' (FRAG. 47) (SEQ. ID NO: 57)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG. 48) (SEQ. ID NO: 58)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG. 49) (SEQ. ID NO: 59)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG. 50) (SEQ. ID NO: 60)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG CAC A-3' (FRAG. 51) (SEQ. ID NO: 61)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG. 52) (SEQ. ID NO: 62)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG CA-3' (FRAG. 53) (SEQ. ID NO: 63)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG C-3' (FRAG. 54) (SEQ. ID NO: 64)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG -3' (FRAG. 55) (SEQ. ID NO: 65)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GG-3' (FRAG. 56) (SEQ. ID NO: 66)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC G-3' (FRAG. 57) (SEQ. ID NO: 67)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC -3' (FRAG. 58) (SEQ. ID NO: 68)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TG -3' (FRAG. 59) (SEQ. ID NO: 69)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG. 60) (SEQ. ID NO: 70)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG. 61) (SEQ. ID NO: 71)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG. 62) (SEQ. ID NO: 72)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG. 63) (SEQ. ID NO: 73)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG. 64) (SEQ. ID NO: 74)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG. 65) (SEQ. ID NO: 75)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG. 66) (SEQ. ID NO: 76)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG. 67) (SEQ. ID NO: 77)

5'-GGC GGC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 68) (SEQ. ID NO: 78)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA G -3' (FRAG 69) (SEQ. ID NO: 79)  
5'-GGC GGC CTG GAA AGC TGA GAT GGA -3' (FRAG 70) (SEQ. ID NO: 80)  
5'-GGC GGC CTG GAA AGC TGA GAT GG -3' (FRAG 71) (SEQ. ID NO: 81)  
5'-GGC GGC CTG GAA AGC TGA GAT G -3' (FRAG 72) (SEQ. ID NO: 82)  
5'-GGC GGC CTG GAA AGC TGA GAT -3' (FRAG 73) (SEQ. ID NO: 83)  
5'-GGC GGC CTG GAA AGC TGA GA-3' (FRAG 74) (SEQ. ID NO: 84)  
5'-GGC GGC CTG GAA AGC TGA G-3' (FRAG 75) (SEQ. ID NO: 85)  
5'-GGC GGC CTG GAA AGC TGA-3' (FRAG 76) (SEQ. ID NO: 86)  
5'-GGC GGC CTG GAA AGC TG-3' (FRAG 77) (SEQ. ID NO: 87)  
5'-GGC GGC CTG GAA AGC T-3' (FRAG 78) (SEQ. ID NO: 88)  
5'-GGC GGC CTG GAA AGC-3' (FRAG 79) (SEQ. ID NO: 89)  
5'-GGC GGC CTG GAA AG-3' (FRAG 80) (SEQ. ID NO: 90)  
5'-GGC GGC CTG GAA A-3' (FRAG 81) (SEQ. ID NO: 91)  
5'-GGC GGC CTG GAA-3' (FRAG 82) (SEQ. ID NO: 92)  
5'-GGC GGC CTG GA-3' (FRAG 83) (SEQ. ID NO: 93)  
5'-GGC GGC CTG G-3' (FRAG 84) (SEQ. ID NO: 94)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC CAC AGG CTG GGC-3' (FRAG 85) (SEQ. ID NO: 95)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC CAC AGG CTG GG-3' (FRAG 86) (SEQ. ID NO: 96)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC CAC AGG CTG G-3' (FRAG 87) (SEQ. ID NO: 97)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC CAC AGG CTG -3' (FRAG 88) (SEQ. ID NO: 98)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC CAC AGG CT-3' (FRAG 89) (SEQ. ID NO: 99)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC CAC AGG C-3' (FRAG 90) (SEQ. ID NO: 100)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC CAC AGG -3' (FRAG 91) (SEQ. ID NO: 101)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC CAC AG-3' (FRAG 92) (SEQ. ID NO: 102)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC CAC A-3' (FRAG 93) (SEQ. ID NO: 103)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC CAC-3' (FRAG 94) (SEQ. ID NO: 104)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC CA-3' (FRAG 95) (SEQ. ID NO: 105)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC C-3' (FRAG 96) (SEQ. ID NO: 106)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC -3' (FRAG 97) (SEQ. ID NO: 107)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 98) (SEQ. ID NO: 108)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 99) (SEQ. ID NO: 109)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 100) (SEQ. ID NO: 110)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 101) (SEQ. ID NO: 111)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 102) (SEQ. ID NO: 112)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 103) (SEQ. ID NO: 113)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 104) (SEQ. ID NO: 114)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 105) (SEQ. ID NO: 115)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 106) (SEQ. ID NO: 116)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 107) (SEQ. ID NO: 117)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 108) (SEQ. ID NO: 118)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 109) (SEQ. ID NO: 119)  
5'-GC GGC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 110) (SEQ. ID NO: 120)  
5'-GC GGC CTG GAA AGC TGA GAT GGA G -3' (FRAG 111) (SEQ. ID NO: 121)  
5'-GC GGC CTG GAA AGC TGA GAT GGA -3' (FRAG 112) (SEQ. ID NO: 122)  
5'-GC GGC CTG GAA AGC TGA GAT GG -3' (FRAG 113) (SEQ. ID NO: 123)  
5'-GC GGC CTG GAA AGC TGA GAT G -3' (FRAG 114) (SEQ. ID NO: 124)  
5'-GC GGC CTG GAA AGC TGA GAT -3' (FRAG 115) (SEQ. ID NO: 125)  
5'-GC GGC CTG GAA AGC TGA GA-3' (FRAG 116) (SEQ. ID NO: 126)  
5'-GC GGC CTG GAA AGC TGA G-3' (FRAG 117) (SEQ. ID NO: 127)  
5'-GC GGC CTG GAA AGC TGA-3' (FRAG 118) (SEQ. ID NO: 128)  
5'-GC GGC CTG GAA AGC TG-3' (FRAG 119) (SEQ. ID NO: 129)  
5'-GC GGC CTG GAA AGC T-3' (FRAG 120) (SEQ. ID NO: 130)  
5'-GC GGC CTG GAA AGC-3' (FRAG 121) (SEQ. ID NO: 131)  
5'-GC GGC CTG GAA AG-3' (FRAG 122) (SEQ. ID NO: 132)  
5'-GC GGC CTG GAA A-3' (FRAG 123) (SEQ. ID NO: 133)  
5'-GC GGC CTG GAA-3' (FRAG 124) (SEQ. ID NO: 134)  
5'-GC GGC CTG GA-3' (FRAG 125) (SEQ. ID NO: 135)  
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC CAC AGG CTG GGC-3' (FRAG 126) (SEQ. ID NO: 136)  
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC CAC AGG CTG GG-3' (FRAG 127) (SEQ. ID NO: 137)  
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC CAC AGG CTG G-3' (FRAG 128) (SEQ. ID NO: 138)  
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC CAC AGG CTG -3' (FRAG 129) (SEQ. ID NO: 139)  
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGC CAC AGG CT-3' (FRAG 130) (SEQ. ID NO: 140)  
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC CAC AGG C-3' (FRAG 131) (SEQ. ID NO: 141)  
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC CAC AGG -3' (FRAG 132) (SEQ. ID NO: 142)  
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGC CAC AG-3' (FRAG 133) (SEQ. ID NO: 143)  
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGC CAC A-3' (FRAG 134) (SEQ. ID NO: 144)  
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGC CAC-3' (FRAG 135) (SEQ. ID NO: 145)  
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGC CA-3' (FRAG 136) (SEQ. ID NO: 146)

5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 137) (SEQ. ID NO: 147)  
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 138) (SEQ. ID NO: 148)  
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 139) (SEQ. ID NO: 149)  
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 140) (SEQ. ID NO: 150)  
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 141) (SEQ. ID NO: 151)  
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 142) (SEQ. ID NO: 152)  
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 143) (SEQ. ID NO: 153)  
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 144) (SEQ. ID NO: 154)  
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 145) (SEQ. ID NO: 155)  
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 146) (SEQ. ID NO: 156)  
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 147) (SEQ. ID NO: 157)  
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 148) (SEQ. ID NO: 158)  
5'-C GGC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 148) (SEQ. ID NO: 159)  
5'-C GGC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 150) (SEQ. ID NO: 160)  
5'-C GGC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 151) (SEQ. ID NO: 161)  
5'-C GGC CTG GAA AGC TGA GAT GGA G -3' (FRAG 152) (SEQ. ID NO: 162)  
5'-C GGC CTG GAA AGC TGA GAT GGA -3' (FRAG 153) (SEQ. ID NO: 163)  
5'-C GGC CTG GAA AGC TGA GAT GG -3' (FRAG 154) (SEQ. ID NO: 164)  
5'-C GGC CTG GAA AGC TGA GAT G -3' (FRAG 155) (SEQ. ID NO: 165)  
5'-C GGC CTG GAA AGC TGA GAT -3' (FRAG 156) (SEQ. ID NO: 166)  
5'-C GGC CTG GAA AGC TGA GA-3' (FRAG 157) (SEQ. ID NO: 167)  
5'-C GGC CTG GAA AGC TGA G-3' (FRAG 158) (SEQ. ID NO: 168)  
5'-C GGC CTG GAA AGC TGA-3' (FRAG 159) (SEQ. ID NO: 169)  
5'-C GGC CTG GAA AGC TG-3' (FRAG 160) (SEQ. ID NO: 170)  
5'-C GGC CTG GAA AGC T-3' (FRAG 161) (SEQ. ID NO: 171)  
5'-C GGC CTG GAA AGC-3' (FRAG 162) (SEQ. ID NO: 172)  
5'-C GGC CTG GAA AG-3' (FRAG 163) (SEQ. ID NO: 173)  
5'-C GGC CTG GAA A-3' (FRAG 164) (SEQ. ID NO: 174)  
5'-C GGC CTG GAA-3' (FRAG 165) (SEQ. ID NO: 175)  
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 166) (SEQ. ID NO: 176)  
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 167) (SEQ. ID NO: 177)  
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 168) (SEQ. ID NO: 178)  
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 169) (SEQ. ID NO: 179)  
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 170) (SEQ. ID NO: 180)  
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 171) (SEQ. ID NO: 181)  
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG CAC AGG -3' (FRAG 172) (SEQ. ID NO: 182)  
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG CAC AG-3' (FRAG 173) (SEQ. ID NO: 183)  
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG CAC A-3' (FRAG 174) (SEQ. ID NO: 184)  
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG CAC-3' (FRAG 175) (SEQ. ID NO: 185)  
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG CA-3' (FRAG 176) (SEQ. ID NO: 186)  
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG C-3' (FRAG 177) (SEQ. ID NO: 187)  
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG -3' (FRAG 178) (SEQ. ID NO: 188)  
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GG-3' (FRAG 179) (SEQ. ID NO: 189)  
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC G-3' (FRAG 180) (SEQ. ID NO: 190)  
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC -3' (FRAG 181) (SEQ. ID NO: 191)  
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TG -3' (FRAG 182) (SEQ. ID NO: 192)  
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT T G -3' (FRAG 183) (SEQ. ID NO: 193)  
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 184) (SEQ. ID NO: 194)  
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 185) (SEQ. ID NO: 195)  
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 186) (SEQ. ID NO: 196)  
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 187) (SEQ. ID NO: 197)  
5'-GGC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 188) (SEQ. ID NO: 198)  
5'-GGC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 189) (SEQ. ID NO: 199)  
5'-GGC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 190) (SEQ. ID NO: 200)  
5'-GGC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 191) (SEQ. ID NO: 201)  
5'-GGC CTG GAA AGC TGA GAT GGA G -3' (FRAG 192) (SEQ. ID NO: 202)  
5'-GGC CTG GAA AGC TGA GAT GGA -3' (FRAG 193) (SEQ. ID NO: 203)  
5'-GGC CTG GAA AGC TGA GAT GG -3' (FRAG 194) (SEQ. ID NO: 204)  
5'-GGC CTG GAA AGC TGA GAT G -3' (FRAG 195) (SEQ. ID NO: 205)  
5'-GGC CTG GAA AGC TGA GAT -3' (FRAG 196) (SEQ. ID NO: 206)  
5'-GGC CTG GAA AGC TGA GA-3' (FRAG 197) (SEQ. ID NO: 207)  
5'-GGC CTG GAA AGC TGA G-3' (FRAG 198) (SEQ. ID NO: 208)  
5'-GGC CTG GAA AGC TGA-3' (FRAG 199) (SEQ. ID NO: 209)  
5'-GGC CTG GAA AGC TG-3' (FRAG 200) (SEQ. ID NO: 210)  
5'-GGC CTG GAA AGC T-3' (FRAG 201) (SEQ. ID NO: 211)  
5'-GGC CTG GAA AGC-3' (FRAG 202) (SEQ. ID NO: 212)  
5'-GGC CTG GAA AG -3' (FRAG 203) (SEQ. ID NO: 213)

5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 206) (SEQ. ID NO: 216)  
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 207) (SEQ. ID NO: 217)  
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 208) (SEQ. ID NO: 218)  
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 209) (SEQ. ID NO: 219)  
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 210) (SEQ. ID NO: 220)  
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 211) (SEQ. ID NO: 221)  
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 212) (SEQ. ID NO: 222)  
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 213) (SEQ. ID NO: 223)  
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 214) (SEQ. ID NO: 224)  
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 215) (SEQ. ID NO: 225)  
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 216) (SEQ. ID NO: 226)  
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 217) (SEQ. ID NO: 227)  
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 218) (SEQ. ID NO: 228)  
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 219) (SEQ. ID NO: 229)  
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 220) (SEQ. ID NO: 230)  
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 221) (SEQ. ID NO: 231)  
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 222) (SEQ. ID NO: 232)  
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 223) (SEQ. ID NO: 233)  
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 224) (SEQ. ID NO: 234)  
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 225) (SEQ. ID NO: 235)  
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 226) (SEQ. ID NO: 236)  
5'- GC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 227) (SEQ. ID NO: 237)  
5'- GC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 228) (SEQ. ID NO: 238)  
5'- GC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 229) (SEQ. ID NO: 239)  
5'- GC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 230) (SEQ. ID NO: 240)  
5'- GC CTG GAA AGC TGA GAT GGA G -3' (FRAG 231) (SEQ. ID NO: 241)  
5'- GC CTG GAA AGC TGA GAT GGA -3' (FRAG 232) (SEQ. ID NO: 242)  
5'- GC CTG GAA AGC TGA GAT GG -3' (FRAG 233) (SEQ. ID NO: 243)  
5'- GC CTG GAA AGC TGA GAT G -3' (FRAG 234) (SEQ. ID NO: 244)  
5'- GC CTG GAA AGC TGA GAT -3' (FRAG 235) (SEQ. ID NO: 245)  
5'- GC CTG GAA AGC TGA GA-3' (FRAG 236) (SEQ. ID NO: 246)  
5'- GC CTG GAA AGC TGA G-3' (FRAG 237) (SEQ. ID NO: 247)  
5'- GC CTG GAA AGC TGA-3' (FRAG 238) (SEQ. ID NO: 248)  
5'- GC CTG GAA AGC TG-3' (FRAG 239) (SEQ. ID NO: 249)  
5'- GC CTG GAA AGC T-3' (FRAG 240) (SEQ. ID NO: 250)  
5'- GC CTG GAA AGC-3' (FRAG 241) (SEQ. ID NO: 251)  
5'- GC CTG GAA AG-3' (FRAG 242) (SEQ. ID NO: 252)  
5'- C CTG GAA AGC TGA GAT GG A GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 243) (SEQ. ID NO: 253)  
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 244) (SEQ. ID NO: 254)  
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 245) (SEQ. ID NO: 255)  
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 246) (SEQ. ID NO: 256)  
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 247) (SEQ. ID NO: 257)  
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 248) (SEQ. ID NO: 258)  
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 249) (SEQ. ID NO: 259)  
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 250) (SEQ. ID NO: 260)  
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 251) (SEQ. ID NO: 261)  
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 252) (SEQ. ID NO: 262)  
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 253) (SEQ. ID NO: 263)  
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 254) (SEQ. ID NO: 264)  
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 255) (SEQ. ID NO: 265)  
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 256) (SEQ. ID NO: 266)  
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 257) (SEQ. ID NO: 267)  
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 258) (SEQ. ID NO: 268)  
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 259) (SEQ. ID NO: 269)  
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 260) (SEQ. ID NO: 270)  
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 261) (SEQ. ID NO: 271)  
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 262) (SEQ. ID NO: 272)  
5'- C CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 263) (SEQ. ID NO: 273)  
5'- C CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 264) (SEQ. ID NO: 274)  
5'- C CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 265) (SEQ. ID NO: 275)  
5'- C CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 266) (SEQ. ID NO: 276)  
5'- C CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 267) (SEQ. ID NO: 277)  
5'- C CTG GAA AGC TGA GAT GGA GG -3' (FRAG 268) (SEQ. ID NO: 278)  
5'- C CTG GAA AGC TGA GAT GGA G -3' (FRAG 269) (SEQ. ID NO: 279)  
5'- C CTG GAA AGC TGA GAT GGA -3' (FRAG 270) (SEQ. ID NO: 280)  
5'- C CTG GAA AGC TGA GAT GG -3' (FRAG 271) (SEQ. ID NO: 281)  
5'- C CTG GAA AGC TGA GAT G -3' (FRAG 272) (SEQ. ID NO: 282)  
5'- C CTG GAA AGC TGA GAT -3' (FRAG 273) (SEQ. ID NO: 283)  
5'- C CTG GAA AGC TGA GA-3' (FRAG 274) (SEQ. ID NO: 284)

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5'- C CTG GAA AGC TGA -3' (FRAG 275) (SEQ. ID NO: 285)  
5'- C CTG GAA AGC TGA -3' (FRAG 276) (SEQ. ID NO: 286)  
5'- C CTG GAA AGC TG -3' (FRAG 277) (SEQ. ID NO: 287)  
5'- C CTG GAA AGC T -3' (FRAG 278) (SEQ. ID NO: 288)  
5'- C CTG GAA AGC -3' (FRAG 279) (SEQ. ID NO: 289)  
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC -3' (FRAG 280) (SEQ. ID NO: 290)  
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG -3' (FRAG 281) (SEQ. ID NO: 291)  
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G -3' (FRAG 282) (SEQ. ID NO: 292)  
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 283) (SEQ. ID NO: 293)  
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT -3' (FRAG 284) (SEQ. ID NO: 294)  
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C -3' (FRAG 285) (SEQ. ID NO: 295)  
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 286) (SEQ. ID NO: 296)  
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG -3' (FRAG 287) (SEQ. ID NO: 297)  
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A -3' (FRAG 288) (SEQ. ID NO: 298)  
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC -3' (FRAG 289) (SEQ. ID NO: 299)  
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA -3' (FRAG 290) (SEQ. ID NO: 300)  
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C -3' (FRAG 291) (SEQ. ID NO: 301)  
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 292) (SEQ. ID NO: 302)  
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG -3' (FRAG 293) (SEQ. ID NO: 303)  
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G -3' (FRAG 294) (SEQ. ID NO: 304)  
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 295) (SEQ. ID NO: 305)  
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 296) (SEQ. ID NO: 306)  
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 297) (SEQ. ID NO: 307)  
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 298) (SEQ. ID NO: 308)  
5'- CTG GAA AGC TGA GAT GGA GGG CGG CA -3' (FRAG 299) (SEQ. ID NO: 309)  
5'- CTG GAA AGC TGA GAT GGA GGG CGG C -3' (FRAG 300) (SEQ. ID NO: 310)  
5'- CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 301) (SEQ. ID NO: 311)  
5'- CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 302) (SEQ. ID NO: 312)  
5'- CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 303) (SEQ. ID NO: 313)  
5'- CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 304) (SEQ. ID NO: 314)  
5'- CTG GAA AGC TGA GAT GGA GG -3' (FRAG 305) (SEQ. ID NO: 315)  
5'- CTG GAA AGC TGA GAT GGA G -3' (FRAG 306) (SEQ. ID NO: 316)  
5'- CTG GAA AGC TGA GAT GGA -3' (FRAG 307) (SEQ. ID NO: 317)  
5'- CTG GAA AGC TGA GAT GG -3' (FRAG 308) (SEQ. ID NO: 318)  
5'- CTG GAA AGC TGA GAT G -3' (FRAG 309) (SEQ. ID NO: 319)  
5'- CTG GAA AGC TGA GAT -3' (FRAG 310) (SEQ. ID NO: 320)  
5'- CTG GAA AGC TGA GA -3' (FRAG 311) (SEQ. ID NO: 321)  
5'- CTG GAA AGC TGA G -3' (FRAG 312) (SEQ. ID NO: 322)  
5'- CTG GAA AGC TGA -3' (FRAG 313) (SEQ. ID NO: 323)  
5'- CTG GAA AGC TG -3' (FRAG 314) (SEQ. ID NO: 324)  
5'- CTG GAA AGC T -3' (FRAG 315) (SEQ. ID NO: 325)  
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC -3' (FRAG 316) (SEQ. ID NO: 326)  
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG -3' (FRAG 317) (SEQ. ID NO: 327)  
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G -3' (FRAG 318) (SEQ. ID NO: 328)  
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 319) (SEQ. ID NO: 329)  
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT -3' (FRAG 320) (SEQ. ID NO: 330)  
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C -3' (FRAG 321) (SEQ. ID NO: 331)  
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 322) (SEQ. ID NO: 332)  
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG -3' (FRAG 323) (SEQ. ID NO: 333)  
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A -3' (FRAG 324) (SEQ. ID NO: 334)  
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC -3' (FRAG 325) (SEQ. ID NO: 335)  
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA -3' (FRAG 326) (SEQ. ID NO: 336)  
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C -3' (FRAG 327) (SEQ. ID NO: 337)  
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 328) (SEQ. ID NO: 338)  
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG -3' (FRAG 329) (SEQ. ID NO: 339)  
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC G -3' (FRAG 330) (SEQ. ID NO: 340)  
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 331) (SEQ. ID NO: 341)  
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 332) (SEQ. ID NO: 342)  
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 333) (SEQ. ID NO: 343)  
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 334) (SEQ. ID NO: 344)  
5'- TG GAA AGC TGA GAT GGA GGG CGG CA -3' (FRAG 335) (SEQ. ID NO: 345)  
5'- TG GAA AGC TGA GAT GGA GGG CGG C -3' (FRAG 336) (SEQ. ID NO: 346)  
5'- TG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 337) (SEQ. ID NO: 347)  
5'- TG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 338) (SEQ. ID NO: 348)  
5'- TG GAA AGC TGA GAT GGA GGG C -3' (FRAG 339) (SEQ. ID NO: 349)  
5'- TG GAA AGC TGA GAT GGA GGG -3' (FRAG 340) (SEQ. ID NO: 350)  
5'- TG GAA AGC TGA GAT GGA GG -3' (FRAG 341) (SEQ. ID NO: 351)  
5'- TG GAA AGC TGA GAT GGA G -3' (FRAG 342) (SEQ. ID NO: 352)  
5'- TG GAA AGC TGA GAT GGA -3' (FRAG 343) (SEQ. ID NO: 353)

5'- TG GAA AGC TGA GAT GG -3' (FRAG 344) (SEQ. ID NO: 354)  
5'- TG GAA AGC TGA GAT G -3' (FRAG 345) (SEQ. ID NO: 355)  
5'- TG GAA AGC TGA GAT -3' (FRAG 346) (SEQ. ID NO: 356)  
5'- TG GAA AGC TGA GA-3' (FRAG 347) (SEQ. ID NO: 357)  
5'- TG GAA AGC TGA G-3' (FRAG 348) (SEQ. ID NO: 358)  
5'- TG GAA AGC TGA-3' (FRAG 349) (SEQ. ID NO: 359)  
5'- TG GAA AGC TG-3' (FRAG 350) (SEQ. ID NO: 360)  
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 351) (SEQ. ID NO: 361)  
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 352) (SEQ. ID NO: 362)  
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 353) (SEQ. ID NO: 363)  
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 354) (SEQ. ID NO: 364)  
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 355) (SEQ. ID NO: 365)  
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 356) (SEQ. ID NO: 366)  
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 357) (SEQ. ID NO: 367)  
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 358) (SEQ. ID NO: 368)  
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 359) (SEQ. ID NO: 369)  
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 360) (SEQ. ID NO: 370)  
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 361) (SEQ. ID NO: 371)  
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 362) (SEQ. ID NO: 372)  
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 363) (SEQ. ID NO: 373)  
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 364) (SEQ. ID NO: 374)  
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 365) (SEQ. ID NO: 375)  
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 366) (SEQ. ID NO: 376)  
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 367) (SEQ. ID NO: 377)  
5'- G GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 368) (SEQ. ID NO: 378)  
5'- G GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 369) (SEQ. ID NO: 379)  
5'- G GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 370) (SEQ. ID NO: 380)  
5'- G GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 371) (SEQ. ID NO: 381)  
5'- G GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 372) (SEQ. ID NO: 382)  
5'- G GAA AGC TGA GAT GGA GGG CG -3' (FRAG 373) (SEQ. ID NO: 383)  
5'- G GAA AGC TGA GAT GGA GGG C -3' (FRAG 374) (SEQ. ID NO: 384)  
5'- G GAA AGC TGA GAT GGA GGG -3' (FRAG 375) (SEQ. ID NO: 385)  
5'- G GAA AGC TGA GAT GGA GG -3' (FRAG 376) (SEQ. ID NO: 386)  
5'- G GAA AGC TGA GAT GGA G -3' (FRAG 377) (SEQ. ID NO: 387)  
5'- G GAA AGC TGA GAT GGA -3' (FRAG 378) (SEQ. ID NO: 388)  
5'- G GAA AGC TGA GAT GG -3' (FRAG 379) (SEQ. ID NO: 389)  
5'- G GAA AGC TGA GAT G -3' (FRAG 380) (SEQ. ID NO: 390)  
5'- G GAA AGC TGA GAT -3' (FRAG 381) (SEQ. ID NO: 391)  
5'- G GAA AGC TGA GA-3' (FRAG 382) (SEQ. ID NO: 392)  
5'- G GAA AGC TGA G-3' (FRAG 383) (SEQ. ID NO: 393)  
5'- G GAA AGC TGA-3' (FRAG 384) (SEQ. ID NO: 394)  
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 385) (SEQ. ID NO: 395)  
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 386) (SEQ. ID NO: 396)  
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 387) (SEQ. ID NO: 397)  
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 388) (SEQ. ID NO: 398)  
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 389) (SEQ. ID NO: 399)  
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 390) (SEQ. ID NO: 400)  
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 391) (SEQ. ID NO: 401)  
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 392) (SEQ. ID NO: 402)  
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 393) (SEQ. ID NO: 403)  
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 394) (SEQ. ID NO: 404)  
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 395) (SEQ. ID NO: 405)  
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 396) (SEQ. ID NO: 406)  
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 397) (SEQ. ID NO: 407)  
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 398) (SEQ. ID NO: 408)  
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 399) (SEQ. ID NO: 409)  
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 400) (SEQ. ID NO: 410)  
5'- GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 401) (SEQ. ID NO: 411)  
5'- GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 402) (SEQ. ID NO: 412)  
5'- GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 403) (SEQ. ID NO: 413)  
5'- GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 404) (SEQ. ID NO: 414)  
5'- GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 405) (SEQ. ID NO: 415)  
5'- GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 406) (SEQ. ID NO: 416)  
5'- GAA AGC TGA GAT GGA GGG CG -3' (FRAG 407) (SEQ. ID NO: 417)  
5'- GAA AGC TGA GAT GGA GGG C -3' (FRAG 408) (SEQ. ID NO: 418)  
5'- GAA AGC TGA GAT GGA GGG -3' (FRAG 409) (SEQ. ID NO: 419)  
5'- GAA AGC TGA GAT GGA GG -3' (FRAG 410) (SEQ. ID NO: 420)  
5'- GAA AGC TGA GAT GGA G -3' (FRAG 411) (SEQ. ID NO: 421)  
5'- GAA AGC TGA GAT GGA -3' (FRAG 412) (SEQ. ID NO: 422)



5'- GAA AGC TGA C G G G -3' (FRAG 413) (SEQ. ID NO: 423)  
5'- GAA AGC TGA GAT G -3' (FRAG 414) (SEQ. ID NO: 424)  
5'- GAA AGC TGA GAT -3' (FRAG 415) (SEQ. ID NO: 425)  
5'- GAA AGC TGA GA-3' (FRAG 416) (SEQ. ID NO: 426)  
5'- GAA AGC TGA G-3' (FRAG 417) (SEQ. ID NO: 427)  
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 418) (SEQ. ID NO: 428)  
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 419) (SEQ. ID NO: 429)  
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 420) (SEQ. ID NO: 430)  
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 421) (SEQ. ID NO: 431)  
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 422) (SEQ. ID NO: 432)  
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 423) (SEQ. ID NO: 433)  
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 424) (SEQ. ID NO: 434)  
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 425) (SEQ. ID NO: 435)  
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 426) (SEQ. ID NO: 436)  
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 427) (SEQ. ID NO: 437)  
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 428) (SEQ. ID NO: 438)  
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 429) (SEQ. ID NO: 439)  
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 430) (SEQ. ID NO: 440)  
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 431) (SEQ. ID NO: 441)  
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 432) (SEQ. ID NO: 442)  
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 433) (SEQ. ID NO: 443)  
5'- AA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 434) (SEQ. ID NO: 444)  
5'- AA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 435) (SEQ. ID NO: 445)  
5'- AA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 436) (SEQ. ID NO: 446)  
5'- AA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 437) (SEQ. ID NO: 447)  
5'- AA AGC TGA GAT GGA GGG CGG C-3' (FRAG 438) (SEQ. ID NO: 448)  
5'- AA AGC TGA GAT GGA GGG CGG -3' (FRAG 439) (SEQ. ID NO: 449)  
5'- AA AGC TGA GAT GGA GGG CG -3' (FRAG 440) (SEQ. ID NO: 450)  
5'- AA AGC TGA GAT GGA GGG C -3' (FRAG 441) (SEQ. ID NO: 451)  
5'- AA AGC TGA GAT GGA GGG -3' (FRAG 442) (SEQ. ID NO: 452)  
5'- AA AGC TGA GAT GGA GG -3' (FRAG 443) (SEQ. ID NO: 453)  
5'- AA AGC TGA GAT GGA G -3' (FRAG 444) (SEQ. ID NO: 454)  
5'- AA AGC TGA GAT GGA -3' (FRAG 445) (SEQ. ID NO: 455)  
5'- AA AGC TGA GAT GG -3' (FRAG 446) (SEQ. ID NO: 456)  
5'- AA AGC TGA GAT G -3' (FRAG 447) (SEQ. ID NO: 457)  
5'- AA AGC TGA GAT -3' (FRAG 448) (SEQ. ID NO: 458)  
5'- AA AGC TGA GA-3' (FRAG 449) (SEQ. ID NO: 459)  
5'- A AGC TGA GAT GGA GGG CG G CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 450) (SEQ. ID NO: 460)  
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 451) (SEQ. ID NO: 461)  
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 452) (SEQ. ID NO: 462)  
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 453) (SEQ. ID NO: 463)  
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 454) (SEQ. ID NO: 464)  
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 455) (SEQ. ID NO: 465)  
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 456) (SEQ. ID NO: 466)  
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 457) (SEQ. ID NO: 467)  
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 458) (SEQ. ID NO: 468)  
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 459) (SEQ. ID NO: 469)  
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 460) (SEQ. ID NO: 470)  
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 461) (SEQ. ID NO: 471)  
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 462) (SEQ. ID NO: 472)  
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 463) (SEQ. ID NO: 473)  
5'- A AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 464) (SEQ. ID NO: 474)  
5'- A AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 465) (SEQ. ID NO: 475)  
5'- A AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 466) (SEQ. ID NO: 476)  
5'- A AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 467) (SEQ. ID NO: 477)  
5'- A AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 468) (SEQ. ID NO: 478)  
5'- A AGC TGA GAT GGA GGG CGG CA-3' (FRAG 469) (SEQ. ID NO: 479)  
5'- A AGC TGA GAT GGA GGG CGG C-3' (FRAG 470) (SEQ. ID NO: 480)  
5'- A AGC TGA GAT GGA GGG CGG -3' (FRAG 471) (SEQ. ID NO: 481)  
5'- A AGC TGA GAT GGA GGG CG -3' (FRAG 472) (SEQ. ID NO: 482)  
5'- A AGC TGA GAT GGA GGG C -3' (FRAG 473) (SEQ. ID NO: 483)  
5'- A AGC TGA GAT GGA GGG -3' (FRAG 474) (SEQ. ID NO: 484)  
5'- A AGC TGA GAT GGA GG -3' (FRAG 475) (SEQ. ID NO: 485)

5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 482) (SEQ. ID NO: 492)  
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 483) (SEQ. ID NO: 493)  
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 484) (SEQ. ID NO: 494)  
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 485) (SEQ. ID NO: 495)  
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 486) (SEQ. ID NO: 496)  
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 487) (SEQ. ID NO: 497)  
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 488) (SEQ. ID NO: 498)  
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 489) (SEQ. ID NO: 499)  
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 490) (SEQ. ID NO: 500)  
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 491) (SEQ. ID NO: 501)  
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 492) (SEQ. ID NO: 502)  
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 493) (SEQ. ID NO: 503)  
5'- AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 494) (SEQ. ID NO: 504)  
5'- AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 495) (SEQ. ID NO: 505)  
5'- AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 496) (SEQ. ID NO: 506)  
5'- AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 497) (SEQ. ID NO: 507)  
5'- AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 498) (SEQ. ID NO: 508)  
5'- AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 499) (SEQ. ID NO: 509)  
5'- AGC TGA GAT GGA GGG CGG CA-3' (FRAG 500) (SEQ. ID NO: 510)  
5'- AGC TGA GAT GGA GGG CGG C-3' (FRAG 501) (SEQ. ID NO: 511)  
5'- AGC TGA GAT GGA GGG CGG -3' (FRAG 502) (SEQ. ID NO: 512)  
5'- AGC TGA GAT GGA GGG CG -3' (FRAG 503) (SEQ. ID NO: 513)  
5'- AGC TGA GAT GGA GGG C -3' (FRAG 504) (SEQ. ID NO: 514)  
5'- AGC TGA GAT GGA GGG -3' (FRAG 505) (SEQ. ID NO: 515)  
5'- AGC TGA GAT GGA GG -3' (FRAG 506) (SEQ. ID NO: 516)  
5'- AGC TGA GAT GGA G -3' (FRAG 507) (SEQ. ID NO: 517)  
5'- AGC TGA GAT GGA -3' (FRAG 508) (SEQ. ID NO: 518)  
5'- AGC TGA GAT GG -3' (FRAG 509) (SEQ. ID NO: 519)  
5'- AGC TGA GAT G -3' (FRAG 510) (SEQ. ID NO: 520)  
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 511) (SEQ. ID NO: 521)  
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 512) (SEQ. ID NO: 522)  
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 513) (SEQ. ID NO: 523)  
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 514) (SEQ. ID NO: 524)  
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 515) (SEQ. ID NO: 525)  
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 516) (SEQ. ID NO: 526)  
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 517) (SEQ. ID NO: 527)  
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 518) (SEQ. ID NO: 528)  
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 519) (SEQ. ID NO: 529)  
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 520) (SEQ. ID NO: 530)  
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 521) (SEQ. ID NO: 531)  
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 522) (SEQ. ID NO: 532)  
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 523) (SEQ. ID NO: 533)  
5'- GC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 524) (SEQ. ID NO: 534)  
5'- GC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 525) (SEQ. ID NO: 535)  
5'- GC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 526) (SEQ. ID NO: 536)  
5'- GC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 527) (SEQ. ID NO: 537)  
5'- GC TGA GAT GGA GGG CGG CAT G -3' (FRAG 528) (SEQ. ID NO: 538)  
5'- GC TGA GAT GGA GGG CGG CAT -3' (FRAG 529) (SEQ. ID NO: 539)  
5'- GC TGA GAT GGA GGG CGG CA-3' (FRAG 530) (SEQ. ID NO: 540)  
5'- GC TGA GAT GGA GGG CGG C-3' (FRAG 531) (SEQ. ID NO: 541)  
5'- GC TGA GAT GGA GGG CGG -3' (FRAG 532) (SEQ. ID NO: 542)  
5'- GC TGA GAT GGA GGG CG -3' (FRAG 533) (SEQ. ID NO: 543)  
5'- GC TGA GAT GGA GGG C -3' (FRAG 534) (SEQ. ID NO: 544)  
5'- GC TGA GAT GGA GGG -3' (FRAG 535) (SEQ. ID NO: 545)  
5'- GC TGA GAT GGA GG -3' (FRAG 536) (SEQ. ID NO: 546)  
5'- GC TGA GAT GGA G -3' (FRAG 537) (SEQ. ID NO: 547)  
5'- GC TGA GAT GGA -3' (FRAG 538) (SEQ. ID NO: 548)  
5'- GC TGA GAT GG -3' (FRAG 539) (SEQ. ID NO: 549)  
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 540) (SEQ. ID NO: 550)  
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 541) (SEQ. ID NO: 551)  
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 542) (SEQ. ID NO: 552)  
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 543) (SEQ. ID NO: 553)  
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 544) (SEQ. ID NO: 554)  
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 545) (SEQ. ID NO: 555)  
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 546) (SEQ. ID NO: 556)  
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 547) (SEQ. ID NO: 557)  
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 548) (SEQ. ID NO: 558)  
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 549) (SEQ. ID NO: 559)  
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 550) (SEQ. ID NO: 560)

5'- C TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 551) (SEQ. ID NO: 561)  
5'- C TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 552) (SEQ. ID NO: 562)  
5'- C TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 553) (SEQ. ID NO: 563)  
5'- C TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 554) (SEQ. ID NO: 564)  
5'- C TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 555) (SEQ. ID NO: 565)  
5'- C TGA GAT GGA GGG CGG CAT GG -3' (FRAG 556) (SEQ. ID NO: 566)  
5'- C TGA GAT GGA GGG CGG CAT G -3' (FRAG 557) (SEQ. ID NO: 567)  
5'- C TGA GAT GGA GGG CGG CAT -3' (FRAG 558) (SEQ. ID NO: 568)  
5'- C TGA GAT GGA GGG CGG CA-3' (FRAG 559) (SEQ. ID NO: 569)  
5'- C TGA GAT GGA GGG CGG C-3' (FRAG 560) (SEQ. ID NO: 570)  
5'- C TGA GAT GGA GGG CGG -3' (FRAG 561) (SEQ. ID NO: 571)  
5'- C TGA GAT GGA GGG CG -3' (FRAG 562) (SEQ. ID NO: 572)  
5'- C TGA GAT GGA GGG C -3' (FRAG 563) (SEQ. ID NO: 573)  
5'- C TGA GAT GGA GGG -3' (FRAG 564) (SEQ. ID NO: 574)  
5'- C TGA GAT GGA GG -3' (FRAG 565) (SEQ. ID NO: 575)  
5'- C TGA GAT GGA G -3' (FRAG 566) (SEQ. ID NO: 576)  
5'- C TGA GAT GGA -3' (FRAG 567) (SEQ. ID NO: 577)  
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 568) (SEQ. ID NO: 578)  
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 569) (SEQ. ID NO: 579)  
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 570) (SEQ. ID NO: 580)  
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 571) (SEQ. ID NO: 581)  
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 572) (SEQ. ID NO: 582)  
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 573) (SEQ. ID NO: 583)  
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 574) (SEQ. ID NO: 584)  
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 575) (SEQ. ID NO: 585)  
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 576) (SEQ. ID NO: 586)  
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 577) (SEQ. ID NO: 587)  
5'- TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 578) (SEQ. ID NO: 588)  
5'- TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 579) (SEQ. ID NO: 589)  
5'- TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 580) (SEQ. ID NO: 590)  
5'- TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 581) (SEQ. ID NO: 591)  
5'- TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 582) (SEQ. ID NO: 592)  
5'- TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 583) (SEQ. ID NO: 593)  
5'- TGA GAT GGA GGG CGG CAT GG -3' (FRAG 584) (SEQ. ID NO: 594)  
5'- TGA GAT GGA GGG CGG CAT G -3' (FRAG 585) (SEQ. ID NO: 595)  
5'- TGA GAT GGA GGG CGG CAT -3' (FRAG 586) (SEQ. ID NO: 596)  
5'- TGA GAT GGA GGG CGG CA-3' (FRAG 587) (SEQ. ID NO: 597)  
5'- TGA GAT GGA GGG CGG C-3' (FRAG 588) (SEQ. ID NO: 598)  
5'- TGA GAT GGA GGG CGG -3' (FRAG 589) (SEQ. ID NO: 599)  
5'- TGA GAT GGA GGG CG -3' (FRAG 590) (SEQ. ID NO: 600)  
5'- TGA GAT GGA GGG C -3' (FRAG 591) (SEQ. ID NO: 601)  
5'- TGA GAT GGA GGG -3' (FRAG 592) (SEQ. ID NO: 602)  
5'- TGA GAT GGA GG -3' (FRAG 593) (SEQ. ID NO: 603)  
5'- TGA GAT GGA G -3' (FRAG 594) (SEQ. ID NO: 604)  
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 595) (SEQ. ID NO: 605)  
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 596) (SEQ. ID NO: 606)  
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 597) (SEQ. ID NO: 607)  
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 598) (SEQ. ID NO: 608)  
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 599) (SEQ. ID NO: 609)  
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 600) (SEQ. ID NO: 610)  
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 601) (SEQ. ID NO: 611)  
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 602) (SEQ. ID NO: 612)  
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 603) (SEQ. ID NO: 613)  
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 604) (SEQ. ID NO: 614)  
5'- GA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 605) (SEQ. ID NO: 615)  
5'- GA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 606) (SEQ. ID NO: 616)  
5'- GA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 607) (SEQ. ID NO: 617)  
5'- GA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 608) (SEQ. ID NO: 618)  
5'- GA GAT GGA GGG CGG CAT GGC G-3' (FRAG 609) (SEQ. ID NO: 619)  
5'- GA GAT GGA GGG CGG CAT GGC -3' (FRAG 610) (SEQ. ID NO: 620)  
5'- GA GAT GGA GGG CGG CAT GG -3' (FRAG 611) (SEQ. ID NO: 621)  
5'- GA GAT GGA GGG CGG CAT G -3' (FRAG 612) (SEQ. ID NO: 622)  
5'- GA GAT GGA GGG CGG CAT -3' (FRAG 613) (SEQ. ID NO: 623)  
5'- GA GAT GGA GGG CGG CA-3' (FRAG 614) (SEQ. ID NO: 624)  
5'- GA GAT GGA GGG CGG C-3' (FRAG 615) (SEQ. ID NO: 625)  
5'- GA GAT GGA GGG CGG -3' (FRAG 616) (SEQ. ID NO: 626)  
5'- GA GAT GGA GGG CG -3' (FRAG 617) (SEQ. ID NO: 627)  
5'- GA GAT GGA GGG C -3' (FRAG 618) (SEQ. ID NO: 628)  
5'- GA GAT GGA GGG -3' (FRAG 619) (SEQ. ID NO: 629)

5'- GA GAT GGA GG -3' (FRAG 620) (SEQ. ID NO: 630)  
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 621) (SEQ. ID NO: 631)  
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 622) (SEQ. ID NO: 632)  
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 623) (SEQ. ID NO: 633)  
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 624) (SEQ. ID NO: 634)  
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 625) (SEQ. ID NO: 635)  
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 626) (SEQ. ID NO: 636)  
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 627) (SEQ. ID NO: 637)  
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 628) (SEQ. ID NO: 638)  
5'- A GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 629) (SEQ. ID NO: 639)  
5'- A GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 630) (SEQ. ID NO: 640)  
5'- A GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 631) (SEQ. ID NO: 641)  
5'- A GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 632) (SEQ. ID NO: 642)  
5'- A GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 633) (SEQ. ID NO: 643)  
5'- A GAT GGA GGG CGG CAT GGC GG-3' (FRAG 634) (SEQ. ID NO: 644)  
5'- A GAT GGA GGG CGG CAT GGC G-3' (FRAG 635) (SEQ. ID NO: 645)  
5'- A GAT GGA GGG CGG CAT GGC -3' (FRAG 636) (SEQ. ID NO: 646)  
5'- A GAT GGA GGG CGG CAT GG -3' (FRAG 637) (SEQ. ID NO: 647)  
5'- A GAT GGA GGG CGG CAT G -3' (FRAG 638) (SEQ. ID NO: 648)  
5'- A GAT GGA GGG CGG CAT -3' (FRAG 639) (SEQ. ID NO: 649)  
5'- A GAT GGA GGG CGG CA-3' (FRAG 640) (SEQ. ID NO: 650)  
5'- A GAT GGA GGG CGG C-3' (FRAG 641) (SEQ. ID NO: 651)  
5'- A GAT GGA GGG CGG -3' (FRAG 642) (SEQ. ID NO: 652)  
5'- A GAT GGA GGG CG -3' (FRAG 643) (SEQ. ID NO: 653)  
5'- A GAT GGA GGG C -3' (FRAG 644) (SEQ. ID NO: 654)  
5'- A GAT GGA GGG -3' (FRAG 645) (SEQ. ID NO: 655)  
5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 646) (SEQ. ID NO: 656)  
5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 647) (SEQ. ID NO: 657)  
5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 648) (SEQ. ID NO: 658)  
5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 649) (SEQ. ID NO: 659)  
5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 650) (SEQ. ID NO: 660)  
5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 651) (SEQ. ID NO: 661)  
5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 652) (SEQ. ID NO: 662)  
5'- GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 653) (SEQ. ID NO: 663)  
5'- GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 654) (SEQ. ID NO: 664)  
5'- GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 655) (SEQ. ID NO: 665)  
5'- GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 656) (SEQ. ID NO: 666)  
5'- GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 657) (SEQ. ID NO: 667)  
5'- GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 658) (SEQ. ID NO: 668)  
5'- GAT GGA GGG CGG CAT GGC GG-3' (FRAG 659) (SEQ. ID NO: 669)  
5'- GAT GGA GGG CGG CAT GGC G-3' (FRAG 660) (SEQ. ID NO: 670)  
5'- GAT GGA GGG CGG CAT GGC -3' (FRAG 661) (SEQ. ID NO: 671)  
5'- GAT GGA GGG CGG CAT GG -3' (FRAG 662) (SEQ. ID NO: 672)  
5'- GAT GGA GGG CGG CAT G -3' (FRAG 663) (SEQ. ID NO: 673)  
5'- GAT GGA GGG CGG CAT -3' (FRAG 664) (SEQ. ID NO: 674)  
5'- GAT GGA GGG CGG CA-3' (FRAG 665) (SEQ. ID NO: 675)  
5'- GAT GGA GGG CGG C-3' (FRAG 666) (SEQ. ID NO: 676)  
5'- GAT GGA GGG CGG -3' (FRAG 667) (SEQ. ID NO: 677)  
5'- GAT GGA GGG CG -3' (FRAG 668) (SEQ. ID NO: 678)  
5'- GAT GGA GGG C -3' (FRAG 669) (SEQ. ID NO: 679)  
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 670) (SEQ. ID NO: 680)  
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 671) (SEQ. ID NO: 681)  
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 672) (SEQ. ID NO: 682)  
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 673) (SEQ. ID NO: 683)  
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 674) (SEQ. ID NO: 684)  
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 675) (SEQ. ID NO: 685)  
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 676) (SEQ. ID NO: 686)  
5'- AT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 677) (SEQ. ID NO: 687)  
5'- AT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 678) (SEQ. ID NO: 688)  
5'- AT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 679) (SEQ. ID NO: 689)  
5'- AT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 680) (SEQ. ID NO: 690)  
5'- AT GGA GGG CGG CAT GGC GGG C-3' (FRAG 681) (SEQ. ID NO: 691)  
5'- AT GGA GGG CGG CAT GGC GGG -3' (FRAG 682) (SEQ. ID NO: 692)  
5'- AT GGA GGG CGG CAT GGC GG-3' (FRAG 683) (SEQ. ID NO: 693)  
5'- AT GGA GGG CGG CAT GGC G-3' (FRAG 684) (SEQ. ID NO: 694)  
5'- AT GGA GGG CGG CAT GGC -3' (FRAG 685) (SEQ. ID NO: 695)  
5'- AT GGA GGG CGG CAT GG -3' (FRAG 686) (SEQ. ID NO: 696)  
5'- AT GGA GGG CGG CAT G -3' (FRAG 687) (SEQ. ID NO: 697)  
5'- AT GGA GGG CGG CAT -3' (FRAG 688) (SEQ. ID NO: 698)

5'- AT GGA GGG CGG CA-3' (FRAG 689) (SEQ. ID NO: 699)  
5'- AT GGA GGG CGG C-3' (FRAG 690) (SEQ. ID NO: 700)  
5'- AT GGA GGG CGG -3' (FRAG 691) (SEQ. ID NO: 701)  
5'- AT GGA GGG CG -3' (FRAG 692) (SEQ. ID NO: 702)  
5'- T GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 693) (SEQ. ID NO: 703)  
5'- T GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 694) (SEQ. ID NO: 704)  
5'- T GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 695) (SEQ. ID NO: 705)  
5'- T GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 696) (SEQ. ID NO: 706)  
5'- T GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 697) (SEQ. ID NO: 707)  
5'- T GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 698) (SEQ. ID NO: 708)  
5'- T GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 699) (SEQ. ID NO: 709)  
5'- T GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 700) (SEQ. ID NO: 710)  
5'- T GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 701) (SEQ. ID NO: 711)  
5'- T GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 702) (SEQ. ID NO: 712)  
5'- T GGA GGG CGG CAT GGC GGG CA-3' (FRAG 703) (SEQ. ID NO: 713)  
5'- T GGA GGG CGG CAT GGC GGG C-3' (FRAG 704) (SEQ. ID NO: 714)  
5'- T GGA GGG CGG CAT GGC GGG -3' (FRAG 705) (SEQ. ID NO: 715)  
5'- T GGA GGG CGG CAT GGC GG-3' (FRAG 706) (SEQ. ID NO: 716)  
5'- T GGA GGG CGG CAT GGC G-3' (FRAG 707) (SEQ. ID NO: 717)  
5'- T GGA GGG CGG CAT GGC -3' (FRAG 708) (SEQ. ID NO: 718)  
5'- T GGA GGG CGG CAT GG -3' (FRAG 709) (SEQ. ID NO: 719)  
5'- T GGA GGG CGG CAT G -3' (FRAG 710) (SEQ. ID NO: 720)  
5'- T GGA GGG CGG CAT -3' (FRAG 711) (SEQ. ID NO: 721)  
5'- T GGA GGG CGG CA-3' (FRAG 712) (SEQ. ID NO: 722)  
5'- T GGA GGG CGG C-3' (FRAG 713) (SEQ. ID NO: 723)  
5'- T GGA GGG CGG -3' (FRAG 714) (SEQ. ID NO: 724)  
5'- GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 715) (SEQ. ID NO: 725)  
5'- GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 716) (SEQ. ID NO: 726)  
5'- GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 717) (SEQ. ID NO: 727)  
5'- GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 718) (SEQ. ID NO: 728)  
5'- GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 719) (SEQ. ID NO: 729)  
5'- GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 720) (SEQ. ID NO: 730)  
5'- GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 721) (SEQ. ID NO: 731)  
5'- GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 722) (SEQ. ID NO: 732)  
5'- GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 723) (SEQ. ID NO: 733)  
5'- GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 724) (SEQ. ID NO: 734)  
5'- GGA GGG CGG CAT GGC GGG CA-3' (FRAG 725) (SEQ. ID NO: 735)  
5'- GGA GGG CGG CAT GGC GGG C-3' (FRAG 726) (SEQ. ID NO: 736)  
5'- GGA GGG CGG CAT GGC GGG -3' (FRAG 727) (SEQ. ID NO: 737)  
5'- GGA GGG CGG CAT GGC GG-3' (FRAG 728) (SEQ. ID NO: 738)  
5'- GGA GGG CGG CAT GGC G-3' (FRAG 729) (SEQ. ID NO: 739)  
5'- GGA GGG CGG CAT GGC -3' (FRAG 730) (SEQ. ID NO: 740)  
5'- GGA GGG CGG CAT GG -3' (FRAG 731) (SEQ. ID NO: 741)  
5'- GGA GGG CGG CAT G -3' (FRAG 732) (SEQ. ID NO: 742)  
5'- GGA GGG CGG CAT -3' (FRAG 733) (SEQ. ID NO: 743)  
5'- GGA GGG CGG CA-3' (FRAG 734) (SEQ. ID NO: 744)  
5'- GGA GGG CGG C-3' (FRAG 735) (SEQ. ID NO: 745)  
5'- GA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 736) (SEQ. ID NO: 746)  
5'- GA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 737) (SEQ. ID NO: 747)  
5'- GA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 738) (SEQ. ID NO: 748)  
5'- GA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 739) (SEQ. ID NO: 749)  
5'- GA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 740) (SEQ. ID NO: 750)  
5'- GA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 741) (SEQ. ID NO: 751)  
5'- GA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 742) (SEQ. ID NO: 752)  
5'- GA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 743) (SEQ. ID NO: 753)  
5'- GA GGG CGG CAT GGC GGG CAC A-3' (FRAG 744) (SEQ. ID NO: 754)  
5'- GA GGG CGG CAT GGC GGG CAC-3' (FRAG 745) (SEQ. ID NO: 755)  
5'- GA GGG CGG CAT GGC GGG CA-3' (FRAG 746) (SEQ. ID NO: 756)  
5'- GA GGG CGG CAT GGC GGG C-3' (FRAG 747) (SEQ. ID NO: 757)  
5'- GA GGG CGG CAT GGC GGG -3' (FRAG 748) (SEQ. ID NO: 758)  
5'- GA GGG CGG CAT GGC GG-3' (FRAG 749) (SEQ. ID NO: 759)  
5'- GA GGG CGG CAT GGC G-3' (FRAG 750) (SEQ. ID NO: 760)  
5'- GA GGG CGG CAT GGC -3' (FRAG 751) (SEQ. ID NO: 761)  
5'- GA GGG CGG CAT GG -3' (FRAG 752) (SEQ. ID NO: 762)  
5'- GA GGG CGG CAT G -3' (FRAG 753) (SEQ. ID NO: 763)  
5'- GA GGG CGG CAT -3' (FRAG 754) (SEQ. ID NO: 764)  
5'- GA GGG CGG CA-3' (FRAG 755) (SEQ. ID NO: 765)  
5'- A GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 756) (SEQ. ID NO: 766)  
5'- A GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 757) (SEQ. ID NO: 767)

- 5'- A GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 758) (SEQ. ID NO: 768)  
5'- A GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 759) (SEQ. ID NO: 769)  
5'- A GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 760) (SEQ. ID NO: 770)  
5'- A GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 761) (SEQ. ID NO: 771)  
5'- A GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 762) (SEQ. ID NO: 772)  
5'- A GGG CGG CAT GGC GGG CAC AG-3' (FRAG 763) (SEQ. ID NO: 773)  
5'- A GGG CGG CAT GGC GGG CAC A-3' (FRAG 764) (SEQ. ID NO: 774)  
5'- A GGG CGG CAT GGC GGG CAC-3' (FRAG 765) (SEQ. ID NO: 775)  
5'- A GGG CGG CAT GGC GGG CA-3' (FRAG 766) (SEQ. ID NO: 776)  
5'- A GGG CGG CAT GGC GGG C-3' (FRAG 767) (SEQ. ID NO: 777)  
5'- A GGG CGG CAT GGC GGG -3' (FRAG 768) (SEQ. ID NO: 778)  
5'- A GGG CGG CAT GGC GG-3' (FRAG 769) (SEQ. ID NO: 779)  
5'- A GGG CGG CAT GGC G-3' (FRAG 770) (SEQ. ID NO: 780)  
5'- A GGG CGG CAT GGC -3' (FRAG 771) (SEQ. ID NO: 781)  
5'- A GGG CGG CAT GG -3' (FRAG 772) (SEQ. ID NO: 782)  
5'- A GGG CGG CAT G -3' (FRAG 773) (SEQ. ID NO: 783)  
5'- A GGG CGG CAT -3' (FRAG 774) (SEQ. ID NO: 784)  
5'- GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 775) (SEQ. ID NO: 785)  
5'- GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 776) (SEQ. ID NO: 786)  
5'- GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 777) (SEQ. ID NO: 787)  
5'- GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 778) (SEQ. ID NO: 788)  
5'- GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 779) (SEQ. ID NO: 789)  
5'- GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 780) (SEQ. ID NO: 790)  
5'- GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 781) (SEQ. ID NO: 791)  
5'- GGG CGG CAT GGC GGG CAC AG-3' (FRAG 782) (SEQ. ID NO: 792)  
5'- GGG CGG CAT GGC GGG CAC A-3' (FRAG 783) (SEQ. ID NO: 793)  
5'- GGG CGG CAT GGC GGG CAC-3' (FRAG 784) (SEQ. ID NO: 794)  
5'- GGG CGG CAT GGC GGG CA-3' (FRAG 785) (SEQ. ID NO: 795)  
5'- GGG CGG CAT GGC GGG C-3' (FRAG 786) (SEQ. ID NO: 796)  
5'- GGG CGG CAT GGC GGG -3' (FRAG 787) (SEQ. ID NO: 797)  
5'- GGG CGG CAT GGC GG-3' (FRAG 788) (SEQ. ID NO: 798)  
5'- GGG CGG CAT GGC G-3' (FRAG 789) (SEQ. ID NO: 799)  
5'- GGG CGG CAT GGC -3' (FRAG 790) (SEQ. ID NO: 800)  
5'- GGG CGG CAT GG -3' (FRAG 791) (SEQ. ID NO: 801)  
5'- GGG CGG CAT G -3' (FRAG 792) (SEQ. ID NO: 802)  
5'- GG CGG CAT GGC GGG CAC AG G CTG GGC-3' (FRAG 793) (SEQ. ID NO: 803)  
5'- GG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 794) (SEQ. ID NO: 804)  
5'- GG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 795) (SEQ. ID NO: 805)  
5'- GG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 796) (SEQ. ID NO: 806)  
5'- GG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 797) (SEQ. ID NO: 807)  
5'- GG CGG CAT GGC GGG CAC AGG C-3' (FRAG 798) (SEQ. ID NO: 808)  
5'- GG CGG CAT GGC GGG CAC AGG -3' (FRAG 799) (SEQ. ID NO: 809)  
5'- GG CGG CAT GGC GGG CAC AG-3' (FRAG 800) (SEQ. ID NO: 810)  
5'- GG CGG CAT GGC GGG CAC A-3' (FRAG 801) (SEQ. ID NO: 811)  
5'- GG CGG CAT GGC GGG CAC-3' (FRAG 802) (SEQ. ID NO: 812)  
5'- GG CGG CAT GGC GGG CA-3' (FRAG 803) (SEQ. ID NO: 813)  
5'- GG CGG CAT GGC GGG C-3' (FRAG 804) (SEQ. ID NO: 814)  
5'- GG CGG CAT GGC GGG -3' (FRAG 805) (SEQ. ID NO: 815)  
5'- GG CGG CAT GGC GG-3' (FRAG 806) (SEQ. ID NO: 816)  
5'- GG CGG CAT GGC G-3' (FRAG 807) (SEQ. ID NO: 817)  
5'- GG CGG CAT GGC -3' (FRAG 808) (SEQ. ID NO: 818)  
5'- GG CGG CAT GG -3' (FRAG 809) (SEQ. ID NO: 819)  
5'- G CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 810) (SEQ. ID NO: 820)  
5'- G CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 811) (SEQ. ID NO: 821)  
5'- G CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 812) (SEQ. ID NO: 822)  
5'- G CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 813) (SEQ. ID NO: 823)  
5'- G CGG CAT GGC GGG CAC AGG CT-3' (FRAG 814) (SEQ. ID NO: 824)  
5'- G CGG CAT GGC GGG CAC AGG C-3' (FRAG 815) (SEQ. ID NO: 825)  
5'- G CGG CAT GGC GGG CAC AGG -3' (FRAG 816) (SEQ. ID NO: 826)  
5'- G CGG CAT GGC GGG CAC AG-3' (FRAG 817) (SEQ. ID NO: 827)  
5'- G CGG CAT GGC GGG CAC A-3' (FRAG 818) (SEQ. ID NO: 828)  
5'- G CGG CAT GGC GGG CAC-3' (FRAG 819) (SEQ. ID NO: 829)  
5'- G CGG CAT GGC GGG CA-3' (FRAG 820) (SEQ. ID NO: 830)  
5'- G CGG CAT GGC GGG C-3' (FRAG 821) (SEQ. ID NO: 831)  
5'- G CGG CAT GGC GGG -3' (FRAG 822) (SEQ. ID NO: 832)  
5'- G CGG CAT GGC GG-3' (FRAG 823) (SEQ. ID NO: 833)  
5'- G CGG CAT GGC G-3' (FRAG 824) (SEQ. ID NO: 834)  
5'- G CGG CAT GGC -3' (FRAG 825) (SEQ. ID NO: 835)  
5'- CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 826) (SEQ. ID NO: 836)



5'- CGG CAT GGC CAC AGG CTG GG-3' (FRAG 827) (SEQ. ID NO: 837)  
5'- CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 828) (SEQ. ID NO: 838)  
5'- CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 829) (SEQ. ID NO: 839)  
5'- CGG CAT GGC GGG CAC AGG CT-3' (FRAG 830) (SEQ. ID NO: 840)  
5'- CGG CAT GGC GGG CAC AGG C-3' (FRAG 831) (SEQ. ID NO: 841)  
5'- CGG CAT GGC GGG CAC AGG -3' (FRAG 832) (SEQ. ID NO: 842)  
5'- CGG CAT GGC GGG CAC AG-3' (FRAG 833) (SEQ. ID NO: 843)  
5'- CGG CAT GGC GGG CAC A-3' (FRAG 834) (SEQ. ID NO: 844)  
5'- CGG CAT GGC GGG CAC-3' (FRAG 835) (SEQ. ID NO: 845)  
5'- CGG CAT GGC GGG CA-3' (FRAG 836) (SEQ. ID NO: 846)  
5'- CGG CAT GGC GGG C-3' (FRAG 837) (SEQ. ID NO: 847)  
5'- CGG CAT GGC GGG -3' (FRAG 838) (SEQ. ID NO: 848)  
5'- CGG CAT GGC GG-3' (FRAG 839) (SEQ. ID NO: 849)  
5'- CGG CAT GGC G-3' (FRAG 840) (SEQ. ID NO: 850)  
5'- GG CAT GGC GGG CAC AGG C TG GGC-3' (FRAG 841) (SEQ. ID NO: 851)  
5'- GG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 842) (SEQ. ID NO: 852)  
5'- GG CAT GGC GGG CAC AGG CTG G-3' (FRAG 843) (SEQ. ID NO: 853)  
5'- GG CAT GGC GGG CAC AGG CTG -3' (FRAG 844) (SEQ. ID NO: 854)  
5'- GG CAT GGC GGG CAC AGG CT-3' (FRAG 845) (SEQ. ID NO: 855)  
5'- GG CAT GGC GGG CAC AGG C-3' (FRAG 846) (SEQ. ID NO: 856)  
5'- GG CAT GGC GGG CAC AGG -3' (FRAG 847) (SEQ. ID NO: 857)  
5'- GG CAT GGC GGG CAC AG-3' (FRAG 848) (SEQ. ID NO: 858)  
5'- GG CAT GGC GGG CAC A-3' (FRAG 849) (SEQ. ID NO: 859)  
5'- GG CAT GGC GGG CAC-3' (FRAG 850) (SEQ. ID NO: 860)  
5'- GG CAT GGC GGG CA-3' (FRAG 851) (SEQ. ID NO: 861)  
5'- GG CAT GGC GGG C-3' (FRAG 852) (SEQ. ID NO: 862)  
5'- GG CAT GGC GGG -3' (FRAG 853) (SEQ. ID NO: 863)  
5'- GG CAT GGC GG-3' (FRAG 854) (SEQ. ID NO: 864)  
5'- G CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 855) (SEQ. ID NO: 865)  
5'- G CAT GGC GGG CAC AGG CTG GG-3' (FRAG 856) (SEQ. ID NO: 866)  
5'- G CAT GGC GGG CAC AGG CTG G-3' (FRAG 857) (SEQ. ID NO: 867)  
5'- G CAT GGC GGG CAC AGG CTG -3' (FRAG 858) (SEQ. ID NO: 868)  
5'- G CAT GGC GGG CAC AGG CT-3' (FRAG 859) (SEQ. ID NO: 869)  
5'- G CAT GGC GGG CAC AGG C-3' (FRAG 860) (SEQ. ID NO: 870)  
5'- G CAT GGC GGG CAC AGG -3' (FRAG 861) (SEQ. ID NO: 871)  
5'- G CAT GGC GGG CAC AG-3' (FRAG 862) (SEQ. ID NO: 872)  
5'- G CAT GGC GGG CAC A-3' (FRAG 863) (SEQ. ID NO: 873)  
5'- G CAT GGC GGG CAC-3' (FRAG 864) (SEQ. ID NO: 874)  
5'- G CAT GGC GGG CA-3' (FRAG 865) (SEQ. ID NO: 875)  
5'- G CAT GGC GGG C-3' (FRAG 866) (SEQ. ID NO: 876)  
5'- G CAT GGC GGG -3' (FRAG 867) (SEQ. ID NO: 877)  
5'- CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 868) (SEQ. ID NO: 878)  
5'- CAT GGC GGG CAC AGG CTG GG-3' (FRAG 869) (SEQ. ID NO: 879)  
5'- CAT GGC GGG CAC AGG CTG G-3' (FRAG 870) (SEQ. ID NO: 880)  
5'- CAT GGC GGG CAC AGG CTG -3' (FRAG 871) (SEQ. ID NO: 881)  
5'- CAT GGC GGG CAC AGG CT-3' (FRAG 872) (SEQ. ID NO: 882)  
5'- CAT GGC GGG CAC AGG C-3' (FRAG 873) (SEQ. ID NO: 883)  
5'- CAT GGC GGG CAC AGG -3' (FRAG 874) (SEQ. ID NO: 884)  
5'- CAT GGC GGG CAC AG-3' (FRAG 875) (SEQ. ID NO: 885)  
5'- CAT GGC GGG CAC A-3' (FRAG 876) (SEQ. ID NO: 886)  
5'- CAT GGC GGG CAC-3' (FRAG 877) (SEQ. ID NO: 887)  
5'- CAT GGC GGG CA-3' (FRAG 878) (SEQ. ID NO: 888)  
5'- CAT GGC GGG C-3' (FRAG 879) (SEQ. ID NO: 889)  
5'- AT GGC GGG CAC AGG CTG GGC-3' (FRAG 880) (SEQ. ID NO: 890)  
5'- AT GGC GGG CAC AGG CTG GG-3' (FRAG 881) (SEQ. ID NO: 891)  
5'- AT GGC GGG CAC AGG CTG G-3' (FRAG 882) (SEQ. ID NO: 892)  
5'- AT GGC GGG CAC AGG CTG -3' (FRAG 883) (SEQ. ID NO: 893)  
5'- AT GGC GGG CAC AGG CT-3' (FRAG 884) (SEQ. ID NO: 894)  
5'- AT GGC GGG CAC AGG C-3' (FRAG 885) (SEQ. ID NO: 895)  
5'- AT GGC GGG CAC AGG -3' (FRAG 886) (SEQ. ID NO: 896)  
5'- AT GGC GGG CAC AG-3' (FRAG 887) (SEQ. ID NO: 897)  
5'- AT GGC GGG CAC A-3' (FRAG 888) (SEQ. ID NO: 898)  
5'- AT GGC GGG CAC-3' (FRAG 889) (SEQ. ID NO: 899)  
5'- AT GGC GGG CA-3' (FRAG 890) (SEQ. ID NO: 900)  
5'- T GGC GGG CAC AGG CTG GGC-3' (FRAG 891) (SEQ. ID NO: 901)  
5'- T GGC GGG CAC AGG CTG GG-3' (FRAG 892) (SEQ. ID NO: 902)  
5'- T GGC GGG CAC AGG CTG G-3' (FRAG 893) (SEQ. ID NO: 903)  
5'- T GGC GGG CAC AGG CTG -3' (FRAG 894) (SEQ. ID NO: 904)

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5'- T GGC GGG CAC AGG C-3' (FRAG 896) (SEQ. ID NO: 906)  
5'- T GGC GGG CAC AGG -3' (FRAG 897) (SEQ. ID NO: 907)  
5'- T GGC GGG CAC AG-3' (FRAG 898) (SEQ. ID NO: 908)  
5'- T GGC GGG CAC A-3' (FRAG 899) (SEQ. ID NO: 909)  
5'- T GGC GGG CAC-3' (FRAG 900) (SEQ. ID NO: 910)  
5'- GGC GGG CAC AGG CTG GGC-3' (FRAG 901) (SEQ. ID NO: 911)  
5'- GGC GGG CAC AGG CTG GG-3' (FRAG 902) (SEQ. ID NO: 912)  
5'- GGC GGG CAC AGG CTG G-3' (FRAG 903) (SEQ. ID NO: 913)  
5'- GGC GGG CAC AGG CTG -3' (FRAG 904) (SEQ. ID NO: 914)  
5'- GGC GGG CAC AGG CT-3' (FRAG 905) (SEQ. ID NO: 915)  
5'- GGC GGG CAC AGG C-3' (FRAG 906) (SEQ. ID NO: 916)  
5'- GGC GGG CAC AGG -3' (FRAG 907) (SEQ. ID NO: 917)  
5'- GGC GGG CAC AG-3' (FRAG 908) (SEQ. ID NO: 918)  
5'- GGC GGG CAC A-3' (FRAG 909) (SEQ. ID NO: 919)  
5'- GC GGG CAC AGG CTG GGC-3' (FRAG 910) (SEQ. ID NO: 920)  
5'- GC GGG CAC AGG CTG GG-3' (FRAG 911) (SEQ. ID NO: 921)  
5'- GC GGG CAC AGG CTG G-3' (FRAG 912) (SEQ. ID NO: 922)  
5'- GC GGG CAC AGG CTG -3' (FRAG 913) (SEQ. ID NO: 923)  
5'- GC GGG CAC AGG CT-3' (FRAG 914) (SEQ. ID NO: 924)  
5'- GC GGG CAC AGG C-3' (FRAG 915) (SEQ. ID NO: 925)  
5'- GC GGG CAC AGG -3' (FRAG 916) (SEQ. ID NO: 926)  
5'- GC GGG CAC AG-3' (FRAG 917) (SEQ. ID NO: 927)  
5'- C GGG CAC AGG CTG GGC-3' (FRAG 918) (SEQ. ID NO: 928)  
5'- GGG CAC AGG CTG GG-3' (FRAG 919) (SEQ. ID NO: 929)  
5'- C GGG CAC AGG CTG G-3' (FRAG 920) (SEQ. ID NO: 930)  
5'- C GGG CAC AGG CTG -3' (FRAG 921) (SEQ. ID NO: 931)  
5'- C GGG CAC AGG CT-3' (FRAG 922) (SEQ. ID NO: 932)  
5'- C GGG CAC AGG C-3' (FRAG 923) (SEQ. ID NO: 933)  
5'- C GGG CAC AGG -3' (FRAG 924) (SEQ. ID NO: 934)  
5'- GGG CAC AGG CTG GGC-3' (FRAG 925) (SEQ. ID NO: 935)  
5'- GGG CAC AGG CTG GG-3' (FRAG 926) (SEQ. ID NO: 936)  
5'- GGG CAC AGG CTG G-3' (FRAG 927) (SEQ. ID NO: 937)  
5'- GGG CAC AGG CTG -3' (FRAG 928) (SEQ. ID NO: 938)  
5'- GGG CAC AGG CT-3' (FRAG 929) (SEQ. ID NO: 939)  
5'- GGG CAC AGG C-3' (FRAG 930) (SEQ. ID NO: 940)  
5'- GG CAC AGG CTG GGC-3' (FRAG 931) (SEQ. ID NO: 941)  
5'- GG CAC AGG CTG GG-3' (FRAG 932) (SEQ. ID NO: 942)  
5'- GG CAC AGG CTG G-3' (FRAG 933) (SEQ. ID NO: 943)  
5'- GG CAC AGG CTG -3' (FRAG 934) (SEQ. ID NO: 944)  
5'- GG CAC AGG CT-3' (FRAG 935) (SEQ. ID NO: 945)  
5'- G CAC AGG CTG GGC-3' (FRAG 936) (SEQ. ID NO: 946)  
5'- G CAC AGG CTG GG-3' (FRAG 937) (SEQ. ID NO: 947)  
5'- G CAC AGG CTG G-3' (FRAG 938) (SEQ. ID NO: 948)  
5'- G CAC AGG CTG -3' (FRAG 939) (SEQ. ID NO: 949)  
5'- CAC AGG CTG GGC-3' (FRAG 940) (SEQ. ID NO: 950)  
5'- CAC AGG CTG GG-3' (FRAG 941) (SEQ. ID NO: 951)  
5'- CAC AGG CTG G-3' (FRAG 942) (SEQ. ID NO: 952)  
5'- AC AGG CTG GGC-3' (FRAG 943) (SEQ. ID NO: 953)  
5'- AC AGG CTG GG-3' (FRAG 944) (SEQ. ID NO: 954)  
5'- C AGG CTG GGC-3' (FRAG 945) (SEQ. ID NO: 955)  
5'- TTT TCC TTC CTT TGT CTC TCT TC (FRAG 946) (SEQ. ID NO: 956)  
5'- GCT CCC GGC TGC CTG (FRAG 947) (SEQ. ID NO: 957)  
5'- CTC GGC CGT GCG GCT CTG TCG CTC CCG GT (FRAG 948) (SEQ. ID NO: 958)  
5'- CCG CCG CCC TCC GGG GGG TC (FRAG 949) (SEQ. ID NO: 959)  
5'- TGC TGC CGT TGG CTG CCC (FRAG 950) (SEQ. ID NO: 960)  
5'- CTT CTG CGG GTC GCC GG (FRAG 951) (SEQ. ID NO: 961)  
5'- TGC TGG GCT TGT GGC (FRAG 952) (SEQ. ID NO: 962)  
5'- GGC CTC TCT TCT GGG (FRAG 953) (SEQ. ID NO: 963)  
5'- CCT GGT CCC TCC GT (FRAG 954) (SEQ. ID NO: 964)  
5'- GGT GGC TCC TCT GC (FRAG 955) (SEQ. ID NO: 965)  
5'- GCT TGG TCC TGG GGC TGC (FRAG 956) (SEQ. ID NO: 966)  
5'- TGC TCT CCT CTC CTT (FRAG 957) (SEQ. ID NO: 967)

#### Human Adenosine A2a Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-TGC TTT TCT TTT CTG GGC CTC TGT GGT CTG TTT TTT TCT G GCC CTG CTG GGG CGC TCT CC GCC GCC CGC CTG  
GCT CCC GGB GCC CBT GBT GGG CBT GCC GTG GTT CTT GCC CTC CTT TGG CTG CCG TGC CCG CTC CCC GGC CTC CTG  
GCG GGT GGC CGT TG GGC CCG TGT TCC CCT GGG -GCC TGG GGC TCC CTT CTC TC GCC CTT CTT GCT GGG CCT C TGC  
TGC TGC TGG TGC TGT GGC CCC C GTA CAC CGA GGA GCC CAT GAT GGG CAT GCC ACA GAC GAC AGG C GTB CBC  
CGB GGB GCC CBT GBT GGG CBT GCC BCB GBC GBC BGG C-3' (FRAG. NO. 1665) (SEQ. ID NO:1678)  
5'-CTG GGC CTC-3' (FRAG 1666) (SEQ. ID NO: 1679)

5'-GCC GCC CGC CTG-3' (FRAG 1667) (SEQ. ID NO: 1680)  
5'-GC CCG CTC CCC GGC-3' (FRAG 1668) (SEQ. ID NO: 1681)  
5'-CBCCGGBGGGCC-3' (FRAG 1669) (SEQ. ID NO: 1682)  
5'-TGC TTT TCT TTT CTG GGC CTC-3' (FRAG 958) (SEQ. ID NO: 968)  
5'-TGT GGT CTG TTT TTT TCT G-3' (FRAG 959) (SEQ. ID NO: 969)  
5'-GCC CTG CTG GGG CGC TCT CC-3' (FRAG 960) (SEQ. ID NO: 970)  
5'-GCC GCC CGC CTG GCT CCC-3' (FRAG 961) (SEQ. ID NO: 971)  
5'-GGB GCC CBT GBT GGG CBT GCC-3' (FRAG 962) (SEQ. ID NO: 972)  
5'-GTG GTT CTT GCC CTC CTT TGG CTG-3' (FRAG 963) (SEQ. ID NO: 973)  
5'-CCG TGC CCG CTC CCC GGC-3' (FRAG 964) (SEQ. ID NO: 974)  
5'-CTC CTG GCG GGT GGC CGT TG-3' (FRAG 965) (SEQ. ID NO: 975)  
5'-GGC CCG TGT TCC CCT GGG-3' (FRAG 966) (SEQ. ID NO: 976)  
5'-GCC TGG GGC TCC CTT CTC TC-3' (FRAG 967) (SEQ. ID NO: 977)  
5'-GCC CTT CTT GCT GGG CCT C-3' (FRAG 968) (SEQ. ID NO: 978)  
5'-TGC TGC TGC TGG TGC TGT GGC CCC C-3' (FRAG 969) (SEQ. ID NO: 979)  
5'-GTACACCGAGGAGCCCATGATGGGCATGCCACAGACGACAGGC-3' (FRAG 970) (SEQ. ID NO: 980)  
5'-GTBCCCGGBGGGCCBTGTTGGGCBTGCBCBGBCBGGC-3' (FRAG 971) (SEQ. ID NO: 981)

### Human Adenosine A2b Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GGC GCC GTG CCG CGT CTT GGT GGC GGC GG GTT CGC GCC CGC GCG GGG CCC CTC CGG TCC GTT CGC GCC CGC  
GCG GGG CCC CTC CGG TCC CGG GTC GGG GCC CCC CGC GGC C GCC TCG GGG CTG GGG CGC TGG TGG CCG GG CCG  
CGC CTC CGC CTG CCG CTT CTG GCT GGG CCC CGG GCG CCC CCT CCC CTC TTG CTC GGG TCC CCG TG ACA GCG CGT  
CCT GTG TCT CCA GCA GCA TGG CCG GGC CAG CTG GGC CCC BCB GCG CGT CCT GTG TCT CCB GCB GCB TGG CCG  
GGC CBG CTG GGC CCC CCCAGCCCCG AGGCTCAGAA GCGGCAGCGG GAGGCGCGGT CCGGGCGCTA TGGCCATGCC  
CGGCGGGTCT CACGCGGCTG CCCCTCGCCC GCGCGCCCTT CGGTAGGGGG CGCCCGGGGC CCAGCTGGGC CGGCCATGCT  
GCTGGAGACA CAGGACGCGC TGTACGTGGC GCTGGAGCTG GTCATCGCCG CGCTTTCGGT GCGGGGCAAC GTGCTGGTGT  
GCGCCGCGGT GGGCACGGCG AACACTCTGC AGACGCCAC CAACTACTTC CTGGTGTCCC TGGCTGCGGC CGACGTGGCC  
GTGGGGCTCT TCGCCATCCC CTTTGCCATC ACCATCAGCC TGGGCTTCTG CACTGACTTC TACGGCTGCC TCTTCCTCGC  
CTGCTTCGTG CTGGTGCTCA CGCAGAGCTC CATCTTCAGC CTCTGGCCG TGGCAGTCGA CAGATACCTG GCCATCTGTG  
TCCCGCTCAG GTATAAAAGT TTGGTCACGG GGACCCGAGC AAGAGGGGTC ATTGCTGTCC TCTGGGTCTT TGCTTTGGC  
ATCGGATTGA CTCCATTCCT GGGGTGGAAC AGTAAAGACA GTGCCACCAA CAATGCACA GAACCCTGGG ATGGAACCAC  
GAATGAAAGC TGCTGCCTTG TGAAGTGTCT CTTGAGAAT GTGGTCCCA TGAGCTACAT GGTATATTTC AATTCTTTG  
GGTGTGTTCT GCCCCACTG CTTATAATGC TGGTGATCTA CATTAAAGATC TTCTGGTGG CCTGCAGGCA GCTTCAGCGC  
ACTGAGCTGA TGGACCACTC GAGGACCACC CTCCAGCGGG AGATCCATGC AGCCAAGTCA CTGGCCATGA TTGTGGGGAT  
TTTTGCCCTG TGCTGGTTAC CTGTGCATGC TGTTAACTGT GTCACTCTT TCCAGCCAGC TCAGGGTAAA AATAAGCCCA  
AGTGGGCAAT GAATATGGCC ATTCTTCTGT CACATGCCAA TTCAGTGTG AATCCCATG TCTATGCTTA CCGGAACCGA  
GACTTCGGCT AACTTTTCA CAAAATTATC TCCAGGTATC TTCTCTGCCA AGCAGATGTC AAGAGTGGGA ATGGTCAGGC  
TGGGGTACAG CTGCTCTCG GTGTGGGCT ATGATCTAGG CTCTCGCTC TTCCAGGAGA AGATACAAAT CCACAAGAAA  
CAAAGAGGAC ACGGCTGGTT TTCAATTGTA AAGATAGCTA CACCTCACA GGAAATGGAC TGCCTCTCTT GAGCACTTCC  
CTGGAGCTAC CACGTATCTA GCTAATATGT ATGTGTCAGT AGTAGACCA AGGATTGACA AATATATTTA TGATCTATT  
AGCTGCTTTT ACTGTGTGGA TTATGCCAAC AGCTTGAATG GATTCTAACA GACTCTTTT TTTTAAAAG TCTGCCTTGT  
TTATGGTGGA AAATACTGA AACTATTTTA CTGTGAAACA GTGTGAACTA TTATAATGCA AATACTTTT AACTTAGAGG  
CAATGAAAA ATAAAAGTTG ACTGTACTAA AAATGTATAC TTGTGCCAG GAAGGTGACC TCAAAAATTA AAAGTATAAT  
TATTCGGCCG GGCATGGTGG CTCACACCTG TAATTCAGC ACTTTGGGAG GCCAAGGCAG GCGGATCAG AGGTCAGGAG  
TTCAAAACCA GCCTGTCCAA TATAGTG GGGCAATTTG TTAGTTATCC GCCGCCACCA AGACGCGGCA CGGCGCCTGG  
ACCGGAGGGG CCGCGCGCG GCGCGAATT TGGGCTCGGG CGAGTGGGTG GTGCTCCGCC CAGCCCGAGA CGGGCGGGCG  
CGCGGGCCAA TGGGTGCCG CTCTTGCCG CGGGGGGCC CGACCCGTGG GTCCCGGCCA CCAGCGCCCC AGCCCCGAGG  
CTCAGAAGCG GCAGGCGGAG GCGCGGTCCG GCGCTATGG CCATGCCCGG CGGGTCTCAC GCGGCTGCCC CTCGCCCGG  
GCGCTTCGG TAGGGGGCGC CCGGGGCCA GCTGGCCCG CCATGCTGCT GGAGACACAG GACGCGCTGT ACGTGGCGCT  
GGAGCTGGTC ATCGCCGCGC TTTCGGTGGC GGGCAACGTG CTGGTGTGCG CCGCGGTGGG CACGGCGAAC ACTCTGCAGA  
CGCCACCAA CTACTTCTG GTGTCCCTGG CTGCGGCCGA CGTGGCCGTG GGGCTCTTCG CCATCCCCIT TGCCATCACC  
ATCAGCCTGG GCTTCTGCAC TGACTTCTAC GGCTGCTCT TCCTCGCTG CTTCGTGCTG GTGCTCACGC AGAGCTCCAT  
CTTCAGCCTT CTGGCCGTGG CAGTCGACAG ATACCTGGCC ATCTGTGTCC CGCTCAGGTA TAAAAGTTTG GTCACGGGGA

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ATG CCCAGCCCCG AGGCTCAGAA GCGGCAGGCG GAGGCGCGGT CCGGGCGCTA TGGCCATGCC CGGCGGGTCT  
CACGCGGGTG CCCCTCGCCC GGCGCGCCTT CGGTAGGGGG CGCCCGGGGC CCAGCTGGCC CGGCCATGCT GCTGGAGACA  
CAGGACGCGC TGTACGTGGC GCTGGAGCTG GTCATCGCCG CGCTTTCGGT GGCGGGCAAC GTGCTGGTGT GCGCCGCGGT  
GGGACGCGCG AACACTCTGC AGACGCCCCA CAACTACTTC CTGGTGTCCC TGGCTGCGGC CGACGTGGCC GTGGGGCTCT  
TCGCCATCCC CTTTGCCATC ACCATCAGCC TGGGCTTCTG CACTGACTTC TACGGCTGCC TTCTCTCGC CTGCTTCGTG  
CTGGTGCTCA CGCAGAGCTC CATCTCAGC CTCTGGCCG TGGCAGTCGA CAGATACCTG GCCATCTGTG TCCCGCTCAG  
GTATAAAAGT TTGGTCACGG GGACCCGAGC AAGAGGGGTC ATTGCTGTCC TCTGGTCTCT TGCCTTTGGC ATCGGATTGA  
CTCCATTCTT GGGGTGGAAC AGTAAAGACA GTGCCACCA CAACTGCACA GAACCTGGG ATGGAACCAC GAATGAAAGC  
TGCTGCCTTG TGAAGTGTCT CTTTGAGAAT GTGGTCCCA TGAGCTACAT GGTATATTTC AATTCTTTG GGTGTGTCT  
GCCCCACTG CTATAATGC TGGTGATCTA CATTAAAGATC TTCTGGTGG CCTGCAGGCA GCTTCAGCGC ACTGAGCTGA  
TGGACCACTC GAGGACCACC CTCCAGCGGG AGATCCATGC AGCCAAGTCA CTGGCCATGA TTGTGGGGAT TTTTGCCTG  
TGCTGGTTAC CTGTGCATGC TGTTAACTGT GTCACTCTTT TCCAGCCAGC TCAGGGTAAA AATAAGCCCA AGTGGGCAAT  
GAATATGGCC ATTCTTCTGT CACATGCCAA TTCAGTTGTC AATCCCATTT TCTATGCTTA CCGGAACCGA GACTTCCGCT  
ACACTTTTCA CAAAATTATC TCCAGGTATC TTCTTGCCA AGCAGATGTC AAGAGTGGGA ATGGTCAGGC TGGGGTACAG  
CTGCTCTCG GTGTGGGCTT ATGATCTAGG CTCTCGCCTC TTCCAGGAGA AGATACAAAT CCACAAGAAA CAAAGAGGAC  
ACGGCTGGTT TTCATTGTGA AAGATAGCTA CACCTCACA GGAATGGAC TGCCTCTCTT GAGCACTTCC CTGGAGCTAC  
CACGTATCTA GCTAATATGT ATGTGTCAGT AGTAGCACA AGGATTGACA AATATATTTA TGATCTATTC AGCTGCTTTT  
ACTGTGTGGA TTATGCCAAC AGCTTGAATG GATTCTAACA GACTCTTTT TTTTAAAAG TCTGCTTGT TTATGGTGA  
AAATTACTGA AACTATTTTA CTGTGAAACA GTGTGAAC TAATAATGCA AATACTTTTT AACTAGAGG CAATGGAAAA  
ATAAAAGTTG ACTGTACTAA AAATGTATAC TTGTGCCAG GAAGGTGACC TCAAAAATTA AAAGTATAAT TATTCGCGC  
GGCATGGTGG CTCACACCTG TAATCCAGC ACTTTGGGAG GCCAAGGCAG GCGGATCAG AGGTCAGGAG TTCAAACCA  
GCCTGTCCAA TATAGTG GGGCAATTG TTAGTTATCC GCCGCCACA AGACGCGGA CCGGCGCTGG ACCGGAGGGG  
CCCCGCGCGG GCGGAACCTT TGGGCTCGGG CGAGTGGGTG GTGCTCCGCC CAGCCGAGA CGGCGGGCG CCGCGGCCAA  
TGGGTGCCG CTCTGGCGG CGGGGGGCCC CGACCCGTGG GTCCCGGCCA CCAGCGCCCC AGCCCCGAGG CTCAGAAGCG  
GCAGGCGGAG GCGCGGTCCG GCGCTATGG CCATGCCCGG CGGGTCTCAC GCGGTGCCC CTCGCCCCGG CCGCCTTCGG  
TAGGGGGCGC CCGGGGCCCA GCTGGCCCGG CCATGCTGCT GGAGACACAG GACGCGCTGT ACGTGGCGCT GGAGCTGGT  
ATCGCCGCGC TTTGGTGGC GGGCAACGTG CTGGTGTGG CCGCGGTGG CACGGCGAAC ACTCTGCAGA CGCCACCAA  
CTACTTCTG GTGTCCCTG CTGCGCCGA CGTGGCCGTG GGGCTCTCG CCATCCCTT TGCCATCACC ATCAGCTGG  
GCTTCTGCAC TGACTTCTAC GGCTGCCTCT TCCTCGCTG CTTCGTGCTG GTGCTCACGC AGAGCTCCAT CTTCAGCCTT  
CTGGCCGTGG CAGTCGACAG ATACCTGGCC ATCTGTGTCC CGCTCAGGTA TAAAAGTTG GTCACGGGGA CCCGAGCAAG  
AGGGGTCAAT GCTGTCTCT GGGTCTTGC CTTTGGCATC GGATTGACTC CATTCTGGG GTGGAACAGT AAAGACAGT  
CCACAACAA CTGCACAGAA CCCTGGGATG GAACCACGAA TGAAAGCTGC TGCCTTGTA AGTGTCTCTT TGAGAATGTG  
GTCCCAATGA GTCATGGT ATATTTCAAT TTCTTGGGT GTGTCTGCC CCCACTGCTT ATAATGCTGG TGATCTACAT  
TAAGATCTTC CTGGTGGCT GCAGGCAGCT TCAGCGCACT GAGCTGATGG ACCACTCGAG GACCACCTC CAGCGGGAGA  
TCCATGCAGC CAAGTCACTG GCCATGATTG TGGGGATTTT TGCCCTGTGC TGGTTACCTG TGCATGCTGT TAACTGTGTC  
ACTCTTTTCC AGCCAGCTCA GGGTAAAAAT AAGCCCAAGT GGGCAATGAA TATGGCCATT CTCTGTGAC ATGCCAATTC  
AGTTGTCAAT CCCATTGTCT ATGCTTACCG GAACCGAGAC TTCCGCTACA CTTTTCACAA AATTATCTCC AGGTATCTTC  
TCTGCCAAGC AGATGTCAAG AGTGGGAATG GTCAGGCTGG GGTACAGCCT GCTCTCGGTG TGGGCTATG ATCTAGGCTC  
TCGCTCTTC CAGGAGAAGA TACAAATCCA CAAGAAACAA AGAGGACACG GCTGGTTTTC ATTGTGAAAG ATAGTACAC  
CTCACAAGGA AATGGACTGC CTCTCTTGA CACTTCCCTG GAGCTACCAC GTATCTAGCT AATATGTATG TGTCAAGT  
AGGCTCAAG GATTGACAAA TATATTTATG ATCTATTAG CTGCTTTTAC TGTGTGGATT ATGCCAACAG CTTGAATGGA  
TTCTAACAGA CTCTTTTGT TTTAAAAGTC TGCCTTGTG ATGGTGGAAA ATTACTGAAA CTATTTTACT GTGAAACAGT  
GTGAACTATT ATAATGCAA TACTTTTAA CTTAGAGGCA ATGGA AAAAGTTGAC TGACTAAAA ATG -3' (FRAG.  
NO: 1670) (SEQ. ID NO:1683)

5'- GGGCAATTG TTAGTTATCC GCCGCCACA AGACGCGGA CCGCGCTGG ACCGGAGGG CCGCGCGG  
GCGGAACCT TGGGCTCGGG CGAGTGGGTG GTGCTCCGCC CAGCCGAGA CCGGCGGGCG CCGGGGCCAA TGGGTGCCG  
CTCTGGCCG CGGGGGGCCC CGACCCGTGG GTCCCGGCCA CCAGCGCCCC AGCCCCGAGG CTCAGAAGCG GCAGGCGGAG  
GCGCGGTCCG GCGGCTATGG CCATGCCCGG CGGGTCTCAC GCGGTGCCC CTCGCCCCGG CCGCCTTCGG TAGGGGGCGC  
CCGGGGGCCA GCTGGCCCGG CCATGCTGCT GGAGACACAG GACGCGCTGT ACGTGGCGCT GGAGCTGGT ATCGCCGCGC  
TTTCGGTGGC GGGCAACGTG CTGGTGTGG CCGCGGTGG CACGGCGAAC ACTCTGCAGA CGCCACCAA CTACTTCTG  
GTGTCCTGG CTGCGCCGA CGTGGCCGTG GGGCTCTCG CCATCCCTT TGCCATCACC ATCAGCTGG GCTTCTGCAC  
TGACTTCTAC GGCTGCCTCT TCCTCGCTG CTTCGTGCTG GTGCTCACGC AGAGCTCCAT CTTCAGCCTT CTGGCCGTGG  
CAGTCGACAG ATACCTGGCC ATCTGTGTCC CGCTCAGGTA TAAAAGTTG GTCACGGGGA CCCGAGCAAG AGGGGTCAAT  
GCTGTCTCT GGGTCTTGC CTTTGGCATC GGATTGACTC CATTCTGGG GTGGAACAGT AAAGACAGT CCACAACAA  
CTGCACAGAA CCCTGGGATG GAACCACGAA TGAAAGCTGC TGCCTTGTA AGTGTCTCTT TGAGAATGTG GTCCCATGA  
GCTACATGGT ATATTTCAAT TTCTTGGGT GTGTTCTGCC CCCACTGCTT ATAATGCTGG TGATCTACAT TAAGATCTTC  
CTGGTGGCCT GCAGGCAGCT TCAGCGCACT GAGCTGATGG ACCACTCGAG GACCACCTC CAGCGGGAGA TCCATGCAGC  
CAAGTCACTG GCCATGATTG TGGGGATTTT TGCCCTGTGC TGGTTACCTG TGCATGCTGT TAACTGTGTC ACTCTTTTC  
AGCCAGCTCA GGGTAAAAAT AAGCCCAAGT GGGCAATGAA TATGGCCATT CTCTGTGAC ATGCCAATTC AGTTGTCAAT  
CCCATTGTCT ATGCTTACCG GAACCGAGAC TTCCGCTACA CTTTTCACAA AATTATCTCC AGGTATCTTC TCTGCCAAGC  
AGATGTCAAG AGTGGGAATG GTCAGGCTGG GGTACAGCCT GCTCTCGGTG TGGGCTATG ATCTAGGCTC  
CAGGAGAAGA TACAAATCCA CAAGAAACAA AGAGGACACG GCTGGTTTTC ATTGTGAAAG ATAGTACAC  
AATGGACTGC CTCTCTTGA CACTTCCCTG GAGCTACCAC GTATCTAGCT AATATGTATG TGTCAAGT AGGCTCAAG  
GATTGACAAA TATATTTATG ATCTATTAG CTGCTTTTAC TGTGTGGATT ATGCCAACAG CTTGAATGGA TTCTAACAGA  
CTCTTTTGT TTTAAAAGTC TGCCTTGTG ATGGTGGAAA ATTACTGAAA CTATTTTACT GTGAAACAGT GTGAACTATT  
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NO:2436)

5'- CCCAGCCCCG AGGCTCAGAA GCGGCAGGCG GAGGCGCGGT CCGGGCGCTA TGGCCATGCC CGGCGGGTCT  
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CAGGACGCGC TGTACGTGGC GCTGGAGCTG GTCATCGCCG CGCTTTCGGT GCGGGGCAAC GTGCTGGTGT GCGCCGCGGT  
GGGCACGGCG AACACTCTGC AGACGCCCAC CAACTACTTC CTGGTGTCCC TGGCTGCGGC CGACGTGGCC GTGGGGCTCT  
TCGCCATCCC CTTTGCCATC ACCATCAGCC TGGGCTTCTG CACTGACTTC TACGGGTGCC TCTTCTCGC CTGCTTCGTG  
CTGGTGCTCA CGCAGAGCTC CATCTTCAGC CTCTGGCCG TGGCAGTCGA CAGATACCTG GCCATCTGTG TCCCGCTCAG  
GTATAAAGT TTGGTCACGG GGACCCGAGC AAGAGGGGTC ATTGCTGTCC TCTGGGTCTT TGCCTTTGGC ATCGGATTGA  
CTCCATTCTT GGGGTGGAAC AGTAAAGACA GTGCCACCAA CAACTGCACA GAACCTGGG ATGGAACCAAC GAATGAAAGC  
TGCTGCCTTG TGAAGTGTCT CTTTGAGAAT GTGGTCCCA TGAGCTACAT GGTATATTC AATTTCTTG GGTGTGTTCT  
GCCCCACTG CTTATAATGC TGGTGATCTA CATTAGATC TTCTGTGGT CCTGCAGGCA GCTTCAGCGC ACTGAGCTGA  
TGGACCACTC GAGGACCACC CTCCAGCGGG AGATCCATGC AGCCAAGTCA CTGGCCATGA TTGTGGGGAT TTTTGCCCTG  
TGCTGGTAC CTGTGCATGC TGTTAACTGT GTCATCTTT TCCAGCCAGC TCAGGGTAAA AATAAGCCCA AGTGGGCAAT  
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5'- GGGCAATTTG TTAGTTATCC GCCGCCACCA AGACGCGGCA CCGCGCCTGG ACCGGAGGGG CCGCGCGCGG  
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GCGCGGTCCG GCGGCTATGG CCATGCCCCG CGGGTCTCAC GCGGCTGCC CTGCCCCGGC GCGCCTTCGG TAGGGGGCGC  
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CTGCACAGAA CCCTGGGATG GAACCACGAA TGAAAGCTGC TGCCTTGTA AGTGTCTCTT TGAGAATGTG GTCCCCATGA  
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AATGGACTGC CTCTTTGAG CACTTCCCTG GAGCTACCAC GTATCTAGCT AATATGTATG TGTCAGTAGT AGGCTCCAAG  
GATTGACAAA TATATTTATG ATCTATTCAG CTGCTTTTAC TGTGTGGATT ATGCCAACAG CTTGAATGGA TTCTAACAGA  
CTCTTTTGT TTTAAAAGTC TGCCTTGTG ATGGTGAAA ATTAAGTAA CTATTTTACT GTGAAACAGT GTGAACTATT  
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NO:2425)

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GGCATGGTGG CTCACACCTG TAATTCCAGC ACTTTGGGAG GCCAAGGCAG GCGGATCAGC AGGTCAGGAG TTCAAAACCA  
GCCTGTCCAA TATAGTG (FRAG. NO: ) (SEQ. ID NO: 2424)  
5'-GCGCGTCTG-3' (FRAG. NO: 1671) (SEQ. ID NO: 1684)  
5'-GCT GGG CCC CGG-3' (FRAG. NO: 1672) (SEQ. ID NO: 1685)  
5'-CGG GTC GGG GCC CCC C-3' (FRAG. NO: 1673) (SEQ. ID NO: 1686)  
5'-CGC GCC CGC G-3' (FRAG. NO: 1674) (SEQ. ID NO: 1687)  
5'-GGC GCC GTG CCG CGT CTT GGT GGC GGC GG-3' (FRAG 972) (SEQ. ID NO: 982)  
5'-GTT CGC GCC CGC GCG GGG CCC CTC CGG TCC-3' (FRAG 973) (SEQ. ID NO: 983)  
5'-GTT CGC GCC CGC GCG GGG CCC CTC CGG TCC-3' (FRAG 974) (SEQ. ID NO: 984)  
5'-CGG GTC GGG GCC CCC CGC GGC C-3' (FRAG 975) (SEQ. ID NO: 985)  
5'-GCC TCG GGG CTG GGG CGC TGG TGG CCG GG-3' (FRAG 976) (SEQ. ID NO: 986)  
5'-CCG CGC CTC CGC CTG CCG CTT CTG-3' (FRAG 977) (SEQ. ID NO: 987)  
5'-GCT GGG CCC CGG GCG CCC CCT-3' (FRAG 978) (SEQ. ID NO: 988)  
5'-CCC CTC TTG CTC GGG TCC CCG TG-3' (FRAG 979) (SEQ. ID NO: 989)  
5'-ACAGCGCTCTGTGTCTCCAGCAGCATGGCCGGGCCAGCTGGGCCCC-3' (FRAG 980) (SEQ. ID NO: 990)  
5'-BCBGCCTCTGTGTCTCCBGCBCBTGGCCGGGCCBGTGGGCCCC-3' (FRAG 981) (SEQ. ID NO: 991)

### Human Adenosine A3 Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-ACA GAG CAG TGC TGT TGT TGG GCA TCT TGC CTT CCC AGG G BCB GBG CB TGC TGT TGT TGG GCB TCT TGC CTT  
CCC BGG GCC CTT TTC TGG TGG GGT GGT GCT GTT GTT GGG CTT TCT TCT GTT CCC BCB GBG CBG TGC TGT TGT TGG  
GCB TCT TGC CTT CCC BGG GCC CTT TTC TGG TGG GGT GGT GCT GTT GTT GGG C TTT CTT CTG TTC CC  
GAATTCACAG ATGGGCAGAG GTGGCTGGGC TGGTGACCCT AAGTGTGTCT CTTGCTTTA TTCTCTCTAG TGGGTTATTC  
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GACTGATTC AAAAGAACTC ACCTATGTAC TGGGTAGGG GAGGGAGGGT TTTTGCAGT ATTTAACTAA GGTTCAAAGA  
GTGCTATATA GTGAGAAAGG CTTCTTTTTT TTTTTTTTTT TTTTGGCA GAGTGTGCC TCCTAGAAAT TTCTCTTGGT  
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CTTTCAAGT TCCAGCAGTG CAGGGATGTG GGCAGAACTG ACATTGGAAA ATACTAGAAT GATGGAAAT CAGTTGGAGA  
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GACTTGGATC AACTTGGGAT ACAGGGTGGG GGTGCGGAGT GGAATCAATG AATGATGCCA GAGCAGATCA ACTAACAAGA  
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TCCATCTTTT TGCTGAGAGT TCTGAGCTCT GTACTTCTC TTGGCCATC TCACTTCTG AAACACCCCT GAAGAGGGTT  
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ACTGTCACTG CACATACC TCTGGGAAGA CGTCTGGCGA GAGCTAGGCC CAGGCCCT ACAGACGGAT CTGTCTGGCT  
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TGCTTCTCAG AGGTGCTGAG TTTTGCCCT TCTGAGCAGG GAATCTTTC TTATCCCTT GACCAAGGAT CTTGCTCCA  
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GGCTGCCACC AAAGTCTCT TTTGTTCT CTGCTTCTC CGTTTGCTC CTATCATGA GATCTTTTG CTAAGCTGGC  
AGAAAGATT CATAATCAGT GCTTCCAGT CCGCTCCAC CTGATCTGC ACTGTCTCT GGTCCCTGAA TGAATGAACT  
CTCATACCA ATCTTCTC GAGCTTCTC TATGCCACTC ATGGCTCTC TTCTGCTCT TCCATCTTT TGCTGAGAGT

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CACCTGTCCC TGTGGAGGTT CCCCTGGGAA GGCAAGATGC CCAACAACAG CACTGCTCTG CGAATTCGGG GGACATCTGT  
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ACAACAGCAC TGCTCTGTCA TTGGCCAATG TTACCTACAT CACCATGGAA ATTTTCATTG GACTCTGCGC CATAGTGGGC  
AACGTGCTGG TCATCTGCGT GGTCAAGCTG AACCCAGCC TGCAGACCAC CACCTTCTAT TTCATTGTCT CTCTAGCCCT  
GGCTGACATT GCTGTTGGGG TGCTGGTCAT GCCTTTGGCC ATTGTTGTCA GCCTGGGCAT CACAATCCAC TTCTACAGCT  
GCCTTTTTAT GACTTGCTA CTGCTTATCT TTACCCAGCG CTCATCATG TCCTTGCTGG CCATCGCTGT GGACCGATAC  
TTGCGGGTCA AGCTTACCGT CAGATACAAG AGGGTCACCA CTCACAGAAG AATATGGCTG GCCCTGGGCC TTGCTGGCT  
GGTGTCACTC CTGGTGGGAT TGACCCCAT GTTTGGCTGG AACATGAAAC TGACCTCAGA GTACCACAGA AATGTCACCT  
TCCTTTCATG CCAATTTGTT TCCGTCACTG GATGGACTA CATGGTATAC TTCAGCTTCC TCACCTGGAT TTTCATCCCC  
CTGGTTGTCA TGTGCGCCAT CTATCTTGAC ATCTTTTACA TCATTCGGAA CAAACTCAGT CTGAACCTAT CTAACCTCAA  
AGAGACAGGT GCATTTTATG GACGGGAGTT CAAGACGGCT AAGTCCTTGT TTCTGTTCT TTCTTGTGTT GCTCTGTCAT  
GGCTGCCCTT ATCTCTCATC AACTGCATCA TCTACTTAA TGGTGAGGTA CCACAGCTTG TGCTGTACAT GGGCATCCTG  
CTGTCCCATG CCAACTCCAT GATGAACCCT ATCGTCTATG CCTATAAAAT AAAGAAGTTC AAGGAAACCT ACCTTTGAT  
CCTCAAAGCC TGTGTGGTCT GCCATCCCTC TGATTCTTTG GACACAAGCA TTGAGAAGAA TTTCTAGTAG TTATCCATCA  
GAGATGACTG TGCTCATTTG ACCTTCAGAT TCCCATCAA CAAACACTTG AGGGCCTGTA TGCCTGGGCC AAGGGATTTT  
TACATCCTTG ATTACTTCCA CTGAGGTGGG AGCATCTCCA GTGCTCCCCA ATTATATCTC CCCCCTCCA CTACTCTCTT  
CCTCCACTTC ATTTTCTCTT TGTCTTTCT CTCTAATTCA GTGTTTGGGA GGCCTGACTT GGGGACAACG TATTATTGAT  
ATTATTGTCT GTTTTCTTTC TTCCAATAG AAGAATAAGT CATGGAGCCT GAAGGGTGCC TAGTTGACTT ACTGACAAAA  
GGCTCTAGTT GGGCTGAACA TGTGTGTTGGT GGTGACTCAT TTCCATGCCA TTGTGGAATT GAGCAGAGAA CCTGCTCTCG  
GAGGATGCCT AGGAGATGTT GGGAACAGAA GAAATAAACT GAGTTTAAGG GGGACTTAAA CTGCTGAATT C-3' (FRAG.  
NO:1675) (SEQ. ID NO:1688)

5'- CGAATTCGGG GGACATCTGT TTGGGGAAC AAGAGCAGCA GCATTTCAG ATTCAGTCCA TATAGAGCTG  
TCCTACAGCA TTCTGGAAAC TTGAGGATGT GCGGTGCATA AACGGGCTGG AAGTGACCCA CCTGTGATGA GCCCTTCTA  
AGGAGAAGGG TTCCAAGAG ATCACCACAC CAGAAAAGGG TAGGAATGAG CAAGTTGGGA ATTTAGACT GTCACTGCAC  
ATGGACCTCT GGAAGACGT CTGGCGAGAG CTAGGCCAC TGGCCCTACA GACGGATCTT GCTGGCTCAC CTGTCCCTGT  
GGAGGTTCCC CTGGGAAGGC AAGATGCCCA ACAACAGCAC TGCTCTGTCA TTGGCCAATG TTACCTACAT CACCATGGAA  
ATTTTCATTG GACTCTGCGC CATAGTGGGC AACGTGCTGG TCATCTGCGT GGTCAAGCTG AACCCAGCC TGCAGACCAC  
CACCTTCTAT TTCATTGTCT CTCTAGCCCT GGCTGACATT GCTGTTGGGG TGCTGGTCAT GCCTTTGGCC ATTGTTGTCA  
GCCTGGGCAT CACAATCCAC TTCTACAGCT GCCTTTTAT GACTTGCTA CTGCTTATCT TTACCCAGCG CTCATCATG  
TCCTTGCTGG CCATCGCTGT GGACCGATAC TTGCGGGTCA AGCTTACCGT CAGATACAAG AGGGTCACCA CTCACAGAAG  
AATATGGCTG GCCCTGGGCC TTGCTGGCT GGTGTCATTC CTGGTGGGAT TGACCCCAT GTTTGGCTGG AACATGAAAC  
TGACCTCAGA GTACCACAGA AATGTCACCT TCCTTTCATG CCAATTTGTT TCCGTCACTG GATGGACTA CATGGTATAC  
TTCAGCTTCC TCACCTGGAT TTTCATCCCC CTGGTTGTCA TGTGCGCCAT CTATCTTGAC ATCTTTTACA TCATTCGGAA  
CAAACCTCAGT CTGAACCTAT CTAACCTCAA AGAGACAGGT GCATTTTATG GACGGGAGTT CAAGACGGCT AAGTCCTTGT  
TTCTGTTCTT TTCTTGTGTT GCTCTGTCAT GGCTGCCCTT ATCTCTCATC AACTGCATCA TCTACTTAA TGGTGAGGTA  
CCACAGCTTG TGCTGTACAT GGGCATCCTG CTGTCCCATG CCAACTCCAT GATGAACCCT ATCGTCTATG CCTATAAAAT  
AAAGAAGTTC AAGGAAACCT ACCTTTGAT CCTCAAAGCC TGTGTGGTCT GCCATCCCTC TGATTCTTTG GACACAAGCA  
TTGAGAAGAA TTCTGAGTAG TTATCCATCA GAGATGACTC TGTCTCATTG ACCTTCAGAT TCCCATCAA CAAACACTTG  
AGGGCCTGTA TGCCTGGGCC AAGGGATTTT TACATCCTTG ATTACTTCCA CTGAGGTGGG AGCATCTCCA GTGCTCCCCA  
ATTATATCTC CCCCCTCCA CTACTCTCTT CCTCCACTTC ATTTTCTCTT TGTCTTCTT CTCTAATCA GTGTTTGGGA  
GGCCTGACTT GGGGACAACG TATTATTGAT ATTATTGCT TTTTCTTTC TTCCAATAG AAGAATAAGT CATGGAGCCT  
GAAGGGTGCC TAGTTGACTT ACTGACAAAA GGCTCTAGTT GGGCTGAACA TGTGTGTTGGT GGTGACTCAT TTCCATGCCA  
TTGTGGAATT GAGCAGAGAA CCTGCTCTCG GAGGATGCCT AGGAGATGTT GGGAACAGAA GAAATAAACT GAGTTTAAGG  
GGGACTTAAA CTGCTGAATT C-3' (FRAG. NO: ) (SEQ. ID NO:2439)

5'- CTGCTGAATT TATTTTGGGA CTGTACATAT TTAGATGCTT AAGGTAAAAA TGATAAAGCC CTCAAGCCAC TGTGTGGGT  
GGGTCCAAGT GTTCTTGTCT GCTGCCTCTC TAACACGCCT GGTAAAAATA ATCCCTTTGG ATGGTGCTGA GAAGCACCTG  
AACCAAGTGG GTCCCAAAAT AACTATGGCG TGCAAGTGTG TGGTTCCAG AAGTTGGTGA CTAGGTAAGC GACTCAGGGA  
GAGGGGCTGA TTCCAGACA GTCGCTGTT CCTGCTGGGA TGGGGCTGAG GCTTGGGGA TGTGGGCAGG AGGATATGCC  
ATTTGATICT GTTGACACAG TTCTTTTCCC TTCTTCTGT ATGCTGGTC ATTCTGCTAT TGTGCTGTC CTCACATAGG  
TTGGACATTG GCCGGCTGCC AGCATAAGTG CCAATGTGAT TTTCTAGGG TGTGAGCTGA GAAAGAGAGG TGGAGGCTAA  
GCAGGTGTGA TGCTTCTCAG AGGTGCTGAG TTTTGGCCT TCTGAGCAGG GAATCTTTGCT TTATCCCTTT GACCAAGGAT  
CTTTGTCCA AAGGCTGGGT ATCGGCTGTG CTCAGCAAAG CGTCAACTCG TGCAAGAACT TAGCAGGAAT AGTTCTGGCT  
AAGGTTAGGA GGCTGCCACC AAAGTCTCTT TTTTGTCTCT CTGCTTCTCC CGTTTGCCTC CTTATCATGA GATCTTTTGT  
CTAAGCTGGC AGAAAGATTG CATAATCAGT GCTTCCAGCT CCGCTCCAC CTGATCCTGC ACTGCTCTCT GGTCCCTGAA  
TGAATGAACT CTGATACCCA ATCTTGTCTC GAGCCTTCTC TATGCCACTC ATGGCTCTC TTCTGCTCTT TCCATCTTTT  
TGCTGAGAGT TACTGAGCTC TGTACTTCCT CTGGGCCAT CTCACTTCCT GAAACACCCC TGAAGAGGGT TGCTTATCTT  
GATGGAACCT AAAAAGCCAA AAGCTGCAG GCAGAGGCGT TGAGGACATC TGTTTGGGGA ACTAAGAGCA GCAGCACTT

CAGATTCAGT CCATAAGAG CTGTCCTACA GCATTCTGGA AACTTGAGGA TCGGGTGC ATAAAGGGGC TGGAAGTGAC  
CCACCTGTGA TGAGCCCTTT CTAAGGAGAA GGGTTTCCAA GAGATCACCC CACCAGAAAA GGGTAGGAAT GAGCAAGTTG  
GGAATTTTAG ACTGTCACTG CACATGGACC TCTGGGAAGA CGTCTGGCGA GAGCTAGGCC CACTGGCCCT ACAGACGGAT  
CTTGCTGGCT CACCTGTCCC TGTGGAGGTT CCCCTGGGAA GGCAAGATGC CCAACAACAG CACTGCTCTG -3' (FRAG. NO.:)  
(SEQ. ID NO:2438)

5'- GAATTCACAG ATGGGCAGAG GTGGCTGGG TGGTGACCCT AAGTGTGTCT CCTGCCCTTA TTCTCTCTAG TGGGTTATTC  
TTTCATGTGG TATCTTGCTT ACAGCATGCT GTGTTTGGAC ACAAACCCCT TTCTTGCTT TCTCTGACCC AGCTGAGATG  
GACTGATTC AAAAGAACTC ACCTATGTAC TGGGGTAGGG GAGGGAGGGT TTTTTCAGT ATTTAACTAA GGTTCAAAGA  
GTGCTATATA GTGAGAAAGG CTCTTTTTT TTTTTTTTT TTTTGGCA GAGTGCTGCC TCCTAGAAAT TTCTTTGGT  
AACTTCCTTC TCTGAAGCAC AGATAAAGAA AACAATTACA GTAGAAACAT TTATGAGGGA CACATTGGAG GCCGATGAAG  
CTTTCAAGT TCCAGCAGTG CAGGGATGTG GGCAGAACTG ACATTGGAAA ATACTAGAAT GATGGAATTT CAGTTGGAGA  
GGACTGCCCT TTTAATGTC TGGGGAGTCT GCTCAGGGAG AAATGACAAG TCTGGCGGGG ACAAGTATGG GATTTGGTAA  
GACTTGGATC AACTTGGGAT ACAGGGTGGG GGTGGGAGT GGAATCAATG AATGATGCCA GAGCAGATCA ACTAACAAGA  
GGACCTGAT GAGCCCCAGG CAGAGGCGTC TCCCTATGC CCCACTCTGA AGTGTGTGT AGTAAACACC AGAACGCCAT  
TGTTGTACT GCTGAATTT ATTTGGGCT GTACATATT AGATGCTTAA GGTAATAATG ATAAAGCCCT CAAGCCACTG  
TGTGGGTTG GGTCCAAGTG TTCTTCTTG CTGCCTCTT AACACGCTG GTTAAATAA TCCCTTTGGA TGGTGCTGAG  
AAGCACCTGA ACCAAGTGGG TCCCAAATA ACAATGGCGT GCAAGTGTCT GGTCCCAGA AGTTGGTGAC TAGGTAAGCA  
GCTTCAGGGA GAGGGGGCTG ATCCAGAC AGTCGCTGT TCTGCGGGG ATGGGGCTGA GGCTGGGGA ATGTGGGCAG  
GAGGATATGC CATTGATTC TGTTGCACAC GTTCTTTCC CTCTTTCTG TATGTCTGGT CATTCTGCTA TTCTGCTGT  
CCTCACATAG GTTGGACATT GGCCGGCTGC CAGCATAAGT GCCAGTGTGA TTTTGCTAGG TGTGAGCTGA GAAAGAGAGG  
TGGAGGCTAA GCAGGTGTGA TGCTTCTCAG AGGTGCTGAG TTTTGCCCT TCTGACAGG GAATCTTTC TTATCCCTTT  
GACCAAGGAT CTTTGCTGCA AAGGCTGGT ATCGGCTGTG CTCAGCAAAG CGTCAACTCG TGCAAGAACT TAGCAGGAAT  
AGTTCTGGCT AAGGTTAGGA GGCTGCCACC AAAGTCTCTT TTTGTTCCT CTGCTTCTCC CGTTTGCCTC CTATCATGA  
GATCTTTTG CTAAGCTGGC AGAAAGATTG CATAGTACAGT GCTTCCAGCT CTGCTCCAC CTGATCCTGC ACTGCTCTCT  
GGTCCCTGAA TGAATGAACT CTGATACCA ATCTTGCTC GAGCCCTCTC TATGCCACTC ATGGCTCCTC TTCTGCTCTT  
TCCATCTTT TGCTGAGAGT TCTGAGCTCT GACTTCTC TTGGCCATC TCACTTCCTG AAACACCCCT GAAGAGGGTT  
GCTTATCTTG ATGGAAGTCA AAAAGCCAAA AAGCTGCAGG CAGAGGCGTT GAGGACATCT GTTTGGGGAA CTAAGAGCAG  
CAGCACTTC AGATTCAGTC CATATAGAGC TGCTCAGG CATTCTGGAA ACTTGAGGAT GTGCGGTGCA TAAAGGGGCT  
GGAAGTGACC CACCTGTGAT GAGCCCTTC TAAGGAGAAG GGTTCGAAG AGATCACCC ACCAGAAAAA GGTAGGAATG  
AGCAAGTTGG GAATTTAGA CTGTCACTGC ACATGGACCT CTGGGAAGAC GTCTGGCGAG AGCTAGGCCC ACTGGCCCTA  
CAGACGGATC TTGCTGGCTC ACCTGTCCCT GTGAGGTTT CCCTGGGAAG GCAAGATGCC CAACAACAGC ACTGCTCTGT  
CATTGGCCAA TGTTACCTAC ATCACCATGG AAATTTTCAT TGGACTCTGC GCCATAGTGG GCAACGTGCT GGTCTCTGC  
GTGGTCAAGC TGAACCCAG CCTGCAGACC ACCACCTTCT ATTTCAATTG CTCTCTAGCC CTGGCTGACA TTGCTGTTGG  
GGTGCTGGT ATGCCCTTGG CCATTGTTGT CAGCCTGGG ATCACAATCC ACTTCTACAG CTGCCCTTT ATGACTTGCC  
TACTGCTTAT CTTTACCCAC GCCTCCATCA TGTCTTGCT GGCCATCGCT GTGGACCGAT ACTTGGGGT CAAGCTTACC  
GTCAGGTAGC CTGCGGCGTG GGGTGGGCAG CAATTGAGGC AGCTGGGAAA TGAGGCTACA AAGCCAGAGC -3' (FRAG.  
NO.:) (SEQ. ID NO:2437)

5'-CGAATTCGGG GGACATCTGT TTGGGGAAGT AAGAGCAGCA GCACCTTCAG ATTCAGTCCA TATAGAGCTG  
TCCTACAGCA TTCTGGAAGC TTGAGGATGT GCGGTGCATA AACGGGCTGG AAGTGACCCA CCGTGATGA GCCCTTCTA  
AGGAGAAGGG TTTCCAAGAG ATCACCAC CAGAAAAGGG TAGGAATGAG CAAGTTGGGA ATTTAGACT GTCACTGCAC  
ATGGACCTCT GGAAGACGT CTGGCAGAG CTAGGCCAC TGGCCCTACA GACGATCTT GCTGGCTCAC CTGTCCTGT  
GGAGTTCCC CTGGGAAGG AAGATGCCA ACAACAGCAC TGCTGTGCA TTGGCAATG TTACCTACAT CACCATGGAA  
ATTTTCATTG GACTCTGCGC CATAGTGGG AACGTGCTGG TCATCTGCGT GGTCAGCTG AACCCAGCC TGCAGACCAC  
CACCTTCTAT TTCTTGTCT CTCTAGCCCT GGCTGACATT GCTGTTGGG TGCTGGTCAT GCCTTGGCC ATTGTTGTC  
GCCTGGCAT CACAATCCAC TTCTACAGCT GCCTTTTAT GACTTGCTA CTGCTTATCT TTACCCACGC CTCCATCATG  
TCCTTGCTGG CCATCGCTGT GGACCGATAC TTGCGGGTCA AGCTTACCGT CAGATACAAG AGGGTCACCA CTCACAGAAG  
AATATGGCTG GCCCTGGGCC TTGCTGGCT GGTGTCATTC CTGGTGGGAT TGACCCCAT GTTGGCTGG AACATGAAAC  
TGACCTCAGA GTACCACAGA AATGTACCT TCCTTTCATG CCAATTTGT TCCGTATGA GGATGGACTA CATGGTATAC  
TTACGCTTCC TCACCTGGAT TTTCATCCCC CTGGTTGTC TGTCGCCAT CTATCTGAC ATCTTTTACA TCATTGGAA  
CAAACCTAGT CTGAACCTAT CTAACCTCAA AGAGACAGGT GCATTTTATG GACGGGAGT CAAGACGGCT AAGTCTTGT  
TTCTGGTTCT TTTCTGTTT GCTCTGTCAT GGCTGCCTT ATCTCTCATC AACTGCATCA TCTACTTAA TGGTGAGGTA  
CCACAGCTTG TGCTGTACAT GGGCATCCTG CTGTCCCAGT CCAACTCCAT GATGAACCT ATCGTCTATG CCTATAAAT  
AAAGAAGTTC AAGGAAACCT ACCTTTTGAT CCTCAAAGCC TGTGTGGTCT GCCATCCCTC TGATTCTTTG GACACAAGCA  
TTGAGAAGAA TTCTGAGTAG TTATCCATCA GAGATGACTC TGTCTCATTG ACCTTCAGAT TCCCATCAA CAAACACTTG  
AGGGCTGTA TGCTGGGCC AAGGGATTTT TACATCCTTG ATTACTTCCA CTGAGGTGG AGCATCTCCA GTGCTCCCCA  
ATTATATCTC CCCCCTCCA CTACTCTCTT CCTCCACTTC ATTTTCTCT TGCTCTTCT CTCTAATTCA GTGTTTGGG  
GGCCTGACTT GGGGACAACG TATTATTGAT ATTATTGTCT GTTTTCTTC TTCCCAATAG AAGAATAAGT CATGGAGCCT  
GAAGGGTGCC TAGTTGACTT ACTGACAAAA GGCTAGATT GGGCTGAACA TGTGTGTGGT GGTGACTCAT TTCCATGCCA  
TTGTGGAATT GAGCAGAGAA CCTGCTCTCG GAGGATGCCT AGGAGATGTT GGAACAGAA GAAATAAAT GAGTTAAGG  
GGGACTTAAA CTGCTGAATT C -3' (FRAG. NO.:) (SEQ. ID NO:2427)

5'-CTGCTGAATT TTATTTTGA CTGTACATAT TTAGATGCTT AAGGTAATAA TGATAAAGCC CTCAGGCCAC TGTGTGGGT  
GGGTCCAAGT GTTCTTGCT GCTGCCTCTC TAACACGCTT GGTAAATAA ATCCCTTGG ATGGTGTGA GAAGCACCTG  
AACCAAGTGG GTCCCAAAAT AACTATGGCG TGCAAGTGTG TGGTCCCAG AAGTTGGTGA CTAGGTAAGC GACTCAGGGA

GCAGGTGTGA TGCTTCTCAG AGGTGCTGAG TTTTGGCCCT TCTGAGCAGG GAATCTTTGC TTATCCCTTT GACCAAGGAT  
 CTTTGCTCCA AAGGCTGGGT ATCGGCTGTG CTCAGCAAAG CGTCAACTCG TGCAAGAACT TAGCAGGAAT AGTTCTGGCT  
 AAGGTTAGGA GGCTGCCACC AAAGTCTCTT TTTTGTTCCT CTGCTTCTCC CGTTTGCCCT CTTATCATGA GATCTTTTGG  
 CTAAGCTGGC AGAAAGATTG CATAATCAGT GCTTCCAGCT CCGTCCAC CTGATCCTGC ACTGTCTCT GGTCCCTGAA  
 TGAATGAACT CTGATACCCA ATCTTGCTC GAGCCTTCTC TATGCCACTC ATGGCTCCTC TTCTGCTCTT TCCATCTTTT  
 TGCTGAGAGT TACTGAGCTC TGTACTTCTT CTGGGCCAT CTCACTTCTT GAAACACCCC TGAAGAGGGT TGCTTATCTT  
 GATGGAATC AAAAAGCCAA AAAGCTGCAG GCAGAGGCGT TGAGGACATC TGTTTGGGGA ACTAAGAGCA GCAGCACTT  
 CAGATTCACT CCATATAGAG CTGTCTACA GCATTCTGGA AACTTGAGGA TGTGCGGTGC ATAAAGGGGC TGGAAGTGAC  
 CCACCTGTGA TGAGCCCTT CTAAGGAGAA GGGTTTCCAA GAGATCACCC CACCAGAAAA GGGTAGGAAT GAGCAAGTTG  
 GGAATTTTAC ACTGTCACTG CACATGGACC TCTGGGAAGA CGTCTGGCGA GAGCTAGGCC CACTGGCCCT ACAGACGGAT  
 CTTGCTGGCT CACTGTCCC TGTGGAGGT CCCCTGGGAA GGCAAGATGC CCAACAACAG CACTGCTCTG-3' (FRAG. NO: )  
 (SEQ. ID NO:2426)

5'-GAATCCCAG ATGGGCAGAG GTGGCTGGGC TGGTGACCCT AAGTGTGTCT CTGCCTTTA TTCTCTCTAG TGGGTTATTC  
 TTTTATGTGG TATCTTGCCT ACAGCATGCT GTGTTTGGAC ACAAACCCTT TTCCTTGGTT TCTCTGACCC AGCTGAGATG  
 GACTGATTCC AAAAGAACTC ACCTATGTAC TGGGGTAGGG GAGGGAGGGT TTTTGCAGT ATTTAACTAA GGTTCAAAGA  
 GTGCTATATA GTGAGAAAGG CTCTTTTTT TTTTGTGCA GAGTGCTGCC TCCTAGAAAT TTCTCTTGGT  
 AACTTCTTC TCTGAAGCAC AGATAAGAA AACAATTACA GTAGAAACAT TTATGAGGGA CACATTGGAG GCCGATGAAG  
 CTTTCAAGT TCCAGCAGTG CAGGGATGTG GGCAGAACTG ACATTGGAAT ATACTAGAAT GATGGAATTT CAGTTGGAGA  
 GGACTGCCCT TTTAATGTC TGGGGAGTCT GCTCAGGAG AAATGACAAG TCTGGCGGGG ACAAGTATGG GATTGTGTA  
 GACTTGGATC AACTTGGGAT ACAGGGTGGG GGTGCGGAGT GGAATGCAATG AATGATGCCA GAGCAGATCA ACTAACAAGA  
 GGACCCTGAT GAGCCCCAGG CAGAGGCGTC TCCCTATGC CCCACTCTGA AGTGTTTGT AGTAAACACC AGAACGCCAT  
 TGTGTACT GCTGAATTT ATTTTGGGCT GTACATATT AGATGCTTAA GGTAAAAATG ATAAAGCCCT CAAGCCACTG  
 TGTGGGTTG GGTCCAAGTG TTCTTCTTG CTGCTCTCT AACACGCTG GTTAAATAA TCCTTTGGA TGGTGTGAG  
 AAGCACCTGA ACCAAGTGGG TCCCCAAATA ACAATGGCGT GCAAGTGTCT GGTCCCAAG AGTTGGTGAC TAGGTAAGCA  
 GCTTCAGGGA GAGGGGGCTG ATTCCAGAC AGTCGCTGT TCTGCGGGG ATGGGGCTGA GGCTTGGGA ATGTGGCAG  
 GAGGATATGC CATTGATTC TGTGACAC GTCCTTTCC CTCTTCTG TATGTCTGGT CATTCTGCTA TTCTGCTGT  
 CCTACATAG GTTGACATT GGCCGGCTGC CAGCATAAGT GCCAGTGTGA TTTTGTAGG TGTGAGCTGA GAAAGAGAGG  
 TGGAGGCTAA GCAGGTGTGA TGCTTCTCAG AGGTGCTGAG TTTTGGCCCT CTGAGCAGG GAATCTTTGC TTATCCCTT  
 GACCAAGGAT CTTTGTGCA AAGGCTGGGT ATCGGCTGTG CTCAGCAAAG CGTCAACTCG TGCAAGAACT TAGCAGGAAT  
 AGTTCTGGCT AAGGTTAGGA GGCTGCCACC AAAGTCTCTT TTTTGTTCCT CTGCTTCTCC CGTTTGCCCT CTTATCATGA  
 GATCTTTTGG CTAAGCTGGC AGAAAGATTG CATAATCAGT GCTTCCAGCT CTGCTCCAC CTGATCCTGC ACTGTCTCT  
 GGTCCCTGAA TGAATGAACT CTGATACCCA ATCTTGCTC GAGCCTTCTC TATGCCACTC ATGGCTCCTC TTCTGCTCTT  
 TCCATCTTTT TGCTGAGAGT TCTGAGCTCT GTACTTCTC TTGGCCATC TCACTTCTG AAACACCCCT GAAGAGGGTT  
 GCTTATCTTG ATGGAATCA AAAAGCCAAA AAGCTGCAGG CAGAGGCGTT GAGGACATCT GTTTGGGGA CTAAGAGCAG  
 CAGCACTTC AGATTCACTC CATATAGAGC TGCTCTACAG CATTCTGGA ACTTGAGGAT GTGCGGTGCA TAAAGGGGCT  
 GGAAGTGACC CACCTGTGAT GAGCCCTTC TAAGGAGAAG GGTTCCAAG AGATCACCCC ACCAGAAAAG GGTAGGAATG  
 AGCAAGTTGG GAATTTAGA CTGTCACTGC ACATGGACCT CTGGGAAGAC GTCTGGCGAG AGCTAGGCCC ACTGGCCCTA  
 CAGACGGATC TTGCTGGCTC ACCTGTCCCT GTGGAGGTTT CCTGGGAAG GCAAGATGCC CAACAACAGC ACTGCTGTG  
 CATTGGCCAA TGTACCTAC ATCACCATGG AAATTTTCAT TGGACTCTGC GCCATAGTGG GCAACGTGCT GGTCTCTGC  
 GTGGTCAAGC TGAACCCAG CCTGCAGACC ACCACCTTCT ATTTATTGT CTCTCTAGCC CTGGCTGACA TTGCTGTTGG  
 GGTGCTGGTC ATGCTTTGG CCATTGTTGT CAGCCTGGGC ATCACAATCC ACTTCTACAG CTGCCCTTTT ATGACTTGGC  
 TACTGCTTAT CTTTACCAC GCCTCCATCA TGTCTTGT GGCATCGCT GTGGACCGAT ACTTGGGGT CAAGCTTACC  
 GTCAGGTAGC CTGCGCGCTG GGGTGGGAG CAATTGAGGC AGCTGGGAAA TGAGGCTACA AAGCCAGAGC-3' (FRAG.  
 NO: ) (SEQ. ID NO:2425)

5'-GBG CB TGC-3' (FRAG. NO:1676) (SEQ. ID NO:1689)

5'-TTG TTG GGC-3' (FRAG. NO:1677) (SEQ. ID NO:1690)

5'-TGC CTT CCC BGG G-3' (FRAG. NO:1678) (SEQ. ID NO:1691)

5'-GTT GTT GGG CAT CTT GCC-3' (FRAG. NO:1679) (SEQ. ID NO:1692)

5'-GTG GGC CTA GCT CTC GCC-3' (FRAG. NO:1680) (SEQ. ID NO:1693)

5'-ACA GAG CA TGC TGT TGT TGG GCA TCT TGC CTT CCC AGG G-3' (FRAG. NO:1681) (SEQ. ID NO:1694)

5'-BCB GBG CB TGC TGT TGT TGG GCB TCT TGC CTT CCC BGG G-3' (FRAG. NO:1682) (SEQ. ID NO:1695)

5'-CCC TTT TCT GGT GGG GTG-3' (FRAG. NO:1683) (SEQ. ID NO:1696)

5'-GTG CTG TTG TTG GGC-3' (FRAG. NO:1684) (SEQ. ID NO:1697)

5'-TTT CTT CTG TTC CC-3' (FRAG. NO:1685) (SEQ. ID NO:1698)

5'-CCC TTT TCT GGT GGG GTG-3' (FRAG. NO:1686) (SEQ. ID NO:1699)

5'-GTG CTG TTG TTG GGC-3' (FRAG. NO:1687) (SEQ. ID NO:1700)

5'-TTT CTT CTG TTC CC-3' (FRAG. NO:1688) (SEQ. ID NO:1701)

#### Human IgE Receptor $\beta$ Nucleic Acid and Antisense Oligonucleotide Fragments

5'-TTT CCC CTG GGT CTT CC CTC CTG CTC TTT TTT C ATT TGC TCT CCT ATT ACT TTC TGT GTC CAT TTT TTC ATT  
 AAC CGA GCT GT BTT TGC TCT CCT BTT BCT TTC TGT GTC CBT TTT TTC BTT BBC CGB GCT GT-3' (FRAG. NO:1681)  
 (SEQ. ID NO:1692)

5'-CCC CTG GG-3' (FRAG. NO:1682) (SEQ. ID NO:1693)

5'-GCTCTCCTBTT-3' (FRAG. NO:1683) (SEQ. ID NO:1694)

5'-CBTTBCCBGGCTG-3' (FRAG. NO:1684) (SEQ. ID NO:1695)

5'-TTT CCC CTG GGT CTT CC-3' (FRAG. NO:1685) (SEQ. ID NO:1696)

5'-CTC CTG CTC TTT TTT C-3' (FRAG. NO:1686) (SEQ. ID NO:1697)



Human High Affinity IgE Recept r Olig nucleotide Fragments

5'-AACAAGAAAA GCGTTGGTAG CTCTGGTGAA TCCCAAAAGA ATGTGGCAGT TGCTAGCCAT GCTCCTGAAT  
ATGTATAAAC AGTACATCAT ATGACTAAGA GTTTGACTTA GGGGTTAGAT TTTATGTGTT TGAACCCCAA ATTAGTTATT  
TAATAGTTGG CACCCCAAAA CAAGTTACTT AACCTCACTA AGGTTTCAGT TTCTGTGTTA TAAAATGTAG ATAGTGATAG  
TATGTACTTT ATAGGATTAT TGTGAAAAAT AAATGAAATA TCAGATTTAT TTAGGATAAC ACCTGGCATA TGTGTTGGTAT  
TCAGAAATTAG TTGCTGCTGT TTTATCTGCT TCTCCCTTGC ATCCCACTTT TCTAAGTTGT AAATAAATA GTTGTACACA  
GATTGACAGA TTAAGAAAGG CTGTGTATTG TGCTAGACCT ATGCCTATGC CTCTGTCTCA CCAGATTCCA GGTGTATATG  
TGGAGGTGGG ATAGGGAGTG GAGTAAGTGG GTAAATATTA AATTGCCAG TTGGGCACCA TCCTGAATAT TATCTCTAAA  
GAAAGAAGCA AAACCAGGCA CAGCTGATGG TGTAAACCAGA TATGATACAG AAAACATTTC CTCTGCTTTT TGGTTTAA  
GCCTATATTT GAAGCCTTAG ATCTCTCCAG CACAGTAAGC ACCAGGAGTC CATGAAGAAG ATG GATCTTCATG  
TGGAATGACT GGTTCATTTC AATAGACTTA ATTCAGCAGT CTGTGGGGAA GAGCAAGGTA TGATAGAATG GTTCCTCAAG  
TGCTTCAGAT GTGAAGTGGG TTTAAATATA CTGTCCCTGT CTCTTCAGA GTTTTGGTAA AGATAAAATA GGACACTCAT  
TTAAAGCAA TCTTTGCAAA TGACAAGCCA CTATAGACAT TAATAGAGTT TTCATTTCCA GTATTATCAT TAATATCAGA  
TCCTGGAAGA AGGTTGAGCC TTGACCTAGA GCAAAAAAAC AGAAGAATTA GTAAAGGAAT CCTGGAGAAA GCCCCTGCTG  
TGTATTTAAA GGAGAAAGGG AGATCATGTT GGGAAATTAT AATATAAAA GTAAACAAA GCTAGGAAT AAAATAAAAT  
AAATTATATG CCCTAGATCC CCATAAGTAA TGGTTAACT TCTGCCTTCC TGTGTTCTGA GCCAGATTAG GGCACAGTAG  
AGAAAGAGGA GTCTCTGAAA ATGTTTCCAA TTTCGCTGGT CAGACAGCGG ATCATCAGTG AATCAGATGA AAATTTGTGG  
ATTTATGCAC TAACTGATCA GCAGGAAATT AAACAAGAAA AGCGTTGGTA GCTCTGGTGA ATCCCAAAAG AATTTGGCAG  
TTGCTAGCCA TGCTCCTGAA TATGTATAAA CAGTACATCA TATGACTAAG AGTTTGACTT AGGGGTTAGA TTTTATGTGT  
TTGAACCCCA AATTAGTTAT TTAATAGTTG GCACCCCAAA ACAAGTTACT TAACCTCACT AAGATTCACT TTCTCTGTTT  
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NO:2500)

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NO: ) (SEQ. ID NO:2501)

5'-TACTAAGAGT CTCCAGCATC CTCCACCTGT CTACCACCGA GCATGGGCTT ATATTTGAAG CCTTAGATCT CTCCAGCACA  
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ACTTGGATTG ATGAGAGGTG TTAGTCTCTT TAAAAACAT GGTAGATAAA GAGTTGACAC TAAGTGGGTC CTTTGGGAA  
GAGCCAGAA CATTCTCTCA TAAAGACTTT AAATGTCTAG GACGAGAATG GCCAACAGGA GTGAAGGATT CATACTTTA  
TCTTTACTTA GATGTAAAGA ACAATTACTG ATGTGTAACA TGACTACATA CATAAAGGCG CATGGAGAAA AGTATGGCC  
TTCCATGCAT TAGGTAGTGC TTGTATCAAT TCTTATAGTG GCTAGGGTAT CCTGGAAAAT CTTACGTGTG GATGATTTCT  
CAGGACAGTC TAGGACACTA ACGCAGTTTC TCATGTTTGG CTTCTATTAT TAAAAATGA TACAATCTCG GGAAAAATTT  
TTTGATTTTC ATGAAATTC TGTGTTTTTC TATAGGTAAC ACAATTTCTG ACTGCTATGA TATGCTTTG TTTTGGAAACA  
GTTGTCTGCT CTGACTTGA TATTCACAC ATTGAGGGAG ACATTTTTTC ATCATTTAAA GCAGGTTATC CATTCTGGGG  
AGCCATATTT GTGAGTATAT ATCTATAATT GTTTCTGAAA TAACACTGAA CATAGGTTTT TCTTTTCTC AGATCTAACC  
AGTTGTTTAT TCCAGTATT AAGATGATAT TTATAATTCT TAATTATAAA TATATGTGAG CATATATAAC ATAGATATGC  
TCATTAACAA CAACAAAAGA TTCTTTTAC AATTAACGGT GGGTTAAACA TTTAGCCAC AGTTTTATCC CATGAGAAAC  
CTGAATCTAA TACAAGTTAA ATGACTTGCC TAAGGGCCAC TTGACTAATA GTAATTGAAC CTAAACTTTC AGAATCCAAC  
TCCAGGAACA TACTTCTAGC ACTATTCATC AATAAAGTTA TATGATAAAT ACATACAAC TATCTGTCA ACTAAAAATA  
ACAACAGAGG CTGGGCATGG TGGCTCACAC CCGTAATCCC AGCACTTTGG GAGGCTGAGG CAGGTGGATC ACCTGAGGTC  
AGGAGTTTGA GACCAGCCTG ACCAACATGG TGAACCTCA TCTCTACTAA ATATAAAAAA TTAGCTGAGT GTGATAGTGC  
ATACCTGTAA TCCAGTACT TAAGAGGCTG AGGCAGGAGG CTGTGTTGAA CTGGAAGGC AGAGGTTGCA GTGAGCTGAG  
ATTGTGCCAT TGCACCTCAG CCTGGGCAAT AAGTGCAAC TCTGTCTCAA AATAATAATA ATAATAAAGT  
TGTCTTCATG AAAAAATGAGG AAAGAGATTG CTGGGGTGAG AAACATTAAG ATCAATGGGC ATATGGTGAC CTTCTATGCC  
CTAGAAATC TTTTANGGTA TTTTCTCTG GTATCTCTT TACNATCGT TCTATCTGGA AAAATAGGTG GATGAGTGAG  
ATAATAACGG TATATACTTT TAAAGGTCT AATTGACATA TATAAATGC AAGTATTCA GATGTCAATT TGCTAACCTT  
GACACACATA GACACACATG AAAACATCAC CACATTAATA CAATGTATGT ATCCATCAT CCAAAGCTT CCCTGTGTAT  
CTTTGTAAT CTTTCTTCT CCTCCACTC CTGTCTCTT CGTCCCAAG AAAACATTGA TCTGCTTCT GTGAATATAA  
ATTAACCTAC ATTTTITAGA GCTTTATATA AGTATGTTCT CTTACTGTT TGTCTTCTT CGCTGCACAG TTATTTGAG  
ATTCTCAAG TTTTCTTCT ATATCGATAC TTCAITCACA AGAATATATT TTAATTCTAG AACTGTGAC ATTAGCTTTG  
TCGTCTGCTA AATCCTTAGT GCTCAGATGA CTGTTCAGG ACTCTCTTG AACCTGTACC TCTGTANAT TGAACCTGT  
CTCTACTGTC TTTTATTTT AAACACAGCT TATTAGGTGT CTCTCAACCC ATCAAACNCA CAATCTGAGT CTTTAGGAGA  
TTGCTTTGAA TTTGTGCTAT TGACTTATAT NTATATNAAA TNGTAAATG TTTGGTAAAA ATATCATCAT GTACNTTTC  
ATAATTACGC TATNTNCACA TGATATATGT CAGACTCTGG AAATATGCAT GCCACAGACA CGTGTTCCT GCCTAAAGGG  
GCTGATGGAA GACNCACATA CNAATAGACG ATTGCAGTAG AATGAGAGTG GTGGTCTAAN CAGTACATGT CCTGATGTTG  
CTCGGACAGT TACTACNCCA AGAGTACCCC CTGCAATTGC AGGGTTAGCA TCTCTGGAA GCCTCATGTA AATGAAGAAT  
TTCATGCTCC ATCCAGGACC TAATGAATAA GAATCTGCAT TTTAGCAAGA CCTCATATG ATTCATATAC ACTTTTITTT  
TTTTTTTTTA GATGGAGTCT CACTCTGTG GCCCAGGCTG GTGTGCAATG GCATGATCTT GGCTCACTG AACCTCTGCC  
TCCCGGGTTC AAGTGATTCT CTTGTCTCAG CCTCCCTAGT AGCTGGGACT ACAGGTGCAT GCCACAGTGG CTGGCTAATT  
TTTGTATTT TAGTAGAGAC AGGGTTTAC CATTTTGGTC AGGCTGGTCT TGAACCTCATG ACCTCCGGTG ATCCCCCGC  
CTCGGCTTCC CAAAGTGCTG GGATTACAGA CATGAGCCAC CACACCGCC TTATTCGTAT ACNCAATTTAA TTCTGAGAAG  
CACTCTATAG AAAATAAGAA TAAGAAAATA TGGGCTCAC AGGTGACATT AATAAGTAAC TTTATCGAGT ACCCAAAT  
TTACCTATGT TTGGAAGATG GGGTAAAAAG GACACATTGA AAACAAGAAC TCATTGTGGC TTTTTTTTCC TCCTTTTGA



ACAGTTTTCT ATTTCTGGAA TGTGTCAAT TATATCTGAA AGGAGAAATG CACATATCT GGTGAGTTGC CCGTTTCTGT  
CTTTGTCCAT CCTTGAAAAG ATAAGAAGAA CAGAGTTTAA AGAGTCTTAA GGGAAACACA TCTTTGTCTC CTATATTACT  
TGTGAATGTG GATATATGAT TTTGTTTCAA TCTATTTTGT GTCCTAAGGC TTTTGTCAAC AGAAGTTGGA TATATCATTA  
GAAACATAAA TTGTACCATT TAACATACAT GAAGTTTATG TTTACCTTGA CGTTCTTCTA AAAAGTGTCC TACACCGGCA  
TTGTCTTGT AGGCATATTC ACATGATCAA ATAAAATAAT TAGTTTTCAA TTAAGGAGAA TATTGAGGA AAGACCGTAC  
GTGTTCAATG GGTTCCTGAA GGCAGTCCAG TGAGAAAGTA ATATATGCTT CATTAAACAA TCGCGACATT TTCAGGGTTT  
CCCTTTTAA CCAAAATTTG GAAGCAATGT GGAATTTACT GGATGCATCC AGCCCTGAAA TGAAGATAGG TTTATTGAAT  
GTGCCAGCAA GTGCAGGCC AGGTCTGAGT GTTCTTCATT ATTATCAGGT GAGAGGAAGC CTGGGAGCAA AACTGCCAG  
CAGCATAGCT GGGGGAACGG GAATTACCAT CCTGATCATC AACCTGAAGA AGAGCTTGGC CTATATCCAC ATCCACAGTT  
GCCAGAAATT TTTTGAGACC AAGTGCTTTA TGGCTTCTT TTCCACTGTA TGTATTTTT TTTGTGTGGG AAGACTAAGA  
TTCTGGGTCC TAATGTAAGT AAGAAGCCCT CTCTCTCTGT TCCATGAACA CCATCCCTTT CTGTAACCTC TATTACACAG  
TATAGTGGTT CTGTAAGTTC ACACAGCCCA GGGAGATGCT GGCTGCCAC TCCCTCAAC CCAGGAAAT CCTCGGGGT  
TAAAGTTATC TACTGCAAGT GACGATCTCT GGGTTTTCT GTGCTGTGT TGTGTGTGT GTGTGTGTGT GTGTGTGTGT  
GTATGTGTCA CTTTAAAGG ACTGGTCAGA TGGTAGGGAG ATGAAAACAG GAGATGCTAT AAGAAAATAA ACTTTTGGGG  
CGAATACCAA TGTACTCTT TTTGTTTGT ATTTGTGCT GTTCAATAGG AAATTGTAGT GATGATGCTG TTTCTACCA  
TTCTGGGACT TGGTAGTGT GTGCTACTCA CAATCTGTGG AGCTGGGAA GAACTCAAAG GAAACAAGGT AGATAGAAGC  
CCGATATAAA ATCTTGAATG ACAGGTTAAC GAATTGGAGC TTTATCTCT AAAATATGGC CTGGGTTTTG TGAACATTT  
CTTCCAGAAA ATAGTTTCTC CAAGTTTAT TACTTTGGTT TACAAATCTC ACATTTAAAT CACATTTTAT ACCATAAGTA  
GCACACATTT CATAATATTC CTCTGAATGA GGGTTGGGAT AATAGGACTG ATATGTTAGA AATGCCTTAA AGTGTGTGGA  
GCATGAGAGA TGGATGTACA GAAGGCTGTG GAGGAAACCA CCCAGGTATC TGGCCTTGT TTTGCCCCA GAACTAGCCG  
CCTATCTCTG TTTCTGTTT ATTCTTTGT TTCTTGACT TTCTTTCCA ACTTGCTCTA AAACCTCAGT TTTCTTCTC  
TTCTGATTCA TGACTACCAA ATGTTTTCAC TTGCCTCACC CGTCCATTAC ACCTTTGATA AGAACCACCA GACCTTGTC  
TCATGTACTT GCCCATGTCT GATGGAAGAA ACATACTCTC TCCATCTGTC CACTTCTCTG AGGCATTCAA GTCTAGCCAC  
CTTTTAAAT CACTCTCTC CAGGCTGGG ACGGTGTAC GCTGTAAATC TCAGCACTT GTGAGGCTGA GGAGGGCGGA  
TCACTGAAG TCAGGAGTTC AAAACCAGCC TGGCCAAATG GCAAAACCA ATCTTCTTCA ATTATAACCA AATCTTAAAC  
CAAATCTCTA CTAATAATA CAACAAACA AAACAACAAC AAAAAACA GAAAGGAAA CATTAGCCCA GCGTGGTGGC  
AGGTACCTGA GGTTCAGAT ACTGGGAGG CTGAAGCAGG AGAATCGCTT GAGCCCAAGA GATGGAGGTT GCAGTGAGCC  
GAGATCATGC CACTGCACCA CAGCCAGGT GACAGAGCCA TACTCCCAG CACATTGGGA GGCCAAAGCT GAAGAATAAT  
TTGAGGTGAG GATTGGAGA CCAGCCTGGC CAACATGGTG AAATCCGTC TGTACTAAAA ATATAAACT TAGTGGGGCA  
TGGGGGCACA CACTGTAAT TTCAGTACT TAGGAGGCTG AGGCAGGAGA ATTGCTTGAA CCGGGAGGC GGAAGTTGCA  
GTGAGCCAAG ATCGTGGCCA CTGACTCCA GCCTGGGTGA CATAGTGAGA TTCTGTCTCA AAAAAATAA AAGAAATTTA  
AAAAATCACT CTCTCCAAA GATAGATAAA TAAGACAGCA GATATACTAA GGAATAACCT CACCAACTTG TCATTGACTG  
ACATGATTTT TTTTGGCCA CTGGCCAGC TAGTCTGGT TGGTTTTCTG GAAATGAAAG AAATAATCAG AGTTTAAATGA  
CAGAGAGCGT GAGACCCAGA AAGACAAAAG TAGATGAGGT AAGTCTCTG AGCGAGACTT CTAGGGATGG GAAATTTGTG  
GTGATTGATA TGAAATGATT TTTCCCTTAT CAGGTTCAG AGGATCTGT TTATGAAGAA TTAACATAT ATTCACTAC  
TTACAGTGAG TTGGAAGACC CAGGGGAAAT GTCTCTCCC ATTGATTTAT AAGAATCAGC GTGCCAGAAC ACTCTGATTC  
ACAGCCAAGG ATCCAGAAGG CCAAGGTTT GTTAAGGGGC TACTGGAAA ATTTCTATTC TCTCCACAGC CTGCTGGTTT  
TACATTAGAT TTATTCGCCT GATAAGAATA TTTTGTITCT GCTGCTCTG TCCACCTTAA TATGCTCCTT CTATTTGTAG  
ATATGATAGA CTCCTATTTT TCTTGTTTAA TATTATGACC ACACACATCT CTGCTGGAAA GTCAACATGT AGTAAGCAAG  
ATTTAACTGT TTGATTATAA CTGTGCAAT ACAGAAAAAA AGAAGGCTGG CTGAAAGTTG AGTTAACTT TGACAGTTG  
ATAATATTTG GTTCTTAGGG TTTTTTTTTT TTTAGCATT CTAAATAGTT ACAGTTGGGC ATGATTGTGA CCATCCACCC  
ATACCCACAC AGTCACAGTC ACACACACAT ATGTATTACT TACATATAT ATAACCTCTT ATGCAATAT TTTACCACCA  
GTCAATAATA CATTTTGGC AAGACATGAA GTTTTATAAA GATCTGTATA ATTGCCTGAA TCACCAGCAC ATTCAGTGAC  
ATGATATTAT TTGCAGATTG ACAAGTAGGA AGTGGGGAAC TTTTATTAAG TTAATCGTTG TCTGGGGAGG TAAATAGGTT  
AAAAACAGG AAATTATAAG TGCAGAGATT AACATTCAC AAATGTTAG TGAAACATTT GTGAAAAAG AAGACTAAAT  
TAAGACCTGA GCTGAAATAA AGTGACGTGG AAATGGAAAT AATGTTTATA TCTAAACAT GTAGAAAAAG AGTAAGTGGT  
AGATTTTGT TACAAATTA AGAATAAAGT TAGACAAGCA ACTGTTTAC TAATACATTA AGCCTTTGAG TCTAAGATGA  
AAGGAGAACA CTGGTTATGT TGATAGAATG ATAAAAAGG GTGGCGCGG AGGCTCAGC CTGTAATCCC AGCCCTTTGG  
GAGGCCGAGG TGGGCAGATC ACGAAGTCAG TAGTTTGAGA CCAGCCTGGC CAACATAGTG AAACCCGTC TCTACTAAAA  
ATACAAAAAA AAAATTAGCT GGGTGTGGT GCAGTCACCT GTAGTCCAG CTACTTGGGA GGATGAGGCA GGAGAATCGC  
TTGAACCTGG GAGGCCGAGG TTGCAGTGAG CCGAGATCGC ACCAGTGCAC TCCAGCCTTG GTGACAATGG GAGACTCCAT  
CTCAAAAAA AAAAAAGATA AAAAGTCAGA AATCTGAAAA GTGGAGGAAG AGTACAAATA  
GACCTAAAT AAGTCTCATT TTTTGGCTT GATTTTGGG AGACAAAGG AAATGCAGCC ATAGAGGGCC TGATGACATC  
CAATACATGA GTTCTGTAA AGATAAAAT TGATACACGG TTTGGTGTCA TTATAAGAGA AATCATTATT AAATGAAGCA  
AGTTAACT CTAAGAGAAT TATTTTGAGA TAGAAGTGAA GCTAAGCTAA ACTTCACATG CCTATAATTG GAGGGAAAAA  
CTAAGGATAA AATCTAGCCT AGAAGATACA ATAATTAGTC ATAAACATGC ATTGTGAAAC TGAGAGAGC AGGTAGCCCA  
AAATAGAGAA AGATTAGATA AAGAGAAAAA AAGTATCCAT CAGAGACAGT ATCTTAGGC TTGGGCAAGA GAAAAGTCCA  
CAGTGATAAG CAATCCACC TAAGGCATGA ATATGCGGCA GAGAAAAAC CAATAGTGAA TGAATGCAAA AGGTGCTGAG  
CAATTTCCAC ACATGAGTAT TGTGCATGAG TAAATGAATA AAACATTTG AAAGACCTT AGAGAAAGAG AATGGGAGCA  
TATGTGCGAA ATAAGATAGT TGATTATGAA TAGAAGGTAG TGAAGAAAAG CAAGCTAAGA AAAAATCTG TTTATAAAAG  
AAGGAAAAA TAGTTTATGT TTTTAGCCTA AGTATAAGAG TCCTACAGAT GGACTGAAAA AAATCAGTCT GAGAGTATTA  
GTCACAATTA ATGAAATAAT TACATTTTAT GTATTGAGGA TGCCAAGATT AAAAGGTGAC AGGTAGATGT TAATTTCCCT  
AGATTGTGAA AGTGATCAGC ACAATCACAC AAAAAATAAT TAAGTACTT GGTATGCTT ATTTAATTGT AGGCTCTGAG  
GTTTTCCATT CTCATTTTTC TAAATACAA TTTTGTITCT CCAATTTGA CAGCAGAATA AAAACCTAC CCTTCACTG  
TGTATCATGC TAAGCTGCAT CTCTACTCTT GATCATCTGT AGGTATTAAT CACATCACTT CCATGGCATG GATGTTTACA  
TACAGACTCT TAACCCTGGT TTACCAGGAC CTCTAGGAGT GGATCCAATC TATATCTTAA CAGTTGTATA GTATATGATA  
TCTCTTTTAT TCACTCAAT TTATATTTT ATCATTGACT ACATATTTCT TATACACAAC ACACAATTTA TGAATTTTTT

CTGAATGAAC ACCTTTTCAT CCAGCCTTAA TTTCTTGCTC CATAACTACT CTATCCCACG ATGCAGTATT GTATCATTAA  
TTATTAGTGT GCTTGTGACC TCCTTATGTA TTCTCAATTA CTGTATTG TGCAATAAAT TGGAATAATG TAACTTGATT  
TCTTATCTGT GTTTGTGTTG GCATGCAAGA TTTAGGTAAT TATCAAGATA ATGGGGAATT AAGGCATCAA TAAAATGATG  
CCAAAGACCA AGAGCAGTTT CTGAAGTCCT CTTTTCATC AGTCTTTAT CAAACAGAAC ACTCTATAAA CAACCCATAG  
CCAGAAAACA GGATGTAGGA ACAATCACCA GCACACTCTA TAAACAACCC ATAGCCAGAA AACAGAAATGT AAGGACAATC  
ACCAGCCATC TTTTGTCAAT AATTGATGGA ATAGAGTTGA AAGGAACTGG AGCATGAGTC ATATTTGACC AGTCAGTCCT  
CACTCTTATT TACTTGCTAT GTAAACTTGA GAAAGCTTTT TTCTCTTGT GAACCTCAGG TTTTACATCT GAAAATGAGA  
AATTTGGAAC AAAAGATTCC TAACGGTCT TTCTGTCCC ATATTCTGTG ATTTTCAAT ATTTAGGATT TTTGGTAATC  
ACAATTACTT AGTTTGTGGT TGAGATAGCA ACACGAATCA GAACTATTG GTGGACATAT TTTCAAAGGA GTAGCTCTCC  
ACTTTGGGTA AAGAAGTGAT GCNGGTCGTG GTGGCTCAGC CCTGTAATCC CAGCACTTA GGGAGGCEAA GCGGGTGGGA  
TCACGAGGTC AGGAGATCGA GACCATCCTG GCTAACACGG TGAAACCCCG TCTCTACTAA AAAATACAAA AAATTAGCCA  
GGCGTGGTGG CGGGCGCCTG TAGTCCCACG TACTCGGGAG GCTGAGGCAG GAGAATGGCA TGAACCAAGG AGCGGAGCT  
TGCCGTGAGC CGAGATAGCG CCACTGCACT CCTCCTGGG CAAAAGAGCA AGACTGCGTC TCAAAAAAAA AAAAAAAA  
AAAAAAGAA GTGTGTGGAG TAGCAGGACA CCTGCAACAA TAATATTTT CTAATCCCT CTGAAAAATG CTAATCAAG  
GGTTTTTTC TAAAAATTG TCTAGAAAT AAAATTCCC CTTTGGGAGA CCGAGGTGG CAGATCACGA GGTGAGGAGA  
TAGAGACCAC GGTGAAACCC CGTCTCTACT AAAATACTA AAAATTAGCC GGGGNGTGGT GGTGGGTACA CCTGTAGTCC  
CAGCTACTTG GAGGCTGAGG CTGGAGAATC ACGTGAAC-3' (FRAG. NO: ) (SEQ. ID NO:2504)

#### Human Histidine Decarboxylase Nucleic Acid and Antisense Oligonucleotide Fragments

5'-TCT CCC TTG GGC TCT GGC TCC TTC TC TCT CTC TCC CTC TCT CTC TGT CGC CTC CGC CCT GGC TGC TGG GGT  
GGT GGT GC TTT TGT TCT TCC TTG CTG CC GCC CCG CTG CTT GTC T TC CTC G CTC TGT CCC TCT CTC TCT GTB CTC  
CTC BGG CTC CBT CBT CTC CCT TGG GC-3' (FRAG. NO:1700) (SEQ. ID NO:1711)  
5'-GGC TCT GGC (FRAG. NO:1701) (SEQ. ID NO: 1712)  
5'-CCC TTG G (FRAG. NO:1702) (SEQ. ID NO: 1713)  
5'- TT TGT TCT TCC (FRAG. NO:1703) (SEQ. ID NO: 1714)  
5'- TCT CCC TTG GGC TCT GGC TCC TTC TC-3' (FRAG. NO:1024) (SEQ. ID NO: 1034)  
5'- TCT CTC TCC CTC TCT CTC TGT -3' (FRAG. NO:1025) (SEQ. ID NO:1035)  
5'- CGC CTC CGC CCT GGC TGC TGG GGT GGT GGT GC-3' (FRAG. NO:1026) (SEQ. ID NO:1036)  
5'- TTT TGT TCT TCC TTG CTG CC-3' (FRAG. NO:1027) (SEQ. ID NO:1037)  
5'- GCC CCG CTG CTT GTC T TC CTC G-3' (FRAG. NO:1028) (SEQ. ID NO:1038)  
5'-CTC TGT CCC TCT CTC TCT GTB CTC CTC BGG CTC CBT CBT CTC CCT TGG GC (FRAG. NO:1029) (SEQ. ID NO:1039)

#### Human Beta Tryptase Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CTT GCT CCT GGG GGC CTC CTG GTC CCT CCG GGT GTT CCC GGC GGG CCT GGC CTG GGG CBG GGG CCG CGT BGG  
CGC GGC TCG CCB GGB CGG GCB GCG CCB GCB GCB GCB GBT TCB GCB TCC TGG-3' (FRAG. NO:1704) (SEQ. ID NO:  
1715)  
5'- GCT CCT GGG GGC CT-3' (FRAG. NO:1705) (SEQ. ID NO: 1716)  
5'-CGT BGG CGC-3' (FRAG. NO:1706) (SEQ. ID NO: 1717)  
5'-T GGC CTG GGG-3' (FRAG. NO:1707) (SEQ. ID NO: 1718)  
5'-CTT GCT CCT GGG GGC CTC CTG-3' (FRAG. NO:1030) (SEQ. ID NO:1040)  
5'-GTC CCT CCG GGT GTT CCC GGC-3' (FRAG. NO:1031) (SEQ. ID NO:1041)  
5'-GGG CCT GGC CTG GGG CBG GGG CCG CGT BGG CGC GGC TCG CCB GGB CGG GCB GCG CCB GCB GCB GCB GBT TCB  
GCB TCC TGG-3' (FRAG. NO:1032) (SEQ. ID NO:1042)

#### Human Tryptase-I Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CTT GCT CCT GGG GGC CTC CTG GTC CCT CTG GCT G TT CCC GGC CCT GGB CTG GGG CBG GGG CCG CGT BGG CGC  
GGC TCG CCB GGB CGG GCB GCG CCB GCB GCB GCB GGC TCB GCB TCC TGG CCB CGG BBT TCC-3' (FRAG. NO: 1708)  
(SEQ. ID NO:1719)  
5'-CT CCT GGG GGC CTC CTG-3' (FRAG. NO:1709) (SEQ. ID NO:1720)  
5'-B TCC TGG CCB CGG BBT TCC -3' (FRAG. NO:1710) (SEQ. ID NO:1721)  
5'-GTC CCT C-3' (FRAG. NO:1711) (SEQ. ID NO:1722)  
5'-CTT GCT CCT GGG GGC CTC CTG-3' (FRAG. NO:1033) (SEQ. ID NO:1043)  
5'-GTC CCT CTG GCT G TT CCC GGC-3' (FRAG. NO:1034) (SEQ. ID NO:1044)  
5'-CCT GGB CTG GGG CBG GGG CCG CGT BGG CGC GGC TCG CCB GGB CGG GCB GCG CCB GCB GCB GCB GGC TCB GCB  
TCC TGG CCB CGG BBT TCC -3' (FRAG. NO:1035) (SEQ. ID NO:1045)

#### Human Prostaglandin D Synthase Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GGT GTG CGG GGC CTG GTG CC CCT GGG CCT CGG GTG CTG CCT GT GCG CTG CCT TCT TCT CCT GG GTC CTC GCC  
GGG GCC CTT GCT GCC CTG GCT GT GCC CTG GGG GTC TGG GTT CGG CTG T CCC CBG CBG GBC CBG TCC CBT CCB  
CBG CGT GTG BTG BGT BGC CBT TCT CCT GCB GCC GBG-3' (FRAG. NO:1712) (SEQ. ID NO:1723)  
5'-T TCT CCT GCB GCC GBG -3' (FRAG. NO:1713) (SEQ. ID NO:1724)  
5'-CTT GCT GCC CTG GCT GT-3' (FRAG. NO:1714) (SEQ. ID NO:1725)  
5'- TCT TCT CCT GG-3' (FRAG. NO:1715) (SEQ. ID NO:1726)  
5'-GGT GTG CGG GGC CTG GTG CC-3' (FRAG. NO:1036) (SEQ. ID NO:1046)  
5'-CCT GGG CCT CGG GTG CTG CCT GT-3' (FRAG. NO:1037) (SEQ. ID NO:1047)  
5'-GCG CTG CCT TCT TCT CCT GG-3' (FRAG. NO:1038) (SEQ. ID NO:1048)  
5'-GTC CTC GCC GGG GCC CTT GCT GCC CTG GCT GT-3' (FRAG. NO:1039) (SEQ. ID NO:1049)  
5'-GCC CTG GGG GTC TGG GTT CGG CTG T-3' (FRAG. NO:1040) (SEQ. ID NO:1050)  
5'-CCC CBG GBC CBG TCC CBT CCB CBG CGT GTG BTG BGT BGC CBT TCT CCT GCB GCC GBG -3'

(FRAG. NO:1041) (SEQ. ID NO:1051)

**Human Cyclooxygenase-2 Nucleic Acid and Antisense Oligonucleotide Fragments**

5'-GGG CGC GGG CGB GCB TCG C TTT GGG CTT TTC TCC TTT GGT T TGB GCG CCB GGB CCG CGC BCB GCB GCB GGG  
CGC GGG CGB GCB TCG CBG CGG CGG GCB GGG-3' (FRAG. NO: 1716) (SEQ. ID NO:1727)

5'-G GCB GGG -3' (FRAG. NO: 1717) (SEQ. ID NO: 1728)

5'-TCC TTT GGT T-3' (FRAG. NO:1718) (SEQ. ID NO:1729)

5'-GGG CGC GGG CGB GCB TCG C-3' (FRAG. NO:1042) (SEQ. ID NO:1052)

5'-TTT GGG CTT TTC TCC TTT GGT T-3' (FRAG. NO:1043) (SEQ. ID NO:1053)

5'-TGB GCG CCB GGB CCG CGC BCB GCB GCB GGG CGC GGG CGB GCB TCG CBG CGG CGG GCB GGG -3'  
(FRAG. NO:1044) (SEQ. ID NO:1054)

**Human Eosinophil Cationic Protein Nucleic Acid and Antisense Oligonucleotide Fragments**

5'-CCT CCT TCC TGG TCT GTC TGC CBG BCB BBT TTG GGB BGT GBB CBG TTT TGG BBC CBT GTT TCC CBG TCT CTG  
BGC TGT GGC-3' (FRAG. NO: 1719) (SEQ. ID NO: 1730)

5'-TTC TCC TTT GGT T-3' (FRAG. NO:1720) (SEQ. ID NO: 1731)

5'-T TTC TCC TTT GGT T-3' (FRAG. NO:1721) (SEQ. ID NO:1732)

5'-GGG CGC GGG CGB GCB TCG C-3' (FRAG. NO:1042) (SEQ. ID NO:1052)

5'-TTT GGG CTT TTC TCC TTT GGT T-3' (FRAG. NO:1043) (SEQ. ID NO:1053)

5'-TGB GCG CCB GGB CCG CGC BCB GCB GCB GGG CGC GGG CGB GCB TCG CBG CGG CGG GCB GGG -3'  
(FRAG. NO:1044) (SEQ. ID NO:1054)

**Human Eosinophil Derived Neurotoxin Nucleic Acid and Antisense Oligonucleotide Fragments**

5'-GCC CTG CTG CTC TTT CTG CT TCC CTT GGT GGG TTG GGC C GCT GGT TGT TCT GGG GTT C TTG CTG CCC CTT CTG  
TCC C TGT TTG CTG GTG TCT GCG C 5'-CCC CBB CBG BBG BBG CBG BCB BBT TTG GGB BGT GBB CBG TTT TGG BBC  
CBT GTT TCC TGT-3'

(FRAG. NO: 1722) (SEQ. ID NO: 1733)

5'-TTC CTG T-3' (FRAG. NO:1723) (SEQ. ID NO: 1734)

5'-CTC TTT CTG CT-3' (FRAG. NO: 1724) (SEQ. ID NO:1735)

5'-CCC CTT CTG TCC C-3' (FRAG. NO:1725) (SEQ. ID NO: 1736)

5'-GCC CTG CTG CTC TTT CTG CT-3' (FRAG. NO:1047) (SEQ. ID NO:1057)

5'-TCC CTT GGT GGG TTG GGC C-3' (FRAG. NO:1048) (SEQ. ID NO:1058)

5'-GCT GGT TGT TCT GGG GTT C-3' (FRAG. NO:1049) (SEQ. ID NO:1059)

5'-TTG CTG CCC CTT CTG TCC C-3' (FRAG. NO:1050) (SEQ. ID NO:1060)

5'-TGT TTG CTG GTG TCT GCG C -3' (FRAG. NO:1051) (SEQ. ID NO:1061)

5'-CCC CBB CBG BBG BBG CBG BCB BBT TTG GGB BGT GBB CBG TTT TGG BBC CBT GTT TCC TGT-3' (FRAG. NO:1052)  
(SEQ. ID NO:1062)

**Human Eosinophil Peroxidase Nucleic Acid and Antisense Oligonucleotide Fragments**

5'-GCG CTC GGC CTG GTC CCG G GGG TCT CCT CTT GTT GTT GC TTG CGC CTC CTG CTG GGG GT CC CTC TGT TCT TGT  
TTT GGG GGC GGG CCC GGC CGT TGT CTT G GTT TGG GGG TTT CCG TTG GGG TTC TCC GGT CCC GGG CCT TGC CC  
GGC CGT GGT CCC GGC TTC GTTCCT GTC TCC GTC TCG GCT CTT CTG GGG CCT TGC GCT TTT GGT G 5'-GCB CCG  
TCC BGT GBT GGT GCG GTB CTT GTC GCT GCB GCG CTC GGC CTG GTC CCG GBG BGC CACCGCTCCT GTCAGCCAAC  
AAATATCCAT TGAGCGACAC CTGTGTCCCA GGTGCTGCTC TGGGCCCTGG GAGAAGTGCA TCAGTGGGCT TGGTAGTAGA  
GGGTAGGGAT GGAGTGAAGG GTAGGCAGGA AGAATGTCCC CAGGCTGGTA GGAGGTGGGG TGGGGGGTTT CAGTCTCAAA  
ACTCCCATGA AAACAGAGA GAAGTTTTCAG AACTCCACCC AAGAGGCTGG GTTCTAGGG CCCAGAGCTG CCCTCCCCCA  
CCCTAGATG GGCTATAAAA GTCCCTTCCC AGCTACGTCC AGAGAAGAGC TGGAGGAAGT GAGAGGTCCG CTGGGGGTCC  
TCAAAGTGAG AGGGGAGCAG AGGATCCTCC CGTGCAGGCT GTGGATGTCA CTCATTCCC AGCTGGTGAA GCCTCGCTGC  
AGAGATGCAT CTGCTCCAG CCCTGGCAGG GGTCTGGCC ACACCTGTC TCGCCAGCC CTGTGAGGGC ACTGACCCAG  
GTAATAGTCC CTTAGACAGG CAAGGAGGAG GGAGGGGAAA TGAAGGGGA AGCACTTGGG TCTTGGAGGG GGTCTGTGG  
CTTGCTGAAC CTTGAGTCCC CATCTCTTTG AACAGCCTCC CTTGGGGCAG TGGAGACCTC GGTCTGCGA GACTGCATAG  
CAGAGGCCAA GTTGCTGGTG GATGCTGCCT ACAATTGGAC CCAGAAGAGG TGGACTTGGG TCTGGGGGCT GCATGGGCT  
GGGAGGATCA GT TAATACCTTG TGGGGTCAGG GAGCCCATGT CCCGTGCTGA TGTTATTTC CCACCAGGTC  
CGGGCTGTCT CCAACCAGAT TGTGCGCTC CCAATGAGA GACTGACCTC CGACCGTGGC CGAGCCCTCA TGITCATGCA  
GTGGGGCCAG TTCAATTGACC ATGACCTGGA CTTCTCCCCG GAGTCCCCGG CCAGAGTGGC CTTACTGCA GCGGTGACT  
GTGAGAGGAC CTGCGCCAG CTGCCCCCT GCTTCCCAT CAAGGTACCT ACCCTAGCC AATCTCCCAT GCCCTGTGT  
GGCCTCCCC AAAGGCAAGG TGCTGGGGGT GGGGATCTGG AAGACTGGAG CACCATCCTT AAGGAGCTGC CTGTGGAGCT  
AGGGTATGAG ACAGAGACAC AAG CACTGTCTCC TCTTCCATCT CAGATCCAC CCAATGACCC CCGCATCAAG  
AACCAGCGTG ACTGCATCCC TTTCTTCCGC TCGGCACCCT CATGCCCCA AAACAAGAAC AGAGTCCGCA ACCAGATCAA  
CGCGTCAAC TCCTTTGTGG ACGCCAGCAT GGTGTATGGC AGTGAGGTCT CCTCTCGCT GCGGCTCCGC AACCAGGACA  
ACTACCTGGG GCTGCTGGCC ATCAACCAGC GCTTCAAGA CAACGGCCGG GCCCTGCTGC CCTTCGACAA CTTGCACGAT  
GACCCCTGTC TCCTACCAA CCGCTCGGCG CGCATCCCCT GCTTCTGGC AGGTCAGACA GGGAGGAAGG TGGTGTCTTC  
CCAGGAAACA GCCATCCCTG GGTCCCAAC TGGGAAGCAA TGGTGGGATG TGGTGAAGGT ACATGGTTTG GGACCTCAGT  
ATTAGGCACA CCATAAGCAT GGATCTGTGC AC TGAAGAGATG GAGGTCCAGT GAGGGCCAGG AGTTTGGCCC  
ACCCGCTCTC TCCCATCCCC AGCCCTGGGT CTACCCTGGT AGAAAGACAT TTCTCTGGGA AAGGCTGCAG TAAATCTGAG  
CTTGGGGTTT TCAAGGTGAC ACCCGATCAA CGGAAACCCC CAACTGGCA GCCATGCACA CCTCTTTAT GCGAGAGCAC  
AACC GGCTGG CCACCGAGCT GAGACGCTG AATCCCCGGT GGAATGGAGA CAACTGTAC AATGAGGCTC GGAAGATCAT

CTTCCGCTTT GGCCACACAA TGCTCCAGCC CTTCATGTTT CGCTTGGACA GTCAGTACCG GGCCTCCGCA CCCAACTCGC  
ATGTCCCACT TAGCTCTGCC TTCTTTGCCA GCTGGCGGAT CGTGTATGAA GGTGACCAGG TTTTCCAGGG GGCAAATGGG  
GGTGAGGGTG GGGAGCATGC CCTCCCTAG GTGG TCCAGCTGCT TCATGTCTCT CCAGAACTCT GTTCTCTGAC  
AAACGTTACT AACATACCCG ACTGGCTTGT CCAGCTCTGG GCTAGCTTGG CATCATGTGA TAACCAAGT AGCTTCCAG  
AGGCTGGTCC AATCTGTGCT GCTCACATTC CTTGCCACCA GGGGGCATCG ACCCATCTCT CCGGGGCTC ATGGCCACCC  
CTGCCAAGCT GAACCGTCAG GATGCCATGT TAGTGGATGA GCTCCGGGAC CGGCTGTTTC GGCAAGTGAG GAGGATTGGG  
CTGGACCTGG CAGCTCTCAA CATGCAACGA AGCCGGGACC ACGGCCTTCC AGGTGAGGGG GCTGTCCACC TCTTCTCCA  
GCTTTGCTCG GGCCAGGCTG CTCAAGGGGT TCTGGGAAGA CCCTGGTACC CGACTGCCTG GTAGTTCTG GTGGCAGAAA  
CGAGGTGTTT TCACCAAAAG ACAGCGCAAG GCCCTGAGCA GAATTTCTT GTCTCGAATT ATATGTGACA ATACCGGTAT  
CACCACGGT TCAAGGGACA TCTTCAGAGC CAACATCTAC CCTCGGGGCT TTGTGAAGTG CAGCCGTATC CCCAGTTGA  
ACCTATCAGC CTGGCGAGGG ACATGAGGCT TCTGACGTA AGGGGAGGCC ACCTCCAGCA CCTGGGCTG GTTAAGCCTC  
ACATCCTTCC CTGGATGGAT GGCTGAGTCC TCTAGGTTCT TAAGCAGAG AAAACAGAAC TTGTACTAG GTACTCTTTC  
CAAGTGGCTT CCAGATGTGC TAGTTTCTGG GCTGACAGTC AATTCAGGC CCTAGGACTT TGGGGGAAA TTAGGAGCAT  
CCAATA GAATTCGTG GCCAGGACCC CTGCCAGGGC ACTGACCCAG CCTCCCTGG GGCAGTGGAG ACCTCGGTCC  
TGCGAGACTG CATAGCAGAG GCCAAGTTGC TGGTGGATGC TGCCTACAAT TGGACCCAGA AGAGCATCAA GCAGCGGCTT  
CGCAGCGGTT CAGCCAGCCC CATGGACCTC CTGTCTACT TCAAACAACC GGTAGCAGCC ACCAGGACAG TTGTCGGGG  
CGCAGATTAT ATGCATGTGG CTTTGGGGCT GCTTGAAGAG AAGTTACAAC CCCAGCGGTC CGGACCCCTT ATTGTACTG  
ATGTGCTAAC AGAACACAG CTGCGGCTGC TGTCCAGGC CAGTGGCTGT GCTCTCCGG ACCAGGCCGA GCGTGCAGC  
GACAAGTACC GCACCATCAC TGGACGGTGC AACAACAAGA GGAGACCTT GCTAGGGGCC TCAACCAGG CTCTGGCTCG  
CTGGCTGCCC GCCGAGTATG AGGATGGGCT GTCGTCCCC TTCGGCTGGA CCCCCAGCAG GAGGCGCAAT GGCTTCTTC  
TCCCTCTGT CCGGGCTGTC TCAACCAGA TTGTGCGCTT CCCCATGAG AGACTGACCT CCGACCGTGG CCGAGCCCTC  
ATGTTTCATGC AGTGGGGCCA GTTCATTGAC CATGACCTGG ACTTCTCCCC GGAGTCCCCG GCCAGAGTGG CCTTCACTGC  
AGGCGTTGAC TGTGAGAGGA CCTGCGCCCA GCTGCCCCC TGCTTTCCA TCAAGATCCC ACCCAATGAC CCCCACATCA  
AGAACCAGCG TGACTGCATC CTTTCTTCC GCTCGGCACC CTCATGCCCC CAAAACAAGA ACAGAGTCCG CAACAGATC  
AACCGCTCA CCTCTTTGT GGACGCCAGC ATGGTGTATG CAGTGGAGGT CTCCTCTCG CTGCGGCTCC GCAACCGGAC  
CAACTACCTG GGGCTGCTGG CCATCAACCA GCGCTTTCAA GACAACGCC GGGCCTGCT GCGCTTCGAC AACCTGCACG  
ATGACCCCTG TCTCTCACC AACCGCTCG CGCGCATCCC CTGCTTCTG GCAGGTGACA CCGATCAAC GGAACCCCC  
AACTGGCAG CCATGCACAC CCTCTTTATG CGAGAGCACA ACCGGCTGGC CACCGAGCTG AGACGCCTGA ATCCCCGGTG  
GAATGGAGAC AAATGTACA ATGAGGCTCG GAAGATCATG GGGGCCATGG TCCAGATCAT CACCTACCGA GACTTCTGC  
CCTGTTCTT GGGCAAGGCC CGGGCCAGGA GAACCTGGG GCACTACAGG GGGTACTGCT CCAATGTGGA CCCAGGGTG  
GCCAATGCT TCACCTGGC CTTCCGCTT GGCCACAAA TGCTCCAGCC CTTCATGTTT CGTGTGACA GTCAGTACCG  
GGCTCCGCA CCAACTCGC ATGTCCCACT TAGTCTGCTT TCTTTGCCA GCTGGCGGAT CGTGTATGAA GGGGGCATCG  
ACCCATCCT CCGGGGCTC ATGGCCACCC CTGCCAAGCT GAACCGTCAG GATGCCATGT TAGTGGATGA GCTCCGGGAC  
CGGCTGTTT GGCAAGTGAG GAGGATTGGG CTGGACCTGG CAGCTCTCAA CATGCAACGA AGCCGGGACC ACGGCCTTCC  
AGGTACAAT GCTTGGAGGC GCTTCTGTGG GCTCTCCAG CCCCAGAAAT TGGCAGAGT TAGCCGGGTG CTGAAAAACC  
AGGACTTGGC AAGGAAGTTC CTGAATTTGT ATGGAACACC TGACAACATT GACATCTGGA TTGGGGCCAT CGCTGAGCT  
CTTTGCCGG GGGCTCGAGT GGGGCTCTT CTGGCTTGT TGTTCGAAA CCAATTGAGA AGAGCCGAGA CGGAGACAGG  
TTCTGGTGG AGAACGAGGT GTTTTACCA AAGACAGCGC AAGCCCTGA GCAGAAATTC CTGTCTCGA ATTATATGTG  
ACAAATACCG TATCACACG GTTTCAAGG ACATCTTCAG AGCCAACATC TACCTCGGG GCTTTGTGAA CTGCAGCCGT  
ATCCCCAGGT TGAACCTATC AGCCTGGCA GGGACATGAG GCTTCTGAG GAGTCTATCC CAAGTCTCCA ACTTTTGGAG  
ACAGGGGAA GGGGAGGACC ATGAGGCTGC CTGTCTCCC TGGAGCAAGT GCAGGCTCGT GACGCTTCTG CTGGCTACAG  
CTCAGAGCTG GGTTCGCCAG CAGGAGTGA AGGCTGGGG CTCTATCAG CAATGGACCT TCCGCTTGG GAGCCTCTTA  
GGTATTAGG TATGAATCAG CGCCACGTGC AAAGGCTTGG GAGCCAAGCC ATGTGGTCTT GCACCCAGG CAAGAAAAGT  
CAGCTGGAGG GTTACAGCA CTTTCTACT TTTCCAGCC CTCCTCCCC TCCTCACA TGAATAAG AGCACTCGGT  
CCTAGCTTC AGACACCCA CAATACTCT CTGAGCTGA GGCCAGGCAG CATGCTCTGC TTCTACCAAT AAAGCACTGC  
CGGAATTC-3' (FRAG. NO: 1726) (SEQ. ID NO: 1737)

5'-CACCGCTCCT GTCAGCCAAC AAATATCCAT TGAGCGACAC CTGTGTCCCA GGTGTGCTC TGGGCCCTGG  
GAGAAGTGCA TCAGTGGGCT TGGTAGTAGA GGGTAGGGAT GGAGTGAAGG GTAGGACAGA AGAATGTCCC CAGGCTGGTA  
GGAGGTGGGG TGGGGGGTTT CAGTCTCAA ACTCCCATGA AAACCAGAGA GAAGTTTCAG AACTCCACCC AAGAGGCTGG  
GTTTCTAGGG CCCAGAGCTG CCTCCCCCA CCTAGAATG GGCTATAAAA GTCCTTCCC AGCTACGTCC AGAGAAGAGC  
TGGAGGAAGT GAGAGGTCCG CTGGGGGTCC TCAAAGTGAG AGGGGAGCAG AGGATCCTCC CTGTCAGGCT GTGGATGTA  
CTCACTTCCC AGCTGGTGAA GCCTCGTGC AGAGATGCAT CTGCTCCAG CCTGGCAGG GGTCTGGCC AACTCGTCC  
TCGCCAGCC CTGTGAGGGC ACTGACCCAG GTAATAGTCC CTTAGACAGG CAAGGAGGAG GGAGGGGAAA TGAAGGGGA  
AGCACTGGG TCTTGGAGGG GGTCTTGTG CTGTGTAAC CTTGAGTCCC CATCTTTT AACAGCCTCC CTGGGGCAG  
TGGAGACCTC GGTCTCGGA GACTGCATAG CAGAGGCCAA GTTGTGGTG GATGCTGCT ACAATTGGAC CCAGAAGAGG  
TGGACTTGGG TCTGGGGGCT GCATGGGCT GGGAGGATCA GT-3' (FRAG. NO: ) (SEQ. ID NO: 2483)

5'-TAATACCTTG TGGGGTCAGG GAGCCCATGT CCCGTGCTGA GTTATTTC CCACAGGTC CGGGCTGTCT CCAACCAGAT  
ATGCGCTTC CCAATGAGA GACTGACCTC CGACGGTGGC CGAGCCCTCA GTTTCATGCA GTGGGGCCAG TTCAATTGACC  
TGACTTGGA CTTCTCCCG GAGTCCCGG CCAGAGTGGC CTTCACTCA GGCCTTGACT GTGAGAGGAC CTGCGCCAG  
CTGCCCCCT CTTTCCCAT CAAGGTACCT ACCCTCAGCC AATCTCCAT GCCCTTGTG GGCCTCCCC AAAGGCAAGG  
TGCTGGGGT GGGGATCTGG AAGACTGGAG CACCATCCTT AAGGAGCTGC CTGTGGAGCT AGGGTATGAG ACAGAGACAC  
AAG-3' (FRAG. NO: ) (SEQ. ID NO: 2484)

5'-CACTGTCTCC TCTTCATCT CAGATCCAC CCAATGACCC CCGCATCAAG AACCAGCGTG ACTGCATCCC TTTCTTCCG  
TCGGCACCT CATGCCCCA AAACAAGAAG AGAGTCCGA ACCAGATCAA CGCGCTACC TCCTTTGTGG ACGCCAGCAT  
GGTGTATGGC AGTGAGGTCT CCTCTCGCT CGCGCTCCG AACCGACCA ACTACCTGG GCTGCTGGCC ATCAACCAG  
GCTTCAAGA CAACGGCCGG GCCCTGTGC CTTTCAGCA CCTGCACGAT GACCCCTGTC TCTCACC AAAGGCAAGG  
CGCATCCCT GCTTCTGGC AGGTGAGACA GGGAGGAAG TGGTGTCTT CCAGGAAACA GCCATCCCTG GGGTCCCAAC  
TGGGAAGCAA TGGTGGATG TGGTGAAGT ACATGGTTT GGACCTCAGT ATTAGGCACA CCATAAGCAT GGATCTGTGC  
AC-3' (FRAG. NO: ) (SEQ. ID NO: 2485)

5'-TGAAGAGATG GATCCAGT GAGGGCCAGG AGTTTGGCCC ACCCGTCTC CATCCCC AGCCCTGGGT CTACCCCTGGT  
AGAAAGACAT TTCTCTGGGA AAGGCTGCAG TAAATCTGAG CTGGGGTTT TCAAAGGTGAC ACCCGATCAA CGGAAACCCC  
CAAACCTGGCA GCCATGCACA CCTCTTTAT GCGAGAGCAC AACCGGCTGG CCACCGAGCT GAGACGCTG AATCCCCGGT  
GGAATGGAGA CAAACTGTAC AATGAGGCTC GGAAGATCAT GGGGGCCATG GTCCAGGTAA GGAGCTCTGC ATCCAGCAT  
CCCC-3' (FRAG.NO: )(SEQ.IDNO:2486)

5'-CTTTGTATCT CCACCCACCA ATAGTAAATT AATGTTGTCA CATTGACGT GATGACAATA AAGAATATGT CTGAGCCACC  
CTTTGAAAAG GCAAGGGTAT GGGTGAGTAG CCTCTGGGA ATGTTCTCC TGTCTTCCCT TCCAGATCAT CACCTACCGA  
GACTTTCTGC CCCTGGTTCT GGGCAAGGCC CGGGCCAGGA GAACCTGGG GCACTACAGG GGGTACTGCT CCAATGTGGA  
CCACCGGGTG GCCAATGTCT TCACCTGGC TTCCGCTTT GGCCACACAA TGCTCCAGCC TTCTATGTTT CGTTGGACA  
GTCAGTACCG GGCCTCCGA CCAACTCGC ATGTCCACT TAGCTCTGCC TTCTTTGCA GCTGGCGGAT CGTGATGAA  
GGTGACCAGG TTTCCAGGG GGCAATGGG GGTGAGGGTG GGGAGCATGC CCTCCCCTAG GTGG-3' (FRAG.NO: )(SEQ.ID  
NO:2487)

5'-TCCAGCTGCT TCATGTCTCT CCAGAACTCT GTTCTCTGAC AAACGTTACT AACATACCCG ACTGGCTTGT CCAGCTCTGG  
GCTAGCTTGG CATCATGTGA TAACCCAAGT AGCTTCCAG AGGCTGGTCC AATCTGTGCT GCTCACATTC CCTGCCACCA  
GGGGGCATCG ACCCATCCT CCGGGGCTC ATGGCCACCC CTGCAAGCT GAACCGTCAG GATGCCATGT TAGTGGATGA  
GCTCCGGGAC CGGCTGTTT GGCAAGTGAG GAGGATTGGG CTGGACCTGG CAGCTCTCAA CATGCAACGA AGCCGGGACC  
ACGGCTTCC AGGTGAGGGG GCTGTCCACC TCTTCTCCA GCTTGTCTG GGCAGGCTG CTCAAGGGGT TCTGGGAAGA  
CCCTGGTACC-3' (FRAG.NO: )(SEQ.ID NO:3488)

5'-CGACTGCTG GTAGTTCTG GTGGCAGAAA CGAGGTGTT TCACCAAAG ACAGCGCAAG GCCCTGAGCA  
GAATTTCTT GTCTCGAATT ATATGTGACA ATACCGGTAT CACCACGGT TCAAGGGACA TCTTCAGAGC CAACATCTAC  
CCTCGGGGCT TTGTGAACTG CAGCCGTATC CCCAGGTTGA ACCTATCAGC CTGGCGAGGG ACATGAGGCT TCTGCAGGTA  
AGGGGAGGCC ACCTCCAGCA CCTGGGCTG GTTAAGCCTC ACATCTTCC CTGGATGGAT GGCTGAGTCC TCTTAGGTCT  
CTAAGCAGAG AAAACAGAAC TTGTCACTAG GTACTTTTC CAATGGCTT CCAATGTGC TAGTTTCTGG GCTGACAGTC  
AATTCAGGC CTAGGACTT TGGGGGGAAA TTAGGAGCAT CCAACTA-3' (FRAG.NO: )(SEQ.ID NO:2489)

5'-GAATTCGTG GCCAGGCC CTGCCAGGC ACTGACCCAG CCTCCCCTGG GGCAGTGGAG ACCTCGGTCC  
TGCGAGACTG CATAGCAGAG GCCAAGTTGC TGGTGGATGC TGCTACAAT TGGACCCAGA AGAGCATCAA GCAGCGGCTT  
CGCAGCGGT CAGCCAGCCC CATGGACCTC CTGTCTACT TCAAACAACC GGTAGCAGCC ACCAGGACAG TTGTTCGGGC  
CGCAGATTAT ATGCATGTGG CTTTGGGGCT GCTTGAAGAG AAGTTACAAC CCCAGCGGTC CGGACCTTC ATTGTCACTG  
ATGTGCTAAC AGAACCACAG CTGCGGCTGC TGTCCAGGC CAGTGGCTGT GCTCTCCGGG ACCAGGCCGA GCGCTGCAGC  
GACAAGTACC GCACCATCAC TGGACGGTGC AACAACAAGA GGAGACCTT GCTAGGGGCC TCCAACCAGG CTCTGGCTCG  
CTGGCTGCCC GCCGAGTATG AGGATGGGCT GTGCTCCCC TTCGGCTGGA CCCCCAGCAG GAGGCGCAAT GGCTTCTTC  
TCCCTCTGT CCGGGCTGTC TCCAACCAGA TTGTGCGCTT CCCAATGAG AGACTGACCT CCGACCGTGG CCGAGCCCTC  
ATGTTTCATG AGTGGGGCCA GTTCATTGAC CATGACCTGG ACTTCTCCC GGAGTCCCC GCCAGTATG CTTCACTGC  
AGGCGTTGAC TGTGAGAGGA CTTGCGCCCA GCTGCCCTCC TGTCTTCCA TCAAGATCCC CCAATGAC CCCCCATCA  
AGAACCAGCG TGACTGCATC CCTTCTTCC GCTCGGCACC CTCATGCCCC CAAAACAAGA ACAGAGTCCG CAACCAGATC  
AACCGCTCA CTCCTTTGT GGACGCCAGC ATGGTGTATG GCAGTGAGGT CTCCTCTCG CTGCGGCTCC GCAACCGGAC  
CAACTACCTG GGGCTGCTGG CCATCAACCA GCGCTTCAA GACAACGGCC GGGCCCTGCT GCCCTTCGAC AACCTGCAGC  
ATGACCCCTG TCTCCTACC AACCGCTCG CGCGCATCCC CTGCTTCTG GCAGGTGACA CCCGATCAAC GGAAACCCCC  
AACTGGCAG CCATGCACAC CCTCTTTATG CGAGAGCACA ACCGGCTGGC CACCGAGCTG AGAGCGCTGA ATCCCCGGTG  
GAATGGAGAC AAATGTACA ATGAGGCTCG GAAGATCATG GGGGCCATGG TCCAGATCAT CACCTACCGA GACTTCTGC  
CCCTGGTTCT GGGCAAGGCC CGGGCCAGGA GAACCTGGG GCACTACAGG GGGTACTGCT CCAATGTGGA CCCACGGGTG  
GCCAATGTCT TCACCTGGC CTCCGCTTT GGCCACACAA TGCTCCAGCC CTTCATGTTT CGCTTGGA GTCAGTACCG  
GGCTCCGCA CCAACTCGC ATGTCCACT TAGCTCTGCC TTCTTTGCA GCTGGCGGAT CGTGATGAA GGGGGCATCG  
ACCCATCCT CCGGGGCTC ATGGCCACCC CTGCCAAGT GAACCGTCAG GATGCCATGT TAGTGAGTGA GCTCCGGGAC  
CGGCTGTTT GGAAGTGAG GAGGATTGGG CTGGACCTGG CAGCTCTCAA CATGCAACGA AGCCGGGACC ACGGCTTCC  
AGGTACAAT AATTGGAGG GCTTCTGTGG GTGTCTCCAG CCGGGAATT TGGCACAGCT TAGCCGGGTG CTGAAAAACC  
AGGACTTGGC GAGGAAGTTC CTGAATTTGT ATGGAACACC TGACAACATT GACATCTGGA TTGGGGCCAT CGCTGAGCCT  
CTTTGCGCG GGGCTCGAGT GGGGCTCTT CTGGCTGTC TGTTGAGAA CCAGTTCAGA AGAGCCGAGA CGGAGACAGG  
TTCTGGTGGC AGAACGAGGT GTTTTACCA AAGACAGCG AAGGCCCTGA GCAGAATTC CTGTCTCGA ATTATATGTG  
ACAATACCGG TATCACCAG GTTTCAAGGG ACATCTTCAG AGCCAACATC TACCCTCGG GCTTTGTGAA CTGCAGCCGT  
ATCCCCAGGT TGAACCTATC AGCCTGGCGA GGGACATGAG GCTTCTGAG GAGTCTATCC CAAGTCTCCA ACTTTTGGAG  
ACAAGGGGAA GGGGAGGACC ATGAGGCTGC TTGTCTCCC TGGAGCAAGT GCAGGCTCGT GACGCTTCTG CTGGCTACAG  
CTCAGAGCTG GGTTCGCCAG CCAGGAGTGA AGGCTGGGG CTCCTATCAG CAATGGACCT TCCGCTTGG GAGCCTCTTA  
GGTATTAGG TATGAATCAG CGCCACGTGC AAAGGCTTGG GAGCCAAGCC ATGTGGTCTT GCACCCAGG CAAGAAAAGT  
CAGCTGGAGG GTTACAGCA CTTTCTACTG TTTCCAGCC CTCCTCCCC TCCCTACCA TGAATAAGAG ACCACTCGGT  
CCTAGCCTCC AGACACCCA CAATACTCT CTGAGCCTGA GGCCAGGCAG CATGCTCTGCT TTCTACCAAT AAAGCACTGC  
CGGAATTC-3' (FRAG.NO: )(SEQ.ID no:2490)

5'-TC GGC CTG GTC CCG G-3' (FRAG. NO: 1727) (SEQ. ID NO:1738)

5'-TGG GGG TTT CCG TTG-3' (FRAG. NO: 1728) (SEQ. ID NO: 1739)

5'-TG GTC CCG GBG BGC -3' (FRAG. NO: 1729) (SEQ. ID NO: 1740)

5'-GCG CTC GGC CTG GTC CCG G-3' (FRAG. NO:1053) (SEQ. ID NO:1063)

5'-GGG TCT CCT CTT GTT GTT GC-3' (FRAG. NO:1054) (SEQ. ID NO:1064)

5'-TTG CGC CTC CTG CTG GGG GT CC-3' (FRAG. NO:1055) (SEQ. ID NO:1065)

5'-CTC TGT TCT TGT TTT GGG GGC-3' (FRAG. NO:1056) (SEQ. ID NO:1066)

5'-GGG CCC GGC CGT TGT CTT G-3' (FRAG. NO:1057) (SEQ. ID NO:1067)

5'-GTT TGG GGG TTT CCG TTG-3' (FRAG. NO:1058) (SEQ. ID NO:1068)

5'-GGG TTC TCC TGG CCC GGG CCT TGC CC-3' (FRAG. NO:1059) (SEQ. ID NO:1069)

5'-GGC CGT GGT CCC GGC TTC GTT GC-3' (FRAG. NO:1060) (SEQ. ID NO:1070)

5'-GCT CTC GGC CTC GGC CTT CTC -3' (FRAG. NO:1061) (SEQ. ID NO:1071)

5'-GGG CCT TGC GCT GTC TTT GGT G-3' (FRAG. NO:1062) (SEQ. ID NO:1072)

5'-GCB CCG TCC BGT GBT GGT GCG GTB CTT GTC GCT GCB GCG CTC GGC CTG GTC CCG GBG BGC -3' (FRAG. NO:1063) (SEQ. ID NO:1073)

#### Human Intercellular Adhesion Molecule-1 (ICAM-1) Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GCG CGG GCC GGG GGC TGC TGG G GGT TGG CCC GGG GTG CCC C GCC GCT GGG TGC CCT CGT CCT CTG CGG TC GTG TCT CCT GGC TCT GGT TCC CC GCT GCG CCC GTT GTC CTC TGG GGT GGC CTT C GCT CCC GGG TCT GGT TCT TGT GT TGG GGG TCC CTT TTT GGG CCT GTT GT GGC GTG GCT TGT GTG TTC GGT TTC TGC CCT GTC CTC CGG CGT CCC CGG BGC CTC CCC GGG GCB GGB TGB CTT TTG BGG GGG BCB CBG BTG TCT GGG CBT TGC CBG GTC CTG GGB BCB GGB CCC GCB GCB GGB CCB GGB GTG CGG GCB GCG CGG GCC GGG GGC TGC TGG GBG CCB TBG CGB GGC TGB G-3' (FRAG. NO: 1730)

(SEQ. ID NO: 1741)

5'-GGG GGC TGC TGG G-3' (FRAG. NO: 1731) (SEQ. ID NO:1742)

5'-T GTC CTC CGG CGT CCC-3' (FRAG. NO:1732) (SEQ. ID NO:1743)

5'-G CCB TBG CGB GGC TGB G-3' (FRAG. NO: 1733) (SEQ. ID NO: 1744)

5'-CTC TGG GGT GGC CTT C-3' (FRAG. NO:1734) (SEQ. ID NO:1745)

5'-GCG CGG GCC GGG GGC TGC TGG G-3' (FRAG. NO:1064) (SEQ. ID NO:1074)

5'-GGT TGG CCC GGG GTG CCC C-3' (FRAG. NO:1065) (SEQ. ID NO:1075)

5'-GCC GCT GGG TGC CCT CGT CCT CTG CGG TC-3' (FRAG. NO:1066) (SEQ. ID NO:1076)

5'-GTG TCT CCT GGC TCT GGT TCC CC-3' (FRAG. NO:1067) (SEQ. ID NO:1077)

5'-GCT GCG CCC GTT GTC CTC TGG GGT GGC CTT C-3' (FRAG. NO:1068) (SEQ. ID NO:1078)

5'-GCT CCC GGG TCT GGT TCT TGT GT-3' (FRAG. NO:1069) (SEQ. ID NO:1079)

5'-TGG GGG TCC CTT TTT GGG CCT GTT GT-3' (FRAG. NO:1070) (SEQ. ID NO:1080)

5'-GGC GTG GCT TGT GTG TTC GGT TTC-3' (FRAG. NO:1071) (SEQ. ID NO:1081)

5'-TGC CCT GTC CTC CGG CGT CCC-3' (FRAG. NO:1072) (SEQ. ID NO:1082)

5'- CGG BGC CTC CCC GGG GCB GGB TGB CTT TTG BGG GGG BCB CBG BTG TCT GGG CBT TGC CBG GTC CTG GGB BCB GBG CCC CGB GCB GGB CCB GGB GTG CGG GCB GCG CGG GCC GGG GGC TGC TGG GBG CCB TBG CGB GGC TGB G-3' (FRAG. NO:1073) (SEQ. ID NO:1083)

#### Human Vascular Cell Adhesion Molecule 1 (VCAM-1)

##### Nucleic Acid and Oligonucleotide Fragments

5'-CCT CTT TTC TGT TTT TCC C CTC TGC CTT TGT TTG GGT TCG CTT CCT TTC TGC TTC TTC C CTG TGT CTC CTG TCT CCG CTT TTT TCT TC GTC TTT GTT GTT TTC TCT TCC TTG CTG BGC BBG BTB TCT BGB TTC TGG GGT GGT CTC GBT TTT BBBB GCT TGB GBB GCT GCB BBC BTT BTC CBB BGT BTB TTT GBG GCT CCB BGG BTC BCG BCC BTC TTC CCB GGC BTT TTB BGT TGC TGT CGT-3' (FRAG. NO: 1735) (SEQ. ID NO: 1746)

5'-C TGT CGT-3' (FRAG. NO:1736) (SEQ. ID NO:1747)

5'-TGC TTC TTC C-3' (FRAG. NO:1737) (SEQ. ID NO:1748)

HSVCAM1A51: 5'-CCT CTT TTC TGT TTT TCC C-3' (FRAG. NO:1074) (SEQ. ID NO:1084)

HSVCAM1A52: 5'-CTC TGC CTT TGT TTG GGT TCG-3' (FRAG. NO:1075) (SEQ. ID NO:1085)

HSVCAM1A53: 5'-CTT CCT TTC TGC TTT C-3' (FRAG. NO:1076) (SEQ. ID NO:1086)

HSVCAM1A54: 5'-CTG TGT CTC CTG TCT CCG CTT TTT TCT TC-3' (FRAG. NO:1077) (SEQ. ID NO:1087)

HSVCAM1A55: 5'-GTC TTT GTT GTT TTC TCT TCC TTG-3' (FRAG. NO:1078) (SEQ. ID NO:1088)

CTG BGC BBG BTB TCT BGB TTC TGG GGT GGT CTC GBT TTT BBBB GCT TGB GBB GCT GCB BBC BTT BTC CBB BGT BTB TTT GBG GCT CCB BGG BTC BCG BCC BTC TTC CCB GGC BTT TTB BGT TGC TGT CGT (FRAG. NO:1079) (SEQ. ID NO:1089)

#### Human Endothelial Leukocyte Adhesion Molecule(ELAM-1)

##### Nucleic Acid and Antisense Oligonucleotide Fragments

5'-BBG TGB GBG CTG BGB GBB BCT GTG BBG CBB TCB TGB CTT CBB GBG TTC TTT TCB CCC GTT CTT GGC TTC TTC TGT C CGT TGG CTT GCT GTT GTC CC TGT GGG CTT CTC GTT GTC CC CCC TTC GGG GGC TGG TGG GGC CGT CCT TGC CTG CTG G GTT CTT GGC TTC TTC TGT CCG T TGG CTT CTC GTT GTC CC TGT GGG CTT CTC GTT GTC CC CCC TTC GGG GGC TGG TGG GGC CGT CCT TGC CTG CTG G CCTGAGACAG AGGCAGCAGT GATACCCACC TGAGAGATCC TGTGTTTGAA CAACTGCTTC CAAAACGGA AAGTATTTCAG AGCCTAAACC TTGGGTGAA AAGAACTCTT GAAGTCATGA TTGCTTCACA GTTCTCTCA GCTCTCATT TGGTGCTTCT CATTAAAGAG AGTGGAGCCT GGTCTTACAA CACCTCCACG GAAGCTATGA CTTATGATGA GGCCAGTGCT TATTGTTCAG AAAGGTACAG ACACCTGGTT GCAATTCAAA ACAAGAAGA GATTGAGTAC CTAACCTCCA TATTGAGCTA TTCACCAAGT TATTACTGGA TTGGAATCAG AAAAGTCAAC AATGTGTGGG TCTGGGTAGG AACCAGAAA CCTCTGACAG AAGAAGCCAA GAAGCTGCTT CCAGGTGAAC CCAACAATAG GCAAAAAGAT GAGGACTGCG TGGAGATCTA CATCAAGAGA GAAAAAGATG TGGGCATGTG GAATGATGAG AGGTGCAGCA AGAAGAAGCT TGCCCTATGC TACACAGCTG CCTGTACCAA TACATCCTGC AGTGGCCACG GTGAATGTGT AGAGACCATC AATAATTACA CTGCAAGTG TGACCCTGGC TTCAGTGGAC TCAAGTGTGA GCAATTGTG AACTGTACAG CCCTGGAATC CCCTGAGCAT GGAAGCCTGG TTGTCAGTCA CCCACTGGGA AACTTCAGCT ACAATTCCTC CTGCTCTATC AGCTGTGATA GGGGTTACCT GCCAAGCAGC ATGGAGACCA TGCAAGTAT GTCCCTCTGGA GAATGGAGTG CTCTATTCC AGCCTGCAAT GTGGTTGAGT GTGATGCTGT GACAAATCCA GCCAATGGGT TCGTGAATG TTTCCAAAAC CCTGGAAGCT TCCCATGGAA CACAACCTGT ACATTGACT GTGAAGAAGG ATTGAACATA ATGGGAGCCC AGAGCCTTCA GTGTACCTCA TCTGGGAATT GGGACAACGA GAAGCCAAAG TGTAAGAGCTG TGACATGCAG GGCCGTCCGC CAGCCTCAGA ATGGCTCTGT GAGGTGCAGC CATTCCCTCTG CTGGAGAGTT CACCTTCAAA TCATCCTGCA ACTTCACCTG TGAGGAAGGC TTCATGTTGC AGGGACCAGC CCAGGTTGAA TGCACCACTC AAGGGCAGTG GACACAGCAA ATCCCAAGTT GTGAAGCTTT CCAGTGCACA GCCTGTGCA ACCCCGAGCG AGGCTACATG AATGTCTCTC CTAGTGCTTC TGGCAGTTTC CGTTATGGGT CCAGCTGTGA GTTCTCCTGT GAGCAGGGTT TTGTGTTGAA GGGATCCAAA AGGCTCCAAT GTGGCCCCAC AGGGGAGTGG GACAACGAGA AGCCACATG TGAAGCTGTG AGATGCGATG CTGTCCACCA GCCCCGAAG GGTGTTGGTGA GGTGTGCTCA TTCCCTATT GGAGAATTCA CCTACAAGTC CTCTGTGCC TTCAGCTGTG AGGAGGGATT TGAATTATAT GGATCAACTC AACTTGAGTG CACATCTCAG GGACAATGGA CAGAAGAGGT TCCTCTCTGC CAAGTGTTAA AATGTTCAAG CCTGGCAGTT CCGGGAAGA TCAACATGAG CTGCAAGTGGG GAGCCCGTGT



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-3' (FRAG. NO: 1738) (SEQ. ID NO: 1749)

5'-GCCACCATGG AAACCCCTTG CCTCAGGGCA TCCTTTTGGC TGGCACTGGT TGGATGTGTA ATCAGTGATA ATCCTGAGAG  
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CGTAACTAGA ATAGTGAATC TGTGATTCT GGGTGTTC ACCTAGTTTC AGACCTTCTC CAGGCTCTTT TCAAGGAGGC  
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AGGTCAAAA TGAGGGATC-3' (FRAG. NO: ) (SEQ. ID NO: 2480)  
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 GTTT-3' (FRAG. NO: ) (SEQ. ID NO: 2479)

5'-CCT TGC CTG CTG G-3' (FRAG. NO: 1739) (SEQ. ID NO: 1750)

5'-GTT GTC CC-3' (FRAG. NO: 1740) (SEQ. ID NO: 1751)

5'-GTT CTT GGC TTC TTC TGT C-3' (FRAG. NO: 1080) (SEQ. ID NO: 1090)

5'-GGC TGG TGG-3' (FRAG. NO: 1083) (SEQ. ID NO: 1093)

5'-CGT TGG CTT CTC GTT GTC CC-3' (FRAG. NO: 1081) (SEQ. ID NO: 1091)

5'-TGT GGG CTT CTC GTT GTC CC-3' (FRAG. NO: 1082) (SEQ. ID NO: 1092)

5'-CCC TTC GGG GGC TGG TGG-3' (FRAG. NO: 1083) (SEQ. ID NO: 1093)

5'-GGC CGT CCT TGC CTG CTG G-3' (FRAG. NO: 1084) (SEQ. ID NO: 1094)

#### Human P Selectin Fragments

5'-TTT TCT CTT TCG CTT TCT TTT CGT CTC CTG TTC CTC CTT TT TTG CTG TTT TTT CTC CTT CTT CTC TCC TTT  
 CTT TTC-3' (FRAG. NO: 1741) (SEQ. ID NO: 1752)

5'-TCC TTT CTT TTC-3' (FRAG. NO: 1742) (SEQ. ID NO: 1753)

5'-CTC CTT TT-3' (FRAG. NO: 1743) (SEQ. ID NO: 1754)

5'-TTT TCT CTT TCG CTT TCT TTT CGT CTC CTG TTC CTC CTT TT-3' (FRAG. NO: 1085) (SEQ. ID NO: 1095)

5'-TTG CTG TTT TTT CTC CTT CTT CTC TCC TTT CTT TTC-3' (FRAG. NO: 1086) (SEQ. ID NO: 1096)

#### Human Endothelial Monocyte Activating Factor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-TTT TCT CTT TCG CTT TCT TTT CGT CTC CTG TTC CTC CTT TT TTG CTG TTT TTT CTC CTT CTT CTC TCC TTT  
 CTT TTC-3' (FRAG. NO: 1744) (SEQ. ID NO: 1755)

5'-CC TTT CTT TTC (FRAG. NO: 1745) (SEQ. ID NO: 1756)

5'-CTG TTC CTC CTT TT-3' (FRAG. NO: 1746) (SEQ. ID NO: 1757)

5'-TTT TCT CTT TCG CTT TCT TTT CGT CTC CTG TTC CTC CTT TT-3' (FRAG. NO: 1087) (SEQ. ID NO: 1097)

5'-TTG CTG TTT TTT CTC CTT CTT CTC TCC TTT CTT TTC-3' (FRAG. NO: 1088) (SEQ. ID NO: 1098)

#### Human IL3\* Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CTC TGT CTT GTT CTG GTC CTT CGT GGG GCT CTG TGT CGC GTG G GTG CGG CCG TGG CC GGC GGB CCB GGB GTT  
 GGB GCB GGB GCB GGB CGG GCB GGC GGC TCB TGT TTG GBT CGG CBG GBG GCB CTC (FRAG. NO: 1747) (SEQ. ID NO:  
 1758)

5'-C CCG CCB CTG-3' (FRAG. NO: 1748) (SEQ. ID NO: 1759)

5'-GT GGG GCT CTG-3' (FRAG. NO:1749) (SEQ. ID NO:1760)

HUMIL3AAS1: 5'-CTC TGT CTT GTT CTG GTC CTT CGT GGG GCT CTG-3' (FRAG. NO:1089) (SEQ. ID NO:1099)

HUMIL3AAS2: 5'-TGT CGC GTG G GTG CGG CCG TGG CC-3' (FRAG. NO:1090) (SEQ. ID NO:1100)

GGC GGB CCB GGB GTT GGB GCB GGB GCB GGB CGG GCB GGC GGC TCB TGT TTG GBT CGG CBG GBG GCB CTC (FRAG. NO:1091) (SEQ. ID NO:1101)

#### Human IL3 Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-TCT GGG GTG TCC TGG CCT TCG TGG TTC CTC TTC CTT CGT TTG CCG TCC GCG GGG GCC CCC GGG CCT GGC TGC GCT CCT GCC CCG CCT CTT TCC CGG GCT CTT GCG CTG GGG GGT GCT CC CGT GTG TTT GCG CCC TC CTC CTG GTC GCG CTT GTC GTT TTG GGG CCG GCT TTG CCC GCC TCC CGG CGC CTG GCC CGG CC TTC CTG GGC TGC GTG CGC GTT CTG TTC TTT TTC CTG GCT CTG GGG TGT CCT GGC CTT CGT GGT TCC TCT TCC TTC GTT TGC CGT CCG CGG GGG CCC CCG GGC CT GGC TGC GCT CCT GCC CCG CCT CTT TCC CGG GCT CTT GCG CTG GGG GGT GCT CCC GTG TGT TTG CGC CCT CCT CCT GGT CGC GCT TGT CGT TTT GG GGC CGG CTT TGC CCG CCT CCC GGC GCC TGG CCC GGC CTT CCT GGG CTG CGT GCG CGT TCT GTT CTT CTT CCT GGC GCA GGA GAC AGG GCA GGG CGA TCA GGA GCA GCG TGA GCC AAA GGA GGA CCA TCG GGA ACG CAG CTC CGG AAC GCA GGA CAG AGG TGC C GC BGG BGB CBG GGC BGG GCG BTC BGG BGC BGC GTG BGC CBB BGG BGG BCC BTC GGG BBC GCB GCT CCG GBB CGC BGG BCB GBG GTG CC-3' (FRAG. NO: 1750) (SEQ. ID NO: 1761)

GBG GTG CC-3' (FRAG. NO: 1751) (SEQ. ID NO: 1762)

5'-GCC CCG C-3' (FRAG. NO:1752) (SEQ. ID NO:1763)

5'-TCTGGGGTGTCTG (FRAG. NO:1092) (SEQ. ID NO:1102)

5'-GCCTTCGTGGTTCC (FRAG. NO:1093) (SEQ. ID NO:1103)

5'-TCTTCCTTCGTTTGC (FRAG. NO:1094) (SEQ. ID NO:1104)

5'-CGTCCGCGGGGGCCCCCGGGCCT (FRAG. NO:1095) (SEQ. ID NO:1105)

5'-GGC TGC GCT CCT GCC CCG C (FRAG. NO:1096) (SEQ. ID NO:1106)

5'-CTCTTTCCCGGGCTCTT (FRAG. NO:1097) (SEQ. ID NO:1107)

5'-GCGCTGGGGGTGCTCC (FRAG. NO:1098) (SEQ. ID NO:1108)

5'-CGTGTGTTTGGCGCCCTCCTCTGGTCGC (FRAG. NO:1099) (SEQ. ID NO:1109)

5'-GCTTGTCTTTTGG (FRAG. NO:1100) (SEQ. ID NO:1110)

5'-GGCCGGCTTTGCCCGCCTCCC (FRAG. NO:1101) (SEQ. ID NO:1111)

5'-GGCGCCTGGCCCGGCC (FRAG. NO:1102) (SEQ. ID NO:1112)

5'-TTCCTGGCTGCGTGCGC (FRAG. NO:1103) (SEQ. ID NO:1113)

5'-GTTCTGTTCTTCTCTGCGC (FRAG. NO:1104) (SEQ. ID NO:1114)

5'-GCB GGB GBC BGG GCB GGG CGB TCB GGB GCB GCG TGB GCC BBB GGB GGB CCB TCG GGB BCG CBG CTC CGG BBC GCB GGB 5'-CBG BGG TGC C (FRAG. NO:1105) (SEQ. ID NO:1115)

#### Human IL-4 Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CTC TGG TTG GCT TCC TTC GCC GGC BCB TGC TBG CBG GBB GBB CBG BGG GGG BBG CBG TTG GGB GGT GBG BCC CBT TBB TBG GTG TCG B-3' (FRAG. NO: 1753) (SEQ. ID NO: 1764)

5'-GCC GGC BCB-3' (FRAG. NO: 1754) (SEQ. ID NO: 1765)

5'-T TCC TTC-3' (FRAG. NO:1755) (SEQ. ID NO:1766)

5'-CTC TGG TTG GCT TCC TTC-3' (FRAG. NO:1106) (SEQ. ID NO:1116)

5'-GCCGGCBCTGCTBGCBBGBBGBBGBBGGGGGGGGGCGTGGGGGGTGBGCCCBTTBBTGGGTGTCGB-3' (FRAG. NO:1107) (SEQ. ID NO:1117)

#### Human IL4 Receptor Nucleic Acid and Antisense Oligonucleotide Fragment

5'-TCT GCC CTG TCC GCC GGC TCT TCG GTG GCT CGG CCC CGC TCC TTG TCT TGC CGC GGG TTG GTT CCT GGG CCT GGT TCT TGC GGG CGT TTC GGT CTG CTG GCT GGT CTG GGC CCG CGG TGC GGC GGG TGG CTT GCT GTT CTG CCT GGG CTC TCC CCT CTC CTC CTT TTC TCC CTT CCT CTG TCT TGC CTC CTT CCT CTG GGT CCT CTT GGC CTG GGC GCT CTT CCC CTC GGG CGG CTG CGG GCG CTC GTG CTG CCT GGT CCG CTC CCT GGG GGT GCT CCT TCC CTT TCC CCG CTC GTG GGG TTT GCG GGG CTG GGC TGC CCT GGG GGG TCT GGG CCT TTT GGG GTC GGC TGG CTG CTG CTT CGG GCC GCC TGG GCT TCC CTG TGC CCC TTT CCT CTG CTG GGT CCC CTT CCC GTT CCA AGC TGC ACC GCA CAG ACC GGC GCT ACA GGA CAG AGC CAG GCA AGC ACC CAT GGG GAT CCA GGC CCA GCT GTT CCB BGC TGC BCC GCB CBG BCC GGC GCT BCB GGB CBG BGC CBG GCB BGC BCC CBT GGG GBT CCB GGC CCB GCT G-3' (FRAG. NO: 1756) (SEQ. ID NO: 1767)

5'-TCTGCGC-3' (FRAG. NO: 1757) (SEQ. ID NO: 1768)

5'-CCT GCT CCT GGG G (FRAG. NO:1758) (SEQ. ID NO:1769)

5'-TCTGCGCGCCCTGTCTC (FRAG. NO:1108) (SEQ. ID NO:1118)

5'-CGCCCGGCTTCTCT (FRAG. NO:1109) (SEQ. ID NO:1119)

5'-CGTGTGGGCTTCGG (FRAG. NO:1110) (SEQ. ID NO:1120)

5'-CCCCGCGCTCCGTTGTTCTC (FRAG. NO:1111) (SEQ. ID NO:1121)

5'-TGCTCGTGGGCTTG (FRAG. NO:1112) (SEQ. ID NO:1122)

5'-GGTTTCTGGGGCCCTGGGTTTC (FRAG. NO:1113) (SEQ. ID NO:1123)

5'-TCTGCCGGGTCTGTTTC (FRAG. NO:1114) (SEQ. ID NO:1124)

5'-GGGTGCTGGCTGCG (FRAG. NO:1115) (SEQ. ID NO:1125)

5'-CTTGGTGTGGGGCTCC (FRAG. NO:1116) (SEQ. ID NO:1126)

5'-GGCGGCTGCGGGCTGGGTTGGG (FRAG. NO:1117) (SEQ. ID NO:1127)

5'-CTTGGCTGGTTCCTGGCCTCGG (FRAG. NO:1118) (SEQ. ID NO:1128)

5'-CCTCCTCCTCCTCCTCGCTCCCTTTTCTTCTCT (FRAG. NO:1119) (SEQ. ID NO:1129)

5'-TCCCTGCTGCTCTC (FRAG. NO:1120) (SEQ. ID NO:1130)

5'-TGCCCTCCTTCCCTCCTGG (FRAG. NO:1121) (SEQ. ID NO:1131)

5'-GGTGCCTCCTTGGGCCTGC (FRAG. NO:1122) (SEQ. ID NO:1132)

5'-GGCTGCTCCTTGCCCC (FRAG. NO:1123) (SEQ. ID NO:1133)

5'-CTCTGGGTCGGGCT (FRAG. NO:1124) (SEQ. ID NO:1134)  
5'-GGGGCGTCTCTGTGC (FRAG. NO:1125) (SEQ. ID NO:1135)  
5'-CTGGCCTGGGTGCC (FRAG. NO:1126) (SEQ. ID NO:1136)  
5'-GCCTCTCCTGGGGGGTGGCTCCCTGTCC (FRAG. NO:1127) (SEQ. ID NO:1137)  
5'-CCTTTTCCCCGGCTCC (FRAG. NO:1128) (SEQ. ID NO:1138)  
5'-GTGGGGGCTTTGGC (FRAG. NO:1129) (SEQ. ID NO:1139)  
5'-GGG GGT CTG TGG CCT GCT CCT GGG G (FRAG. NO:1130) (SEQ. ID NO:1140)  
5'-AGGGGTCTGGGGCCCTC (FRAG. NO:1131) (SEQ. ID NO:1141)  
5'-TTTTGGGGGTCTGGCTTG (FRAG. NO:1132) (SEQ. ID NO:1142)  
5'-GCCTGGCTGCCTTCC (FRAG. NO:1133) (SEQ. ID NO:1143)  
5'-GGGGCCTGCCGTGGGGC (FRAG. NO:1134) (SEQ. ID NO:1144)  
5'-TGCTCTGTGTGCTCCCTT (FRAG. NO:1135) (SEQ. ID NO:1145)  
5'-TGCTGTGTGTGCTG (FRAG. NO:1136) (SEQ. ID NO:1146)  
5'-GGTTCCCGCCTTCCCT (FRAG. NO:1137) (SEQ. ID NO:1147)  
5'-GTT CCC AGA GCT TGC CAC CTG CAG CAG GCA GCT CAC AGG GAA CAG GAG CCC AGA GCA AAG CCA CCC  
CAT TGG GAG ATG CCA AGG CAC CAG GCT G (FRAG. NO:1138) (SEQ. ID NO:1148)  
5'-GTT CCC BGB GCT TGC CBC CTG CBG CBG GBC CBG GCB GCT CBC BGG GBB CBG GBG CCC BGB GCB BBG CCB CCC  
CBT TGG GBG BTG CCB BGG CBC CBG GCT G-3' (FRAG. NO:1139) (SEQ. ID NO:1149)

#### Human IL5\* Nucleic Acid and Antisense Oligonucleotide Fragments

5'-TCCCTGTTTCCCCCTTTCG TTCTGCGTTT GCCTTTGGCG TTTTGTGTTT GTTTTCTCTC TCCGTCTTTC TTCTCCCT  
GTGGGGBTTT CTGTGGGGBT GGCBTBCBG TBGGCBGCTC CBBGBGCTBG CBBBCTCBBB TGCBBBGBCB TCCTCBTGGC  
TCTGBBBCCG TGGGAATTC TGTGGGGBTG GCATACAGT AGGCAGCTCC AAGAGCTAGC AAACCTCAAAT GCAGAAGCATC  
CTCATGGCTC TGAACG-3' (FRAG. NO: 1759) (SEQ. ID NO: 1770)  
5'-GCC CCG GG-3' (FRAG. NO: 1760) (SEQ. ID NO: 1771)  
5'-G GGT TTC T-3' (FRAG. NO: 1761) (SEQ. ID NO: 1772)  
5'-GTG GGG BTG GC-3' (FRAG. NO: 1762) (SEQ. ID NO: 1773)  
5'-CCB BGB GCT BGC-3' (FRAG. NO: 1763) (SEQ. ID NO: 1774)  
5'-TCC CTG TTT CCC CCC TTT-3' (FRAG. NO:1140) (SEQ. ID NO:1150)  
5'-CGT TCT GCG TTT GCC TTT GGC-3' (FRAG. NO:1141) (SEQ. ID NO:1151)  
5'-GTT TTT TGT TGT TTT TCT-3' (FRAG. NO:1142) (SEQ. ID NO:1152)  
5'-CTC TCC GTC TTT CTT CTC C-3' (FRAG. NO:1143) (SEQ. ID NO:1153)  
5'-CCT CCT GCC TGT GTC CCT GCT CCC C-3' (FRAG. NO:1144) (SEQ. ID NO:1154)  
5'-GAG GGT TTC TGG CTT CCT CTC T-3' (FRAG. NO:1145) (SEQ. ID NO:1155)  
5'-TGT CTC TCT GTC CTT TTG TT-3' (FRAG. NO:1146) (SEQ. ID NO:1156)  
5'-TGT TGT GCG GCC TGG TGC TGC CCT GCC CCG GG-3' (FRAG. NO:1147) (SEQ. ID NO:1157)  
5'-GTG GGA ATT TGT GTG GGG BTG GCA TAC ACG TAG GCA GCT CCA AGA GCT AGC AAA CTC AAA TGC AGA AGC ATC  
CTC ATG GCT CTG AAA CG-3' (FRAG. NO: 1764) (SEQ. ID NO: 1775)  
5'-GTG GGB BTT TCT GTG GGG BTG GCB TBC BCG TBC GCT CCB BGB GCT BGC BBB CTC BBB TGC BGB BGC BTC  
CTC BTG GCT CTG BBB CG-3' (FRAG. NO:1148) (SEQ. ID NO:1158)

#### Human IL-5 Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CTCAGTGGCC CCAAAAGGA TGAGTAATAC ATGCGCCACG ATGATCATAT CCTTTTACT ATGAGGCCGT GTCTGTCTGTG  
TCTTTCCTTT GCTCTTGGTG TGTCTTTGCT GTGCCCTGCC TCTCTGCCCG TGTCTGTCTG GTCTTTCCTT TGCTTTGGT  
GTGTCTTTC TGTGCCCTGC CTCTCTGCC CGTGTCTGTC GTGTCTTTC TTTGCTCTTG GTGTGTCTTT GCTGTGCCCT  
GCCTCTCTGC-3' (FRAG. NO: 1765) (SEQ. ID NO: 1776)  
5'-CCG TGT C-3' (FRAG. NO: 1766) (SEQ. ID NO: 1777)  
5'-GCCCTGCC-3' (FRAG. NO: 1767) (SEQ. ID NO: 1778)  
5'-CCG TGT CTG TCG TGT CT-3' (FRAG. NO:1149) (SEQ. ID NO:1159)  
5'-TTCCTTTGCTCTTG-3' (FRAG. NO:1150) (SEQ. ID NO:1160)  
5'-GTGTGTCTTTGCTGT-3' (FRAG. NO:1151) (SEQ. ID NO:1161)  
5'-GCCCTGCCTCTCTGC-3' (FRAG. NO:1152) (SEQ. ID NO:1162)  
5'-CT CBGTGGCCCC CBBBGGBTG BGTBBTBCBT GCGCCBCGBT GBTCBTBTCC TTTTBTCTBT GBGG (FRAG. NO: 1768)  
(SEQ. ID NO: 1779)

#### Human IL-6 Receptor Fragments

5'-GGGGGTGGCT TCCTGCCGCG TCTCTGGGCC GTCCCGTCCC TCGGCCCCGC GCCGCGCTCG GTCCTCTCC CTCTGGCCCC  
GCTCGGGGCG GGGCGGGGCG GTGGGCGGGC GCGCTGCC TCGCGCGCGC GCTGGCCCCCT GTGGCCGTC GGCTGCGCGC  
TGCTGGCTGC CCTGCTGGCC GCGCCGGGCG CTGTCCGCTC CTGCGGGGCG TGCTCTCTGG CTGTCTTCC GGCTCTTCTG  
CTGGGGTGGG GCTGGGCGGC CGGCCGGTG CTGGGGCTCC TCGGGGGGGG GGGCTCTTCC GGGCTGTCTC CCTCCGGGGC  
GGGGGTTTCT GGCCGTGGGG GTCTTGCTG GCCTCCGGGC TCTGCTTG CTGGCTTCC TTCTCTGGT GGTGTGTGGT  
CGGGGCTCCG TGGGTCCCTG GCGCCCGTTT GTGTTTGT TTTTCCCTG GCGTCCCTG GCGCTCTCC TCTCCTCT  
CTGCTTCTCG CTCTCTTTG TGGGGCCCTC CCGCTGCTC TTGGTTTGG GCTTTTTTTC TCTCTCTCT TTTCTGTGCG  
TGGGCTCCG CACGCTCTT GCCACTCCT GCGCAGGCA GCGCCTTG GGCCAGCGCC GCTCCGGCG CGGCCAGCAG  
GGCAGCCAGC AGCGCGCAGC CGACGGCCAG CATGCTTCT CCGCGCTAC CACTCCATGG TCCCGCAGAG GCGGACAGGC  
GCBGCTC TTGCCBCTC CTGCGCBGG GCGCGCTTG GGGCCBGGC CGTCCCGGC GCGGCCBGB GGGCBGCCB  
CBGCGCGCG CCGCGGCCB GCBTGTCTTCT CCGCGCTB CCBCTCCBTG GTCCGCBGB GCGGCBGG C-3'  
(FRAG. NO: 1769) (SEQ. ID NO: 1780)  
5'-CCCGGCGC-3' (FRAG. NO:1184) (SEQ. ID NO:1194)  
5'-GGCCBGBGG-3' (FRAG. NO:1186) (SEQ. ID NO:1196)  
5'-GCBGCCBGBGG-3' (FRAG. NO: 1770) (SEQ. ID NO: 1781)

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5'-C GCBGCCBGGCC -3' (FRAG. NO: 1771) (SEQ. ID NO: 1782)  
5'-GGGGGTGGCTTCTGCCC- (FRAG. NO:1153) (SEQ. ID NO:1163)  
5'-GCGTCTCTGGGCGTCCC-3' (FRAG. NO:1154) (SEQ. ID NO:1164)  
5'-GTCCCTCGGCCCCGCGCCGCTCGGCTCCTCTCCC-3' (FRAG. NO:1155) (SEQ. ID NO:1165)  
5'-TCTGGCCCGGCTC-3' (FRAG. NO:1156) (SEQ. ID NO:1166)  
5'-GGGGCGGGGCGGGCGGTGGGCGGGC-3' (FRAG. NO:1157) (SEQ. ID NO:1167)  
5'-GGCGGTGCCCTGCGC-3' (FRAG. NO:1158) (SEQ. ID NO:1168)  
5'-GCGGCGTGGCCCC-3' (FRAG. NO:1159) (SEQ. ID NO:1169)  
5'-TGCTGGCCGTGCGCTGCGCGCTGCTGGCTGCCCT-3' (FRAG. NO:1160) (SEQ. ID NO:1170)  
5'-GCTGGCCGCGCCGGG-3' (FRAG. NO:1161) (SEQ. ID NO:1171)  
5'-GCCTGTCCGCTCTGCGGG-3' (FRAG. NO:1162) (SEQ. ID NO:1172)  
5'-CGCTGTCTCTGGC-3' (FRAG. NO:1163) (SEQ. ID NO:1173)  
5'-TTGTCTTCCGGCTCT-3' (FRAG. NO:1164) (SEQ. ID NO:1174)  
5'-TCTGCTGGGTGGG-3' (FRAG. NO:1165) (SEQ. ID NO:1175)  
5'-GCTGGGCGGCCGCGCCGGT-3' (FRAG. NO:1166) (SEQ. ID NO:1176)  
5'-GCTGGGGCTCCTCGGGGG-3' (FRAG. NO:1167) (SEQ. ID NO:1177)  
5'-GGGGGCTCTCCGG-3' (FRAG. NO:1168) (SEQ. ID NO:1178)  
5'-GCTGTCTCCCTCCGGG-3' (FRAG. NO:1169) (SEQ. ID NO:1179)  
5'-GCGGGGGTTTCTGGCC-3' (FRAG. NO:1170) (SEQ. ID NO:1180)  
5'-GTGGGGGTCTTGCC-3' (FRAG. NO:1171) (SEQ. ID NO:1181)  
5'-TGGCCTCCGGGCTCC-3' (FRAG. NO:1172) (SEQ. ID NO:1182)  
5'-TGCTTGTCTTGCCCTTCTTC-3' (FRAG. NO:1173) (SEQ. ID NO:1183)  
5'-TCTGGTGGTGTGGCTCG-3' (FRAG. NO:1174) (SEQ. ID NO:1184)  
5'-GGGCTCCGTGGGTCCCTGGC-3' (FRAG. NO:1175) (SEQ. ID NO:1185)  
5'-GCCCCGTTGTGTTTGTGTC-3' (FRAG. NO:1176) (SEQ. ID NO:1186)  
5'-TTTTCCCTGGCGT-3' (FRAG. NO:1177) (SEQ. ID NO:1187)  
5'-CCCTGTGCCCCCTCTCCTCTCCTCTGCTTCTC-3' (FRAG. NO:1178) (SEQ. ID NO:1188)  
5'-GCTCTCTTTGTGGG-3' (FRAG. NO:1179) (SEQ. ID NO:1189)  
5'-GCCCTCCCTGCTGCT-3' (FRAG. NO:1180) (SEQ. ID NO:1190)  
5'-CTTGGTTTGGGCT-3' (FRAG. NO:1181) (SEQ. ID NO:1191)  
5'-TTTTTCTCTCTCCTTTTTC-3' (FRAG. NO:1182) (SEQ. ID NO:1192)  
5'-GTGCGTGGGCTCC-3' (FRAG. NO:1183) (SEQ. ID NO:1193)  
5'-  
GCACGCTCTTGCCACCTCTGCGCAGGGCAGCGCTTGGGGCCAGCGCCGCTCCCGGCGGGCCAGCAGGGCAGCCAGCAGCG  
CGCAGCCGACGGCCAGCATGCTTCTCCTCGGCTACCACTCCATGTTCCCGCAGAGGCGGACAGGC-3'  
(FRAG. NO:1185) (SEQ. ID NO:1195)  
5'-  
GCBGCGCTCTTGCCBCCTCTGCGCBGGGCBGCGCCTTGGGGCCBGCGCCGCTCCCGGCGGGCCBGCBGGGCBGCCBGCGCGC  
GCBGCCBGGCCBGCBGTGCTTCTCCTCGGCTBCCBCTCCBTGGTCCCGCBGCGGGCBGCGC-3'  
(FRAG. NO:1187) (SEQ. ID NO:1197)

#### Human IL-6 Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GGGGGTGGCT TCTGCGCG TCTTGGGCC GTCCGCTCCC TGGCCCCGC GCCGCGCTCG GCTCCTCTCC CTCTGGCCCC  
GCTCGGGGCG GGGCGGGGCG GTGGGCGGGC GCGCTGCCC TGCGCGCGG GCTGGCCCT GCTGGCCGTC GGCTGCGCGC  
TGCTGGCTGC CTTGCTGGCC GCGCCGGGGC CTGTCCGCT CTGCGGGGCG TGCTCTCTGG CTGTCTTCC GGCTCTTCTG  
CTGGGGTGGG GCTGGGCGGC CGGCCGGTG CTGGGGTCC TCGGGGGGG GGGCTCTTCC GGGCTGTCTC CTCCGGGGC  
GGGGGTTTCT GGCCGTGGGG GTCTGCTG GCCTCCGGGC TCCTGCTTGT CTGCTTCC TTCTGTGTC GGTGTGGCT  
CGGGGCTCCG TGGGTCCCTG GCGCCGTTT GTGTTTGTG TTTCCCTG GCGTCCCTGT GCCCTCTCC TCTCTTCT  
CTGCTTCTG CTCTCTTTG TGGGGCCCTC CTGCTGCTC TTGGTTTGG GCTTTTTC TCTCTCTCT TTTCTGTCG  
TGGGCTCC GCACGCTCT TGCCACCTCC TGCCAGGGC AGCGCTTG GGCAGCGCC GCTCCCGCG CGGCCAGCAG  
GGCAGCCAGC AGCGCGCAGC CGACGGCCAG CATGCTTCT CCTCGGCTAC CACTCATGG TCCCGCAGAG GCGGACAGGC  
GCBGCGCTC TTGCCBCTC CTGCGCBGG CBGCGCCTG GGGCCBGCG CGTCCCGCG GCGGCCBGB GGGCBGCCB  
CBGCGCGCB CGBCGGCCB GCBTGCTTC TCTCGGCTB CCBCTCCBTG GTCCCGCBG GCGGBCBGG C-3' (FRAG.  
NO:1772) (SEQ. ID NO:1783)  
5'-GGGGCBGG-3' (FRAG. NO:1773) (SEQ. ID NO:1784)  
5'-GBBGGCBG CBGGC-3' (FRAG. NO:1774) (SEQ. ID NO:1785)  
5'-CCBGGBGBG CCCC-3' (FRAG. NO:1775) (SEQ. ID NO:1786)  
5'-BGGG BGGGGCBBC-3' (FRAG. NO:1776) (SEQ. ID NO:1787)  
5'-GCT TCT CTT TCG TTC CCG GTG GGC TCG-3' (FRAG. NO:1188) (SEQ. ID NO:1188)  
5'-GTG GCT GTC TGT GTG GGG CGG CT-3' (FRAG. NO:1189) (SEQ. ID NO:1189)  
5'-GTG CCT CTT TGC TGC TTT C-3' (FRAG. NO:1190) (SEQ. ID NO:1200)  
5'-GAT TCT TTG CCT TTT TCT GC-3' (FRAG. NO:1191) (SEQ. ID NO:1201)  
5'-CTCCTGGGGG TBCTGGGGCB GGGBBGGCBG CBGGCBBCB CBGGBGBGCB CCCBGGGBGB BGGCBCTGG BCCGBGGCG  
CTTGTGGBGB BGGGTTCBT BGCTGGGCTC CTGGBGGGB GBTBGGC-3' (FRAG. NO:1777) (SEQ. ID NO:1788)

#### Human Monocyte-derived Neutrophil Chemotactic Factor

##### Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GGGGTGGBBB GGTTTGGBGT BTGTCTTBT GCBCTGBCBT CTBBGTTCTT TBGCBCTCCT TGGCBBBCT GCBCTTCBC  
BCBGBGCTGC BGGBBTGBG BGGCTGCCB BGBBGCCBC GGCCBGCTTG GBBGTCTGT TTBCBCBGB TGBGTGGTT  
CCTTCCGGGCT TGTGTGCTC TGCTGTCTT TGGTTCCTC CGGTGGTTT TTCTGGCTC TTGTCTTTC TCTTGG CCCT  
TGCC-3' (FRAG. NO:1778) (SEQ. ID NO: 1789)



5'-GGGTG BTG-3' (FRAG. NO:1779) (SEQ. ID NO: 1790)  
5'-GCBCTGCBCT CT-3' (FRAG. NO:1780) (SEQ. ID NO:1791)  
5'-CCG GTG G-3' (FRAG. NO:1781) (SEQ. ID NO: 1792)  
5'-GG CCC TTG GC-3' (FRAG. NO:1782) (SEQ. ID NO: 1793)  
5'-GCT TGT GTG CTC TGC TGT CTC T-3' (FRAG. NO:1192) (SEQ. ID NO:1202)  
5'-TGG TTC CTT CCG GTG GTT TCT TCC TGG CTC TTG TCC T-3' (FRAG. NO:1193) (SEQ. ID NO:1203)  
5'-TTC TCT TGG CCC TTG GC-3' (FRAG. NO:1194) (SEQ. ID NO:1204)  
5'-GGGGTGGBBB GGTTTGGBT BTGTCTTTBT GCBCTGCBCT CTBBGTTCTT TBGCBCTCCT TGGCBBBCT GCBCTTCBC BCBGBC-3' (FRAG. NO:1783) (SEQ. ID NO: 1794)

#### Human Neutrophil Elastase (Medullasin) Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GGGCTCCCGC CGCGBGBGGT TBTGGGCTCC CBGBBCCBCC CGCBCCGCGC GGBCGTTTBC BTTCGCCBCG CBGTGCGCGG  
CCGCBCTGBC GBBGTGGGC GCBTTCBGGG TGGCGCCGCB GBBGTGGCCT CCGCGCBGCT GCBGGGBCBC CBTGBBGGGC  
CBGCGTGGG GCCGCGCTCG CCGGCCCCC CBCTCTCCG BGGCCBGGC GGTGCCCCC BGCBCBBGG CCGGCBGGC  
BCBGGCGBG BGCBCGCGB GTCGGCGGCC GBGGTCTBG GTGGGCTGG GGCTCCGGG TCTCTGCCC TCCGTGCTGG  
TGGGCTGGG GCTCCGGG TCTCTGCCC TCCGTGCGC GTGGGCGCG GCTCGCCGG CCCCCCTGC CGGGTGGGCT  
CCCCCGCGC GCCGGCTGC CGGCCCTCG TGGTCTCTG TGGCCGGTC CGGTCCCGG GGTGGGGCG CGBGTCCGGC  
GCCBGGGTC-3' (FRAG. NO:1784) (SEQ. ID NO: 1795)  
5'-GG TGG GGC-3' (FRAG. NO:1785) (SEQ. ID NO: 1796)  
5'-G GGG CCG-3' (FRAG. NO:1786) (SEQ. ID NO:1797)  
5'-GGC CGG GTC CGG G-3' (FRAG. NO:1787) (SEQ. ID NO: 1798)  
5'-TGG TGG GGC TGG GGC TCC GGC GTC TCT GCC CCT CCG TGC-3' (FRAG. NO:1195) (SEQ. ID NO:1205)  
5'-CGC GTG GGG CCG CGC TCG CCG GCC CCC C-3' (FRAG. NO:1196) (SEQ. ID NO:1206)  
5'-CCT GCC GGG TGG GCT CCC GCC GCG-3' (FRAG. NO:1197) (SEQ. ID NO:1207)  
5'-CGC CGG CCT GCC GGC CCC TC-3' (FRAG. NO:1198) (SEQ. ID NO:1208)  
5'-GTG GGT CCT GGC CGG GTC CGG GTC CCG GGG GTG GGG-3' (FRAG. NO:1199) (SEQ. ID NO:1209)  
5'-CGC GBG TCG GCG GCC GBG GGT C-3' (FRAG. NO:1200) (SEQ. ID NO:1210)  
5'-GGGCTCCCGC CGCGBGBGGT TBTGGGCTCC CBGBBCCBCC CGCBCCGCGC GGBCGTTTBC BTTCGCCBCG CBGTGCGCGG  
CCGCBCTGBC GBBGTGGGC GCBTTCBGGG TGGCGCCGCB GBBGTGGCCT CCGCGCBGCT GCBGGGBCBC CBTGBBGGGC  
CBGCGTGGG GCCGCGCTCG CCGGCCCCC CBCTCTCCG BGGCCBGGC GGTGCCCCC BGCBCBBGG CCGGCBGGC  
BCBGGCGBG BGCBCGCGB GTCGGCGGCC GBGGTCTBG GTGGGCTGG GGCTCCGGG TCTCTGCCC TCCGTGCTGG  
(FRAG. NO:1788) (SEQ. ID NO: 1799)

#### Human Neutrophil Oxidase Factor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CGGGGTGGG GGTCTGGBC GGCCTGBBG GCBTCCBGGG CTCCCTTCCB GTCCTTCTT TCCGTGCCB GCBCCCTTC  
BTTCCBGGG CTGTTGGCT CCBCCBGGG CBTGTTBGG TBGBBCTBG GBGGCCGCC TCCBCCBGG CBTGTTCTT  
TCTGTCCG TGCCTCTG GGGTTTCGG TCTGGGTGG CTTTCTCTT GGGCTGCTG CTGGGCTCTT CTTTGTGT  
CTGGCTGGT GCTCTCTG GCCCTTCCC TTGGTGTCT TGTTTTGTG GCCTCCBCCB GGBCBTG-3' (FRAG. NO:1789)  
(SEQ. ID NO: 1800)  
5'-CGGGGTGGG GG-3' (FRAG. NO:1790) (SEQ. ID NO: 1801)  
5'-GCCBGCBCCC-3' (FRAG. NO:1791) (SEQ. ID NO: 1802)  
5'-C CBC CBG-3' (FRAG. NO:1792) (SEQ. ID NO: 1803)  
5'-GGC CTC CBC CBG GGB CBT G-3' (FRAG. NO:1201) (SEQ. ID NO:1211)  
5'-GTC CTT CTT GTC CGC TGC C-3' (FRAG. NO:1202) (SEQ. ID NO:1212)  
5'-TCT CTG GGG TTT TCG GTC TGG GTG G-3' (FRAG. NO:1203) (SEQ. ID NO:1213)  
5'-GCT TTC CTC TGT GGG CTG CTG CTG-3' (FRAG. NO:1204) (SEQ. ID NO:1214)  
5'-GGC TCT TCT TTT TGT TTT TGG CCT GGT G-3' (FRAG. NO:1205) (SEQ. ID NO:1215)  
5'-CTC TCT CGT GCC CTT TCC-3' (FRAG. NO:1206) (SEQ. ID NO:1216)  
5'-CTT GGG TGT CTT GTT TTT GT-3' (FRAG. NO:1207) (SEQ. ID NO:1217)  
5'-GGC CTC CBC CBG GGB CBT G-3' (FRAG. NO:1208) (SEQ. ID NO:1218)  
5'-CGGGGTGGG GGTCTGGBC GGCCTGBBG GCBTCCBGGG CTCCCTTCCB GTCCTTCTT TCCGTGCCB GCBCCCTTC  
BTTCCBGGG CTGTTGGCT CCBCCBGGG CBTGTTBGG TBGBBCTBG GBGGCC-3' (FRAG. NO:1793) (SEQ. ID NO:  
1804)

#### Human Cathepsin G Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CCCTCCBCBT CTGCTCTGBC CTGCTGGBCT CTGGTCTGB BGTBCGCCB TGTBGGGGCG GGBGTGGGGC CTGCTCTCC  
GGCCTCCGT GBTCTCCCT GCCTCBGCCC CBGTGGGTBG GBGBBGGCC BGCBBBGC BGBGTGGCTG CBTCTTCTT  
GGTGGGGCT GCTCTCCCG CCGCTGTG TTGCTGGGTG TTTCCCGTC TCTGGTCTG CTTCGGGGT CGT-3' (FRAG.  
NO:1794) (SEQ. ID NO: 1805)  
5'-GBBGTBCGCC-3' (FRAG. NO:1795) (SEQ. ID NO: 1806)  
5'-CBGCCCCBG-3' (FRAG. NO:1796) (SEQ. ID NO: 1807)  
5'-TCC CGT CTC TGG-3' (FRAG. NO:1797) (SEQ. ID NO: 1808)  
5'-GTG GGG CCT GCT CTC CCG GCC TCC G-3' (FRAG. NO:1209) (SEQ. ID NO:1219)  
5'-TGT GTT GCT GG GTG TTT TCC CGT CTC TGG-3' (FRAG. NO:1210) (SEQ. ID NO:1220)  
5'-TCT GCC TTC GGG GGT CGT-3' (FRAG. NO:1211) (SEQ. ID NO:1221)  
5'-CCCTCCBCBT CTGCTCTGBC CTGCTGGBCT CTGGTCTGB BGTBCGCCB TGTBGGGGCG GGBGTGGGGC CTGCTCTCC  
GGCCTCCGT GBTCTCCCT GCCTCBGCCC CBGTGGGTBG GBGBBGGCC BGCBBBGC BGBGTGGCTG-3' (FRAG.  
NO:1798) (SEQ. ID NO: 1809)

CTG GGG GCC TGG GCC TGC BGG GCC GCT CTT GCC TGG BGT GGC TC GCC CBG BGT CTT CCC TGG T GCTCAGCCTC  
CAAAGGAGCC AGCCTCTCCC CAGTTCCTGA AATCCTGAGT GTTGCTGCTC AGTCGCCATG AGAAGTTCCT ACCTTCTGCT  
GTTTACTCTC TGCTTACTTT TGCTGAGAT GGCCTCAGGT GGTAACCTTC TCACAGGCCT TGGCCACAGA TCTGATCATT  
ACAATTGCGT CAGCAGTGGG GGGCAATGTC TCTATTCTGC CTGCCCGATC TTTACCAAAA TTCAAGGCAC CTGTTACAGA  
GGGAAGGCCA AGTGCTGCAA GTGAGCTGGG AGTGACCAGA AGAAATGACG CAGAAGTGAA ATGAAGTTT TATAAGCATT  
CTTTAATAA AGGAAAATTG CTTTGAAGT AT CTGAGTGGT AAAAGATTG TATATCTGCT GTTTGATGAA  
TGCAGCACCC ACTAGCCACA TAGTGCTCGT GAGCACTTGC AATGCGGCTA GGGTATTTC AATTAACCTA AAAGAGAACA  
GCCACAGGGA GCATGTGGCT GCCATATTGG ATGGTGCTGC TTTGAGAACA AAATGAGAGA AATGAAGCCT CTATTACCT  
TGGTTGGCGG AACACATTGA AGGGACTCTG TATTGATACC AGGCTTCAAA CTTTGGGAAG TGTACTGGCC AACTTAAACA  
CATCCACAGG AGAATGAAGA GGTGGGGAA GGGACCAGAA AACCAGCATT GAGGACAATG AGAAGAGTTT TTCAAAAGTG  
GAATTACTGC AAAAAGTGGG AAAATAGCCT TTGGATGGAA GTTACTGATG AGACAATTTC CATCGGTGT AAAGCCATCT  
TTCCAACAGA GATCTGCAAC ATGAGAATGT ACTGTCTCCT AGGGTAGCGA TGGCCTCTTG TATTAGTCCG CTCAGGCTAC  
CAGATTTATC GTTTAACTG CCCATAAACA GACCAGGCAG TTTAAACAAC AGAAATTTAT TTCCTCGCAG TCCTGGAGGC  
AGGAAGTCTG CGATCAAGGT GGAAGCAGGG TTGGCTTCTT CTCAGGTGTC TGTCTTGGC TGGTAGATGA CCGCCGCTC  
CCTGGGCTCT CACATGGTCT TTCCTCTGTG TGTGTCTGTC CCAATCTCTT CTTATAAGGA TGCAAGTCTT ATGGATCAGA  
GCACACCCA ATGACCGTGT TTAAGTTGAA TCACCTCTT AAAGTTTCTC TCTCAAATA CAATCACCTC CTGAGGCACT  
GTTAGGGCTT CGACACAGGA ATTCTTTCC TAGGGGATTC AGTTCAGTCC AAAACGCCTA CCAGTGAGA CTGTCAACAT  
GGCGGCTGCG TGGTCCCTCG CCAGGAATAT CACAGGCGAC TGTTCCTGT TGCATGGAAT AGAAGGCTAT TCCAGAGTAC  
TGCTCTATT TATCAGATCT GGGATACTGG GAGAAGGGCA AAATAAGTC CAAGTAGAAA AAAAACTAT GAAAGTTTAA  
GAGAGTAACC ATAATTTAG CCCGATGTGA AACGATCCTA GATTTCAGCT GAAATAGTGA TGTGGGAAGT GAGGGGGCCG  
GGATTCAAGG CAGAGGGAAC AGCGTAAGT AAGGCATGGA AGGAGGGAAG TGTAGGCTGT GTTTGAAGAG TGCCAGCTGC  
TTCCACATTT CTAACACACA GGATGTGATT TTGGGGTGTG TTGAGACAAG GCAGAAAACT TGTGGGAAA AATAACTTGA  
ATTCCCTGCA CATTAAAAAT CTCTCAGCAG AAGAAAACCC CACTCAGAAC CCCACTGTTC ATTCTTGGC TTGATTGGG  
SCACAGCTGG CATAGCCCCA GACTGAGTAA GCTCTCAGA CACTCATT CATGAGTAGC CCAAGAGAT AATCATGGG  
CAATTTCTTG GAAGAGAAGA CTCTCCGTG TTTGTCAGT ATTGTCTG CTTTCGCGAG ATGTTCTCAA ATCGTTGCAG  
CTACAAGCCA TGAGTCTGAA GTGTTGTGT TCCCTCCTA CAGGTGGTAA CTTTCTCACA GGCCTTGGCC ACAGATCTGA  
TCATTACAAT TCGCTCAGCA GTGGAGGCA ATGTCTCTAT TCTGCTGCC CGATCTTTAC CAAAATTCAG GGCACCTGTT  
ACAGAGGGAA GGCCAAGTGC TGCAAGTGAG CTGAGAGTGA CCAGAAGAAA TGACGCAGAA GTGAAATGAA CTTTTATAA  
GCATTTCTTT AATAAGGAA AATTGCTTT GAAGTATACC TCCTTGGGC CAAAATGAAT CTGTGTCTC AATTGGAAGA  
GGTAAAGAAG TAGGGGTTA GGGTGCATGG GTTGAACGT GAGACAGGTC GAACCAAAA GCCTGCCTGG AAAAGGGGAG  
TGACGTCCTA GGCTTCAGTG ATGTACCTC CACTTTGTTT GATCCACAAA CCAACAGGTG ACTGATTTTG GTGAGCTCAG  
CCTCCAAAGG AGCCAGCCTC TCCCAGTTC CTGAAATCCT GAGTGTGTC TGCCAGTGC CATGAGAACT TCCTACCTTC  
TGCTGTTTAC TCTCTGCTTA CTTTGTCTG AGATGGCCTC AGGTGGTAAC TTTCTCACAG GCCTTGGCCA CAGATCTGAT  
CATTACAAT GCGTCAGCAG TGGAGGGCAA TGTCTCTATT CTGCTGCC GATCTTTACC AAAATTCAG GCACCTGTTA  
CAGAGGGAAG GCAAGTGCT GCAAGTGAGC TGGGAGTGAC CAGAAGAAAT GACGCAGAAG TGAAATGAAC TT

-3' (FRAG.NO.:1799) (SEQ. ID NO: 1810)

5'-GTCAGCTCAG CCTCAAAGG AGCCAGCCTC TCCCAGTTC CTGAAATCCT GAGTGTGCTC TGCCAGTGC CATGAGAAT  
TCCTACCTTC TGCTGTTTAC TCTCTGCTTA CTTTGTCTG AGATGGCCTC AGGTGGTAAC TTTCTCACAG GCCTTGGCCA  
CAGATCTGAT CATTACAAT GCGTCAGCAG TGGAGGGCAA TGTCTCTATT CTGCTGCC GATCTTTACC AAAATTCAG  
GCACCTGTTA CAGAGGGAAG GCAAGTGCT GCAAGTGAGC TGGGAGTGAC CAGAAGAAAT GACGCAGAAG TGAAATGAAC  
TT-3' (FRAG.NO.: ) (SEQ. ID NO: 2475)

5'-CTGAGTGGT AAAAAGATTG TATATCTGCT GTTTGATGAA TGCAGCACCC ACTAGCCACA TAGTGCTCGT GAGCACTTGC  
AATGCGGCTA GGGTGATTTC AATTAACCTA AAAGAGAACA GCCACAGGGA GCATGTGGCT GCCAATTGG ATGGTGCTGC  
TTTGAGAACA AAATGAGAGA AATGAAGCCT CTATTACCT TGGTTGGCGG AACACATTGA AGGAGATCTG TATTGATACC  
AGGCTTCAAA CTTTGGGAAG TGTACTGGCC AACTTAAACA CATCCACAGG AGAATGAAGA GGTGGGGAA GGGACCAGAA  
ACCAGGCATT GAGGACAATG AGAAGAGTTT TTCAAAAGTG GAATTACTGC AAAAAGTGGG AAAATAGCCT TTGGATGGAA  
GTACTGATG AGACAATTTC CATCGGTGTG AAAGCCATCT TTCCAACAGA GATCTGCAAC ATGAGAATGT ACTGTCTCCT  
AGGGTAGCGA TGGCCTCTTG TATTAGTCCG CTCAGGCTAC CAGATTTATC GTTTAACTG CCCATAAACA GACCAGGCAG  
TTTAAACAAC AGAAATTTAT TTCCTCGCAG TCCTGGAGGC AGGAAGTCTG CGATCAAGGT GGAAGCAGGG TTGGCTTCTT  
CTCAGGTGTC TGTCTTGGC TGGTAGATGA CCGCGCCTC CTGGGCTCT CACATGGTCT TTCCTCTGTG TGTGTCTGTC  
CCAATCTCTT CTTATAAGGA TGCAAGTCTT ATGGATCAGA GCACACCCA ATGACCGTGT TAACTTGAA TCACCTCTTT  
AAAGTTTCTC TCTCAAATA CAATCACCTC CTGAGGCACT GTTAGGGCTT CGACACAGGA ATTCTTTCC TAGGGGATTC  
AGTTCAGTCC AAAACGCCTA CCAGTGAGGA CTGCAACAT GCGCGCCTGC TGGTCCCTCG CCAGGAATAT CACAGGCGAC  
TGTTCCTGT TGCATGGAAT AGAAGGCTAT TCCAGAGTAC TGTCTCTATT TATCAGATCT GGGATACTGG GAGAAGGGCA  
AAATAAGTC CAAGTAGAAA AAAAACTAT GAAAGTTTAA GAGAGTAACC ATAATTTAG CCCGATGTGA AACGATCCTA  
GATTTCAGT GAAATAGTGA TGTGGGAAGT GAGGGGGCCG GGATTCAGG CAGAGGGAAC AGCGTAAGT AAGGCATGGA  
AGGAGGGAAG TGTAGGCTGT GTTTGAAGAG TGGCAGTCTC TTCCACATT CTAAACACA GGATGTGATT TTGGGTTGTG  
TTGAGACAAG GCAGAAAAGT GTTTGGAAA AATAACTTGA ATTCCTGCA CATTAAAAAT CTCTCAGAG AAGAAAAACC  
CACTCAGAAC CCCACTGTTC ATTCTTGGC TTGATTTGG SCACAGCTGG CATAGCCCCA GACTGAGTAA GCTCTCAGA  
CACCTCATT CATGAGTAGC CCAAGATC AATCATGGG CAATTTCTG GAAGAGAAGA CTCTCCGTG TTTGTCAGTT  
ATTGTCTG CTTTCGCGAG ATGTTCTCAA ATCGTTGCAG CTACAAGCCA TGAGTCTGAA GTGTTGTGT TCCCTCCTA  
CAGGTGGTAA CTTTCTCACA GGCCTTGGCC ACAGATCTGA TCATTACAAT TCGTCAGCA GTGGAGGCA ATGTCTCTAT  
TCTGCTGCC CGATCTTTAC CAAAATTCAG GGCACCTGTT ACAGAGGGAA GGCCAAGTGC TGCAAGTGAG CTGAGAGTGA  
CCAGAAGAA TGACGCAGAA GTGAAATGAA CTTTTATAA GCATTTCTT AATAAGGAA AATTGCTTT GAAGTATACC  
TCCTTGGGC CAAAATGAAT CTGTGTCTC AATTGGAAGA GGTAAAGAAG TAGGGGGTTA GGGTGCATGG GTTGAACGT  
GAGACAGGTC GAACCAAAA GCCTGCCTGG AAAAGGGGAG TGACGTCCTA GGCTCAGTG ATGTACCTC CACTTTGTTT  
GATCCACAAA CCAACAGGTG ACTGATTTTG-3' (FRAG.NO.: ) (SEQ. ID NO: 2474)

5'-GCTCAGCCTC CAAAGGAGCC AGCCTCTCCC CAGTTCCTGA AATCCTGAGT GTTGCTGCTC AGTCGCCATG AGAAGTTCCT  
ACCTTCTGCT GTTACTCTC TGCTTACTTT TGCTGAGAT GGCCTCAGGT GGTAACCTTC TCACAGGCCT TGGCCACAGA

TCTGATCATT ACAATTGCGT CAGCAGTGA GGGCAATGTC TCTATTCTGC CTGCCCCGATC TTTACCAAAA TTCAAGGCAC  
CTGTTACAGA GGGAAAGGCCA AGTGCTGCAA GTGAGCTGGG AGTGACCAGA AGAAATGACG CAGAAGTGAA ATGAACTTTT  
TATAAGCATT CTTTAAATAA AGGAAAATTG CTTTTGAAGT AT-3' (FRAG.NO: \_\_) (SEQ. ID NO: 2472)

5'-CCGGGGC-3' (FRAG.NO:1800) (SEQ. ID NO: 1811)

5'-GG GCCTGCBGGG CC-3' (FRAG.NO:1801) (SEQ. ID NO: 1812)

5'-GGCBGCB BGG-3' (FRAG.NO:1802) (SEQ. ID NO: 1813)

5'-GGG TCC TCB TGG CTG GGG-3' (FRAG. NO:1212) (SEQ. ID NO:1222)

5'-GCC TGG GCC TGC BGG GCC-3' (FRAG. NO:1213) (SEQ. ID NO:1223)

5'-GCT CTT GCC TGG BGT GGC TC-3' (FRAG. NO:1214) (SEQ. ID NO:1224)

5'-GCC CBG BGT CTT CCC TGG T-3' (FRAG. NO:1215) (SEQ. ID NO:1225)

5'-CCGGGGCTGC BGCBBCTCB TCBGCTCTG CCTGGBGTGG CTCBGCCTGG GCCTGCBGGG CCBCCBGGBG BBTGGCBGCB  
BGGBTGGCB GGGTCTCTBT GGCTGGGGTC BCBGTCCTC TBGCTBGGCB GGGTGBCCBG BGBGGGC-3' (FRAG.NO:1803)  
(SEQ. ID NO: 1814)

### Human Defensin 2 Nucelic Acid and Antisense Oligonucleotide Fragments

5'-ATCCTTTAAG TCAATGGACT TTGCATCAGT CACACCATCT TTTGTTACTT TGGACTTCCC CAGCTATGTT CAATAATTAC  
TGTTCTTCCC TTGGGCCCCA TTGTAATGGC TACAGCCTCG AAAAAAGTC TACACTTTGA AGCATTAAAG CTCGGACATC  
AGCACCAAAT TTTACATCTT TACCATCACT TCAAGTGAGG TGAGGAGCCA GTAGCCTGGA CACTGGTCTC ATCTGGTGAA  
AGACTGTGGG TAATGGAAGC ATTTCTGTGG GGTGCTGGCA GGACATGTGC ATGGCGAGGC AGGTCATCAG CAGCAAGTGA  
GAGCTGCCTC TTACTTTCTA AAGGTGACAT AGCAAATATA CAAAAAATAA TAAATAAATT ATTAATTTAG GTAGAGCACA  
TAAAGGCTTT ATTTCATATT CCATTTCTCT GTATGCTTTC TTCACCAGGA AGAAATAGTT TTAGTGTGAG GAATGAATGA  
GTCTGCCCT CAATTCCAGC CTGCTCAACA CACAAGGAAA CAAAGCCCTG ACAATCAGAG TGAATCCCTG GTGACTAAGC  
TCCCAGTCCT GGATGCATAT TTGTTTAGCA GTTCTGACAG CATTGACCC AGCCCTCTCT CTGCATATCC CATCAGAACC  
TTCTTTTTTT TTTTTTCTT TGAGACTGAG TCTTGCTCTG TCGGAAGCGA CTCTGTGCC TCAGCCTCCC AAATACCTGG  
AATTATAGGC GTAAGCCATC ATGCTGGCT AATTTTGTGA TTTTTCATGG AGATGGGGTT TTGCCATGTT GGTCAAATTG  
GTCTCACT CTGACCTCA TGTGATCCAC CTGCTCAGC CTCCCAAAT GCTGGGATGA CAGGTGTAAG CCACCATGCT  
AGGCTCAGAA ATTTCTTTT ATAAAAATGT CATTAGGAT CTGGCTGCA CAATATCGTT ACCAGCTTCC TTAAATCCA  
CTTCTGGCT GCCAGGAATC AGGTTCTCA GAACCTGACA TTTAAATGA AGAGGTCAGG CAGTTTATGA GGAAAGCCTC  
ATTGTCCCA TGTCTCTGTC ACTGCTGCAC CCTGAGACA TCACAGACAT GGACACTGGG GCCTGCTGT TTTCAAAT  
GCCCTAGAT CGAAAGAGGG AGGAACCAGG ATGAATGCCA CTCATTTCC CAAGAAAGGC CCTCTCTGA GTGCCCGGA  
TGGGGCTCTG TCCATTGCCT GGGGCCGCCA ATTGCTACTC TGGGTACGG AGGAAGGACA GGGTCTGAG AGACACCAGA  
GACCTCACAC AGCCCTGAAA ACATGGGGCT CTTTATAAG TGTTCCTCAT CACCAACAGG GAGACCAGT GGAGGCCTTG  
CAGCCCCACT CGGTGCTTCT CCACCAAATC CCAAGGGCAG TGACGCTGAC GTCTGTGGA AGCAGAGAAA GCCCTGGCTC  
CCAAAGCCCT GAAGTCCCTG TGGAGCTGAC ATTCCCTGAG TGACGGTGTG AATGGAAGGA ACTCAAGTGC GGGTGGTAGG  
CCACCTCTG GCCAGGCCT GGGTGAATC TGAGGGGACA CATGTAGTCA CAATCCATC CTCCATTCT CTTTCTCAGA  
GGAAGGAAGT GGGCATCCAT CTGCTCATC TCTCTCCGT GGGGAAGATG GGGAGTTTCA GGGGAATTT CACATAAAT  
TCACCAGCTC AGATCTCTG TGAGGATGGG GCCCACCATG CTCCGGTGC TGCCAGAGGC CCTGAGCCCC TCCCAGGGTC  
CCTGGGTTTG AGCCAGCCCT GTATCATCCC CAGGAGCTGA ATGTCAGAGC AATGGATAGA ATTAGATGGA AAGAGCTCTC  
AATTTGACCT GAGACTGTCC CCAGATACTC AGGAAAAACA GGACGTCGCA CAGAGTGGG AGCAGGTGAG TGGCAGGTTA  
TAGGTCTGA GTTTGAGTT GTTCTCAGT GAGACAGACC CAGCCCTCA CTCCATTAC ACTGGGTT TAAATGGTG  
CAAGATAGGA GCAATTTTCT GGTCCAAGA GCAGGAGGAA GGGATTTTCT GGGGTTTCT GAGTCCAGAT TTGCATAAGA  
TCTCTGAGT GTGCATTGTT CTTTGAGGAC CATTCTCTGA CTCACCAGT AAGTGGCTGA ATTCTAACCT CTGTAATGAG  
CATTGCACCC AATACCAGTT CTGAATCTA CCTGGTGACC AGGGACCAGG ACCTTTATAA GGTGGAAGGC TTGATGTCCT  
CCCCAGACTC AGCTCTGGT GAAGCTCCA GCCATCAGC ATGAGGGTCT TGTATCTCT CTCTCTGTT CTCTCATAT  
TCCTGATGCC TCTTCAGGT GAGATGGGCC AGGGAATAG GAGGGTTGGC CAAATGGAAG AATGGCGTAG AAGTTCTCTG  
TCTCTCTCA TTCCCTCCA CTTATCTCT CCTCATCCCT CTCTCTCTT CTCTCTCTG TGTGTCCCT CCATCCTTT  
CTCTGCTT TCTCTCTT TCCCTCTCT TCTTTTCT GTCTTTCTT TTCTCTCTC CTTAGAGCAT GTCTTTCTT  
CTTTCTCTT CTTTCTTCT ACCCACAT TTAGACTGAA TGCCCTATTT AATTGAACAA AGCATTGCTT CTTCAATAG  
AAAAGGAGTT TGAGAACCCA ATGGACACT CACTCGTCT TCTAAGCCAA TATGAAGGAG CCCAGTAGCT TGAAATATC  
ATCTCTTAC TCTTTGCA CTGACACTC CTCACACTAT CTTTCAACC TCTTACTCA CTTTAAAT AAAAGGCAGA

TCCAGGGTCA CAGGCATCTG TATTCTTTGG ATTCTTGAC CTTCGCCATT TATTCGCCGGC ATTTTCCTAA AACGTGTGCT  
TTGCTCCTCC TGCATCCTCC CTTGTCATGC CTTACCTAC CCCACATCTT CCCTAAAAAA AGCAAGCCCA ACTCAAAGAC  
CAGTTCCTC ATGGAATCAT AGTGGATCTG CCAAGGGAGG GGATGCCAG TCCTCTGTTT TACACAAGAC TCCCTTCTTC  
TGGCTAAGGT TTCTTATGCA ATTAT GAATTCACAT TTCTCACCTT TGATGTATT AAGAAAGTAT GGAGAAATAT  
ATCCTCTATC AAATTTTCAT GCCTTCAATA ATTTCTAATT CATCAGTCAG TGTTTTTCCA TCCTTTACTG TGATGATGCC  
CTTTCTTCCA AACTTTTTCA TTGCATCAGA GATGATGTTA CCAATTTCTT TGTCTCCATT TGCAGAAATT GTAGCAACCT  
GTGCAATTC TTCAAGTTTG GTCACAGGTT TAGACTGCTT TTTAAGTTCA GCAATTACAG CATCAACAGC TAACATCACA  
CCTCTCTGA TTCCCACTGG ATTAGCACCT TTGCTAACCT TTGGAAGGC TTATTTGGAA ATAGAGCATA CCAGTACAGC  
AGCAGTGATA GTGCCATCCC CCAGTCTCTC CATTTGTGTT ATTGGCAACA TCTGGGACAA GTTTAGCTCC AATGCTTTTA  
TATTTATCCT TTAAGTCAAT TGACTTTGCA TCAGTCACAC CATCTTTTGT TACTTTGGGA CTTCGCCAGC TATGTTCAAT  
AATTACTGTT CTTCCTTTG GCCCATTGT AATGGCTACA GCATCGACAA AAAGTCTACA CTTTGAAGCA TTAAGGCTCA  
GACATCAGCA CCAAATTTTA CATCTTACC ATCACTTCAA GTGAGGTGAG GAGCCAGTAG CCTGGACACT GGTCTCATCT  
GGTGAAGAC TGTGGTAAT GGAAGCATT CTGTGGGGTG GTGGCAGGAC ATGTGCATGG TGAGGCAGGT CATCAGCAGC  
AAGTGAGAGC TGCCTTTAC TTCTAAAGG TGACATAGCA AGTATACAAA AAAAAATAAA ATATTAATTT AGGCAGAGCA  
CATAAAGGCT TTATTTCTA TTCCATTTCT CTGTATGCTT TCTTGACCAG GAAGAAATAG TTTAGTGTC AGGAATGAAT  
GAGTCTGCCC CTCAATTCCA GCCTGCTCAG CACACAAGGA AACAAAGCCC TGACAATCAG AGTGACTCCC TGGTGACTAA  
GCTCCAGTCC TGGATGCATA TTTGTTAGC AGTCTGACA GCATCTGACC CAGCCCTCTC TTTGCATACC CCACCAGAAC  
CTCTTTTTT TTTTTTTT TTTGAGACTG AGTCTTGCTC TGTGGGAAGC GATTCCCGTG CCTCAGCCTC CCAAATACCT  
GGAATTATAG GCGTAAGCCA TCATGCCTGG CTAATTTTGT TATTTTTCAT GGAGATGGGG TTTTGCCATG TTGGTCAAAT  
TGGTCTCACA CTCTGACCT CATGTGATCC ACCTGCCTCA GCCTCCCAA GTGCTGGGAT GACAGGTGTA AGCCACCATG  
CTAGGCTCAG AAATTTCTT TTATAAAAA TCATTAAGG ATCTTGCTG CACAATATCG TTACCAGGTT CCTTTAAATC  
CACCTCTGGC CTGCCAGGAA TCAGGGTTCT TGACAACCTG ACATTTTAAA TGAAGAGGTC AGGCAGGTTA TGAGGAAAGC  
CTCATTTGCC CCATGTCTCT GTCAGTCTG CACCCCTGAG ACATCACAGA CATGGACACT GGGGCTGCT TTTTCTCAA  
ACTGCCCTTA GATCGAAAGA GGGAGGAACC AGGATGAATG CCACTCATT TCCCAAGAAA GGCCCTCTCC TGAGTGCCCG  
GGATGGGGCT CTGTCCATTG CCTGGGGCCG CCAATTGCTA CTCTGGGTTA CGGAAGAAAG ACAGGGTCTC GAGAGACACC  
AGAGACCTCA CACAGCCCTG AAAACATGGG GTCCTTCAT AAGTGTTC CATCACCAAC AGGGAGACCA CGTGGAGGCC  
TTGACGCCCT ACTCGTGCT TCTCCACCA ATCCCAAGGG CAGTGACGCT GACGTCTGTG GAAAGCAGAG AAAGCCCTGG  
CTCCCAAAGC CTGGAAGTCC TGTGGAGCTG ACATTCCTG AGTGACGGTG TGAATGGAAG GAATCAAGT GCGGGTGGA  
GGCCACCTCC TGGCCAGGC CTGGGTGAAC TCTGAGGGGA CACATGTAGT CACAATCCCA TCCTCCATT CTCCTTCTCA  
GAGGAAGGAA GTGGGCATCC ATCTGCCTCA TCTCTCTCC GTGGGAAGA TGGGGAGTT CAGGGGAACT TTCACATAAA  
TTTACCAGC TCAGATCTCC TGTGAGGATG GGGCCACCA TGCTCCCGT GTCGCCAGAG GCCCTGAGCC CCTCCAGGGT  
CCCTGGGTTT GAGCCAGCCC TGATCATCC CCAGGAGCTG AATGTCCGAA CAATGGATAG AATTAGATGG AAAGAGCTCT  
CAATTTGGCC TGAGACTGTC CCCAGATACT CAGGAAAAAC AGGACGTGCG ACAGAGTGGG CAGCAGGTGA GTGGCAGGTT  
ATAGTCTCTG AGTTTGTGTT TGTCTCAG TGAGACAGAG CCAGCCCTC ACTCCATTCA CACATGGGGT TTTAAATGGT  
GCAAGATAGG AGGAATTTT TGTCCCAAAG AGCAGGAGGA AGGGATTTT TGGGGTTTCC TGAGTCCGA TTTGATAAG  
ATCTCTGAG TGTGCATTGT TCTTTGAGGA CCATTCTCTG ACTCACCAGG TAAGTGGCTG AATTCTAACC TTGTAAATGA  
GCATTGCACC CAATACCAGT TCTGAATCT ACCTGGTGAC CAGGGACCAG GACCTTTATA AGGTGGAAGG CTGTATGCC  
TCCCCAGACT CAGCTCCTGG TGAAGCTCCC AGCCATCAGC CATGAGGGTC TTGTATCTCC TCTTCTGTT CCTCTCATA  
TTCTTGATGC CTCTCCAGG TGAGATGGG CAGGGAAATA GGAAGGTTGG CCAAATGGAA GAATGGCGTA GAAGTTCTCT  
GTCTCTCTC ATTCCCTCC ACCTATCTCT CCTCATCCC TCTCTCTCT TCCTCTCTCT GTGTGTCCC TCCATCCTTT  
TCTCTGCTT CTCTCTCTC TTCCCTCTCT CTCTTTTCT TGTCTTTCT TTTTCTCTC TCCTAGAGC ATGTCTTCT  
TTCTTCTCT TTCTTTCT CTACCCACAC TTTAGACTG AGTAGACTGA ATGCCCTATT TAATTGAACC AAGCTAGTCT  
TCCTTCAATA GAAAAGGAGT TTGAGAACC AATGGACAAC TCACCTGTTT TTCTAAGCCA ATATGAAGGA GCCCAGTAGT  
TTGTAATAT CATCTCTCA CTGCTTTCCA TGCTACAACT GCTGAGACTA TGGTTGAAAC CTGTAGGTG ACTTTTAAA  
TAAAAGGCAG AAATTTTGT TTTATCTAAA GAAAGTAGTA TAGAATGTC TTTCTAAAT TTTATATTT AAAGAGTAGA  
TACTGCAACC TAGAGAATC CAGATAATCT TAAGGCCAG CCTATACTGT GAGAACTACT GCAGCAGACA CTCTGCCCC  
AGGACTTTT TGATCAGAG CCTGAGAAC GTCCCTGCC ACTAGGCCAC TGCAGGTTCA CAGGACAGG ACAGCCCAT  
GAAACCACT TTTAAACCTG GATGCCATA CTGATTTTCT CTCTGATAT TATGAAAATA AAATAAAAC CATGAAAGGA  
TAAAAGAGG AGAGTGAAG GGAAGGATG AGAAAGGGA AAAGAAATT TGAGAGTAAA TCCTAAACAA  
ATTAATCTAA TAGATATCAT CTGTGAAAT CCTCATTTA CCAATCTTAT TTATGAGTCC TGGGTTTGT GAGAACAAATG  
GGGTTCTGAG AGGCACCAGA GACCTCATAT TTTCCAAAC CTAGAACAGT ATAATGAAGG AAGGAGGGA GGAGGGAGG  
AGGGAGGGA GGAGGGAAG AGGGAGGAG GGAGGGAAC AAAAGAAGA ATGAGGTGA AACCAGGACT  
TAGATATTAG AAACAAGCCA TTACAAAT TATTTCTATG GTTAATTGTG GTTTTCACT GTAAGTTACT TGGTGTAAAT  
TTCTATTAA ACAATTTAG TAAGTTGCAT CTTTTTAT CCATCTCAGA TCAAATACTT AACAGACTAA ATGATTTGAA  
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 NO:2473)

#### Human Defensin 3 Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CGCTGCBTC TGCTCCGGG CTGCBGCBBC CTCBTCBGCTC TTGCTGGBGTG GCTCBGCCTGG GCCTGCBGGG  
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 CTGTTCCACA TAGCAACAGA AGCCCAGGTA GCACTCAGTC TCACCTGGGT GTTCTCCAAC ATCCAGCTC AGCCAAATGG  
 CTTTCATTAG TTTTATGGT TAGACCCAG GTCTCGGGA CACTGCTTTA GAAACACATT CCAAATCTC CTCTGTGTG  
 AGGTGGCATT CCTATCCAA TCTCTTGA GGGCGTATAC TGTGATACGC AGCCAGGCTG TCCAGAGGC CTAAATATT  
 CCTTGGTGC AGGTAGTTCA GCTTAGCCAC AGCCAATGCA TCACAGGCTC AACTGTGTTA GGAGCCATTG AGAATCCATA  
 GTTGGTGTCT GCCTGGGCT GGCCAGGGCT GACCAAGGTA GATGAGAGGT TCCTCTGTGG AGTTCTACTT TAACCTCACC  
 TCCCACCAA ATTCTCAAC TGTCCTTGGC ACCACAATTA TTTAATGGAC CCAACAGAAA GTAACCCCGG AAATTAGGAC  
 ACCTCATCCC AAAAGACCTT TAAATAGGGG AAGTCCACTT GTGCAGGCT GCTCCTGCT ATAGAAGACC TGGGACAGAG  
 GACTGCTGTC TGCCCTCTCT GTTCACCTG CTTAGCTAGA GATCTGTAA GTACTACAAA ACTTAACTT TACACTGAGT  
 TTTATCATT GAAGCTATGC CTCCAATCTG ACCTCTGACT GTGGGGCCGC CCCAGAGGGA CCCAGCGGGT GAATCCCTGC  
 TAGGAACGTC TGTCCGACC TCTGGTGAAT GCTGGGACG ATGGCTTCCA GCTAACTTA TAGAGAACT CAAGCAGTTT  
 CTTCTAAAT ACACATGTC CATGTCCTGG TTGACATGTC CAGTAAGAAG ACTATCACAG GTCTTTGGAA CATTCTTTG  
 AGAGAAACCT ATTAGGTCC TTGGTCTGTT TTCAATCAG GTTGTGTTGAT TTTGCTATT GAGTTGTGG AATTCTTAT  
 GTATTGAGT ATTTGCCCC TCTGCCATGT AGGTTTGA AATATTTCT CTCATTTCT GGGTATCTT TCACTCGGT  
 TCACTCTCTG CTTTCTCTG CAGATGCTT AGCTTAAAT CAAGGACAG TCTCTATT TCCCTTTAT TGCCTGTGCC

CTTCAGAAAA TAAGAAGCAT TTGTTCCCTG AGCCTGTGTA ATCAAAGTGC AATTTCTATT CTTTTTGGAA TGTTAAAAAG  
 TGAATCATAA TATTTAAGCA GGTGAACCCA CGAGTAACAT AGCAGGGTCT TTCTTGTCAT TATTAGCTCC AACCTAGCAC  
 AGACATTAAG GGTACAGATG TATACTAGCA TGAAGTGGG AGAACAGGAG CATTGAGCA ACCTTGAGAC CAATGGGCCT  
 CTCTTATAAA ATGCACACCT CCTCTCACTG AGATTGAGGA AGGTTTCTTG TCTCCGAGCC TTCTCCCATG AGAGCTATAA  
 ATCCAGGCTG GCTCCTCCCT CCCCACACAG CTGCTCCTGC TCTCCCTCT CCAGGTGACC CCAGCCATGA GGACCTCGC  
 CATCCTTGCT GCCATTCTCC TGGTGGCCCT GCAGGCCAG GCTGAGCCAC TCCAGGCAAG AGCTGATGAG GTTGCTGCAG  
 CCCCAGGAGCA GATTGCAGCG GACATCCAG AAGTGGTGT TTCCCTGCA TGGGACGAAA GCTTGGCTCC AAAGCATCCA  
 GGTGAGAGAG GCAGGCATGC AGAGCTGCTA AGTCTAGAGG GAAGGACGGG AGAGAGGTTT CAGAGTTGGG TCTCAGCAGT  
 CTATGTCACT GAGGTGGCTT CACTTAGAAT CTCTGGGCAT TGATTTCTC ATCTAGAAAT TGAACAGAGA GCCAAATAAA  
 CCTGAGAAAC TTTATTTCTC CAAAGACTTG ATTCCAAGAA ACATCTGTGA AATTCATAA GTTTAAGATA TGAAGAGACA  
 GACTAGTTAT TTCTGGATCT AAACAAGTAG ACTTAGTTGT AAAGAGAAACA TTTACTCTA TCTACAGAAG AGCTTTTAAA  
 AACTGCAGCC AAGCTGAGG GTAAGTTCAG GTGTGTGTGT GATGGGGCAG GAATGCAAAA ATGAGAGCAA AGGAGAATGA  
 GTCTCAAATT CTGTGTGACA AGCACTGCTC TCGTGTTTA TTCCTATCGA CTGAGGTGTG TCGTGCTACC GGCTGCAATG  
 CAGCCAGCAT CACCTGTCAG CTAGCATGTG ACTTCCCGA GATTTCTTTT CTACCCACT GCTAACTCCA TACTCAATTT  
 CTCATGCTCT CCGTGTCCA GGCTCAAGGA AAAACATGGA CTGCTATTGC AGAATACCAG CGTGCAATGC AGGAGAACGT  
 CGCTATGGAA CCTGCATCTA CCAGGGAAGA CTCTGGGCAT TCTGCTGCTG AGCTTGCGA AAAAGAAAAA TGAGCTCAAA  
 ATTTGCTTTG AGAGCTACAG GGAATTGCTA TTACTCTGT ACCTTCTGCT CAATTTCTT TCCTCATCTC AAATAAATGC  
 CTGTATCAA GATTTCTGTG TTTCCACCTC TTTAATGTGT GATATGTGTC TGTGTCAAGA CACTGGGAT ACACGTACCA  
 AAACGCAAAA TCAAATTTT GAACAATATA-3' (FRAG. NO: ) (SEQ. ID NO:2477)  
 5'-GGCBGCBGG-3' (FRAG. NO:1805) (SEQ. ID NO:1816)  
 5'-GG CTG GGG-3' (FRAG. NO:1806) (SEQ. ID NO:1817)  
 5'-GGGGTCBCC-3' (FRAG. NO:1807) (SEQ. ID NO:1818)  
 5'-GGG TCC TCB TGG CTG GGG TC-3' (FRAG. NO:1216) (SEQ. ID NO:1226)  
 5'-CCT CTC TCC CGT CCT-3' (FRAG. NO:1217) (SEQ. ID NO:1227)  
 5'-CGCTGCBTC TGCTCCGGGG CTGCBGCBBC CTCBTCBGCTC TTGCCTGGBGTG GCTCBGCCTGG GCCTGCBGGG  
 CCBCCBGGGB BTGGCBGCBG GBTGGCBGGG TCCTCBTGGC TGGGGTCBCT GGBGGBGGGB GBGCBGG-3' (FRAG.  
 NO:1808) (SEQ. ID NO:1819)

### Human Macrophage Inflammatory Protein-1-alpha/RANTES

#### Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GTCTTTGTT CTGGGCTCGT GCCCBTCCC GGCTTCTCTC TGGTTCGTC CTCTGTGGTG TTTGGCCCTG CTTCCTTTTG  
 CCTGTTGAGG GGGCAGCAGT TGGGCCCAA AGGCCCTCTC GTTCACCTC TGGCACGGAGT GCATCCCCATA  
 GTCAAACCT GTGGTCTGT CATAGTCTC TGTGTGTTT GGAGTTTCCA TCCCGGCTC TCTCTGGTTC CAAGGGAGB  
 GGGGGCBGB GTTGGGCCCB BBBGGCCCTC TCGTTCBCT TCTGGCBGG BGTTCBCTCC CBTBGTCTBB BCTCTGTGGT  
 CGTGTCTBG TCCTCTGTGG TGTGGBGT TTCBTCCCG GCTTCTCTCT GTTCCBBGG GB-3' (FRAG. NO:1809) (SEQ. ID  
 NO:1820)  
 5'-GGGCC CC-3' (FRAG. NO:1810) (SEQ. ID NO:1821)  
 5'-GGGGCBGC-3' (FRAG. NO:1811) (SEQ. ID NO:1822)  
 5'-CCCGGCTTC-3' (FRAG. NO:1812) (SEQ. ID NO:1823)  
 5'-GTC TTT GTT TCT GGG CTC GTG CC-3' (FRAG. NO:1218) (SEQ. ID NO:1228)  
 5'-CCB TCC CGG CTT CTC TCT GGT TCC-3' (FRAG. NO:1219) (SEQ. ID NO:1229)  
 5'-GTC CTCTGT GGT GTT TGG-3' (FRAG. NO:1220) (SEQ. ID NO:1230)  
 5'-CCC TGC TTC CTT TTG CCT GTT-3' (FRAG. NO:1221) (SEQ. ID NO:1231)  
 5'-GAGGGGGCAG CAGTTGGGCC CAAAGGCC TCTCGTTCAC CTCTGGCAC GGAGTTGCAT CCCCATAGTC AAACCTCTGTG  
 GTCGT-3' (FRAG. NO:1222) (SEQ. ID NO:1232)  
 5'-GTCATAGTCTCTGTGGTGTGGAGTTCCATCCCGGCTTCTCTGTTCCAAGGGA-3' (FRAG. NO:1223) (SEQ. ID  
 NO:1233)  
 5'-GBGGGGGCBG CBGTTGGGCC CBBBGGGCC TCTCGTTCBC CTCTGGCBC GGBGTTGCBT CCCCBTBGT BBCTCTGTG  
 GTCGTG-3' (FRAG. NO:1224) (SEQ. ID NO:1234)  
 5'-TCBTGCTCTGTGGTGTGGGTTTCCBTCCCGGCTTCTCTGTTCCBBGGGB-3' (FRAG. NO:1225) (SEQ. ID NO:1235)

#### RANTES Antisense Oligonucleotide Fragments

5'-GGGCBGGGG CBGTGGGCGG GCBTGTBGG CBBGCBGCB GGGTGTGGT TCCBGGBBT BTGGGGGGC BGTGCBGGB  
 GCGCBGGBG CBGTGCBBT GBGBTGBCB GCGBGGCGT CCGCBGBC CTCTBTGGT CCTGTGGBG GGCTGTCCGB  
 GGGGTGTGG TGTCGCTTG GCGGTCTTT CCGGTGTTT TTCTGTGGT TGGCCTGCT CTCGTCTGGT CGCTCCGCTC  
 CCGGTTCTG CTGCTCTGT GCGCCCTTCC TTCCTGTGCG TGTTCTCCC TTCCTGCT CT-3' (FRAG. NO: 1813) (SEQ. ID  
 NO: 1824)  
 5'-GGGTGGC-3' (FRAG. NO: 1814) (SEQ. ID NO: 1825)  
 5'-CGGG CBG-3' (FRAG. NO: 1815) (SEQ. ID NO: 1826)  
 5'-CCCGGTTCTG-3' (FRAG. NO: 1816) (SEQ. ID NO: 1827)  
 5'-GGGTGTGGT-3' (FRAG. NO: 1817) (SEQ. ID NO: 1828)  
 5'-GGGCBGGGG CBGTGGGCGG GCBTGTBGG CBBGCBGCB GGGTGTGGT TCCBGGBBT BTGGGGGGC BGTGCBGGB  
 GCGC-3' (FRAG. NO:1226) (SEQ. ID NO:1236)  
 5'-BGBGGGCBGTGCBTGBGGBTGCBGCGGCGTCCGCGGBGBCCTTCTBTGGTBCCTGTGGBGGGCTGTCGGBGG-3'  
 (FRAG. NO:1227) (SEQ. ID NO:1237)  
 5'-GGGTGTGGTGTCCGCTTGGCGGTTCTTTCGGGTGTTTCTCTGTTGGCTGCTGCTCGTCTGTCGTCGTCGTCGTC-3' (FRAG. NO:1228)  
 (SEQ. ID NO:1238)  
 5'-GCTCCGCTCCCGGTTCTGCTCTGCTGCGCCCTTCTTCTGTCGTTCTCCCTTCTTCTGCTCT-3' (FRAG. NO:1229)  
 (SEQ. ID NO:1239)  
 5'-GGGTGTGGTGTCCG-3' (FRAG. NO:1230) (SEQ. ID NO:1240)

5'-CTTGGCGGTTCTTTCGGGTG-3' (FRAG. NO:1231) (SEQ. ID NO:1241)  
 5'-TTTCTTCTCTGGGTGGC-3' (FRAG. NO:1232) (SEQ. ID NO:1242)  
 5'-CTGCTGCTCGTCGTGGTC-3' (FRAG. NO:1233) (SEQ. ID NO:1243)  
 5'-GCTCCGCTCCCGGGTTC-3' (FRAG. NO:1234) (SEQ. ID NO:1244)  
 5'-GTCTCGCTCTGTGCCC-3' (FRAG. NO:1235) (SEQ. ID NO:1245)  
 5'-CTTCTTCTCTGTGTC-3' (FRAG. NO:1236) (SEQ. ID NO:1246)  
 5'-GTGTTCCTCCCTTCTTGCCTCT-3' (FRAG. NO:1237) (SEQ. ID NO:1247)  
 5'-GGGCBGCGGG CBGTGGGCGG GCBGTGTGG CBBGCBGCB GGGTGTGGT TCCBGGBBT BTGGGGGGC BGBTGCBGG  
 GCGCBGGG CBGTGCBBT GBGGTGBCB GCGGGCGTG CCGCBGGBC CTTCBTGGT CCTGTGGGB GGCTGTGCGG  
 GG-3' (FRAG. NO:1818) (SEQ. ID NO:1829)

#### Human Muscarinic Acetylcholine Receptor HM1\* Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GCTGCCCCGGC GGGGTGTGCG CTGGCGCTC CCGTCTCGG TTCTCTGTCT CCCGGTCCCC CTGCTGGC GTCTCGGGC  
 TTCGTCTCT TCCTCTCTT CCTCCGCTC CGTGGGGGCT GCTGTGGTGG GGCCTGTGCT CGGGGTCCCG GGGCTTCTGG  
 CCCTTCCCGT TCATGTGGC TAGGTGGGG GTTCBTGGT GCTBGGTGG GC-3' (FRAG. NO:1819) (SEQ. ID NO: 1830)  
 5'-GGTGGGGC-3' (FRAG. NO:1820) (SEQ. ID NO: 1831)  
 5'-GCCCGCGGGG-3' (FRAG. NO:1821) (SEQ. ID NO: 1832)  
 5'-CGG GGC TTC TGG CCC-3' (FRAG. NO:1822) (SEQ. ID NO: 1833)  
 5'-GTT CBT GGT GGC TBG GTG GGC C-3' (FRAG. NO:1238) (SEQ. ID NO:1248)  
 5'-GCT GCC CGG CGG GGT GTG CGC TTG GC-3' (FRAG. NO:1239) (SEQ. ID NO:1249)  
 5'-GCT CCC GTG CTC GGT TCT CTG TCT CCC GGT-3' (FRAG. NO:1240) (SEQ. ID NO:1250)  
 5'-CCC CCT TTG CCT GGC GTC TCG G-3' (FRAG. NO:1241) (SEQ. ID NO:1251)  
 5'-GCC TTC CTC TTC CTC TTC CTT CC-3' (FRAG. NO:1242) (SEQ. ID NO:1252)  
 5'-GCT CCG TGG GGG CTG CTT GGT GGG GGC CTG TGC CTC GGG GTC C-3' (FRAG. NO:1243) (SEQ. ID NO:1253)  
 5'-CGG GGC TTC TGG CCC TTG CC-3' (FRAG. NO:1244) (SEQ. ID NO:1254)  
 5'-GTT CAT GGT GGC TAG GTG GGG C-3' (FRAG. NO: 1245) (SEQ. ID NO:1255)

#### Human Muscarinic Acetylcholine Receptor HM3\* Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GGG GTG GGT BGG CCG TGT CTG GGGTT GGC CBT GTT GGT TGC CTCT TGG TGG TGC GCC GGG CGCG TCT TGG CTT  
 TCT TCT CCT TCG GGC CCT CGG GCC GGT GCT TGT GGGCT CCT CCC GGG CGG CCT CCC CGG GCG GGG GCT TCT  
 TGGCG CTG GCG GGG GGG CCT CCGCT CTG TGG CTG GGC GTT CCT TGG TGT TCT GGG TGGTGG CGG GCG TGG TGG  
 CCT CTG TGGGGG CCC GCG GCT GCB GGG GTTG CCT GTC TGC TTC GTCCTT TGC GCT CCC GGG CCG CCGG GTG GGT  
 AGG CCG TGT CTG GGGTT GGC CAT GTT GGT TGC CCGG CCC GCG GCT GCA GGG G-3' (FRAG. NO:1823) (SEQ. ID  
 NO:1934)  
 5'-CCC GGG CGG-3' (FRAG. NO:1824) (SEQ. ID NO:1835)  
 5'-G GCG GGG GGG CC-3' (FRAG. NO:1825) (SEQ. ID NO:1836)  
 5'-CCC GGG CCG CC-3' (FRAG. NO: 1826) (SEQ. ID NO: 1837)  
 5'-GG CCG TGT-3' (FRAG. NO:1827) (SEQ. ID NO:1838)  
 5'-GGG GTG GGT BGG CCG TGT CTG GGG-3' (FRAG. NO:1246) (SEQ. ID NO:1256)  
 5'-GTT GGC CBT GTT GGT TGC C-3' (FRAG. NO:1247) (SEQ. ID NO:1257)  
 5'-TCT TGG TGG TGC GCC GGG C-3' (FRAG. NO:1248) (SEQ. ID NO:1258)  
 5'-GCG TCT TGG CTT TCT TCT CCT TCG GGC CCT CGG GCC GGT GCT TGT GG-3' (FRAG. NO:1249) (SEQ. ID NO:1259)  
 5'-GCT CCT CCC GGG CGG CCT CCC CGG GCG GGG GCT TCT TG-3' (FRAG. NO:1250) (SEQ. ID NO:1260)  
 5'-GCG CTG GCG GGG GGG CCT CCT CC-3' (FRAG. NO:1251) (SEQ. ID NO:1261)  
 5'-GCT CTG TGG CTG GGC GTT CCT TGG TGT TCT GGG TGG C-3' (FRAG. NO:1252) (SEQ. ID NO:1262)  
 5'-TGG CGG GCG TGG TGG CCT CTG TGG TGG-3' (FRAG. NO:1253) (SEQ. ID NO:1263)  
 5'-GGG CCC GCG GCT GCB GGG G-3' (FRAG. NO:1254) (SEQ. ID NO:1264)  
 5'-TTG CCT GTC TTC GTC-3' (FRAG. NO:1255) (SEQ. ID NO:1265)  
 5'-CTT TGC GCT CCC GGG CCG CC-3' (FRAG. NO:1256) (SEQ. ID NO:1266)  
 5'-GGG GTG GGT AGG CCG TGT CTG GGG-3' (FRAG. NO:1257) (SEQ. ID NO:1267)  
 5'-GTT GGC CAT GTT GGT TGC C-3' (FRAG. NO:1258) (SEQ. ID NO:1268)  
 5'-GGG CCC GCG GCT GCA GGG G-3' (FRAG. NO:1259) (SEQ. ID NO:1269)

#### Human Fibronectin\* Antisense Oligonucleotide Fragments

5'-CGG TTT CCT TTG CGG TC TTG GCC CGG GCT CCG GGT G CCC GCC CGC CCG CCG GCC GCC GC CCC GCC GGG CTG  
 TCC CCG CCC CGC CCC GGC CCG GGG CGC GGG GG CGG CCC TCC CGC CCC TCT GG GCC GGC GCG GGC GTC GG CCG  
 CTC GCG CCT GGG GTT CCC TCT CCT CCC CCT GTG C GCC TGC CTC TTG CTC TTCTGC GTC CGC TGC CTT CTC CC CTC  
 TCC TCG GCC GTT GCC TGT GC TGT CCG TCC TGT CGC CCT TCC GTG GTG C TGT TGT CTC TTC TGC CCT C GGT GTG  
 CTG GTG CTG GTG GTG GTG CCT CTG CCC GTG CTC GCCCTG CCT GGG CTG GCC TCT TCG GGT GTG GCT TTG GGG CTC  
 TCT TGG TTG CCC TTT CTT CTC GTG GTG CCT CTC CTC CCT GGC TTG GTC GT TGT CTG GGG TGG TGC TCC TCT CCC  
 TTT CCC TGC TGG CCG TTT GT  
 CCT GTT TTC TTT CCT CT TTC CTC CTG TTT CTC CGT TTG GCT TGC TGC TTG CGG GGC TGT CTC C CTT GCC CCT  
 GTG GGC TTT CCC TGG TCC GGT CTT CTC CTT GGG GGT C GCC CTT CTT GGT GGG CTGGCT CGT CTG TCT TTT TCC TTC  
 C TGG GGG TGG CCG TTG TGG GCG GTG TGG TCC GCC T TGC CTC TGC TGG TCT TTC-3' (FRAG. NO:1828) (SEQ. ID NO:  
 1839)

5'-GGCCCGGGC-3' (FRAG. NO:1829) (SEQ. ID NO: 1840)  
 5'-GCCGGCGCGGGCGC-3' (FRAG. NO:1830) (SEQ. ID NO:1841)  
 5'-GCCTGGGCTGGCC-3' (FRAG. NO:1831) (SEQ. ID NO: 1842)  
 5'-GGGGG TGGCCG-3' (FRAG. NO:1832) (SEQ. ID NO: 1843)  
 5'-GG GGG TGG CCG TTG TGG GCG G-3' (FRAG. NO:1833) (SEQ. ID NO: 1844)  
 5'-CCC TTT CCT TTG CCG TG-3' (FRAG. NO:1834) (SEQ. ID NO: 1845)

5'-TTG GCC CGG GCT CCG GGT G-3' (FRAG. NO:1261)(SEQ. ID NO:1271)  
5'-CCC GCC CGC CCG CCG GCC GC-3' (FRAG. NO:1262)(SEQ. ID NO:1272)  
5'-CCC GCC GGG CTG TCC CCG CCC CGC CCC-3' (FRAG. NO:1263)(SEQ. ID NO:1273)  
5'-GGC CCG GGG CGC GGG GG-3' (FRAG. NO:1264)(SEQ. ID NO:1274)  
5'-CGG CCC TCC CGC CCC TCT GG-3' (FRAG. NO:1265)(SEQ. ID NO:1275)  
5'-GCC GGC GCG GGC GTC GG-3' (FRAG. NO:1266)(SEQ. ID NO:1276)  
5'-CCG CTC GCG CCT GGG GTT CCC TCT CCT CCC CCT GTG C-3' (FRAG. NO:1267)(SEQ. ID NO:1277)  
5'-GCC TGC CTC TTG CTC TTC-3' (FRAG. NO:1268)(SEQ. ID NO:1278)  
5'-TGC GTC CGC TGC CTT CTC CC-3' (FRAG. NO:1269)(SEQ. ID NO:1279)  
5'-CTC TCC TCG GCC GTT GCC TGT GC-3' (FRAG. NO:1270)(SEQ. ID NO:1280)  
5'-TGT CCG TCC TGT CGC CCT TCC GTG GTG C-3' (FRAG. NO:1271)(SEQ. ID NO:1281)  
5'-TGT TGT CTC TTC TGC CCT C-3' (FRAG. NO:1272)(SEQ. ID NO:1282)  
5'-GGT GTG CTG GTG CTG GTG GTG GTG-3' (FRAG. NO:1273)(SEQ. ID NO:1283)  
5'-CCT CTG CCC GTG CTC GCC-3' (FRAG. NO:1274)(SEQ. ID NO:1284)  
5'-CTG CCT GGG CTG GCC TCT TCG GGT-3' (FRAG. NO:1275)(SEQ. ID NO:1285)  
5'-GTG GCT TTG GGG CTC TCT TGG TTG CCC TTT-3' (FRAG. NO:1276)(SEQ. ID NO:1286)  
5'-CTT CTC GTG GTG CCT CTC CTC CCT GGC TTG GTC GT-3' (FRAG. NO:1277)(SEQ. ID NO:1287)  
5'-TGT CTG GGG TGG TGC TCC TCT CCC-3' (FRAG. NO:1278)(SEQ. ID NO:1288)  
5'-TTT CCC TGC TGG CCG TTT GT-3' (FRAG. NO:1279)(SEQ. ID NO:1289)  
5'-CCT GTT TTC TGT CTT CCT CT-3' (FRAG. NO:1280)(SEQ. ID NO:1290)  
5'-TTC CTC CTG TTT CTC CGT-3' (FRAG. NO:1281)(SEQ. ID NO:1291)  
5'-TTG GCT TGC TGT CCG GGC TGT CTC C-3' (FRAG. NO:1282)(SEQ. ID NO:1292)  
5'-CTT GCC CCT GTG GGC TTT CCC-3' (FRAG. NO:1283)(SEQ. ID NO:1293)  
5'-TGG TCC GGT CTT CTC CTT GGG GGT C-3' (FRAG. NO:1284)(SEQ. ID NO:1294)  
5'-GCC CTT CTT GGT GGG CTG-3' (FRAG. NO:1285)(SEQ. ID NO:1295)  
5'-GCT CGT CTG TCT TTT TCC TTC C-3' (FRAG. NO:1286)(SEQ. ID NO:1296)  
5'-TGG GGG TGG CCG TTG TGG GCG GTG TGG TCC GCC T-3' (FRAG. NO:1287)(SEQ. ID NO:1297)  
5'-TGC CTC TGC TGG TCT TTC-3' (FRAG. NO:1288)(SEQ. ID NO:1298)

**Human Interleukin-1 (IL-1) Nucleic Acid and antisense Oligonucleotide Fragments**

5'-AAGCTTCTAC CCTAGTCTGG TGCTACACTT ACATTGCTTA CATCCAAGTG TGGTATTTC TGTGGCTCCT GTTATAACTA  
TTATAGCACC AGGTCTATGA CCAGGAGAAT TAGACTGGCA TTAATCAGA ATAAGAGATT TTGCACCTGC AATAGACCTT  
ATGACACCTA ACCAACCCCA TTATTTACAA TTAACAGGA ACAGAGGGAA TACTTTATCC AACTCACACA AGGTGTTTTT  
CTCCAGATC CATGCTTTTT TCGTTTTATT ATTTTTTAGA GATGGGGGCT TCACTATGTT GCCCAGACTG GACTAAAACT  
CTGGGCTCA AGTGATTGTC CTGCCTCAGC CTCCTGAATA GCTGGGACTA CAGGGGCATG CCATCACACC TAGTTCATTT  
CCTCTATTTA AAATATACAT GGCTTAACT CCACTGGGA ACCCAAACA TTCATTGCT AAGAGTCTGG TGTTCTACCA  
CCTGAAGTAG GCTGGCCACA GGAATTATAA AAGCTGAGAA ATCTTTAAT AATAGTAACC AGGCAACATC ATTGAAGGCT  
CATATGTAAA AATCCATGCC TTCCTTCTC CCAATCTCCA TTCCCAAACCT TAGCCACTGG TTCTGGCTGA GGCCTTACGC  
ATACCTCCC GGGCTTGCAC ACACCTTCTT CTCAGAGA GACACCTTGG GCATATCTCA CAGAAGACCA GGCTTCTCTC  
TGGTCTTGG TAGAGGGCTA CTTTACTGTA ACAGGGCCAG TCTCTCTGA AGTCCATCC CCTCTATAGG  
AAATGTGTTG ACAATATTCA GAAGAGTAAG AGGATCAAGA CTTCTTGTG CTCAAATACC ACTGTTCTCT TCTTACCCT  
GCCCTAACCA GGAGCTTGT ACCCAAACCT CTGAGGTGAT TTATGCCTTA ATCAAGCAAA CTTCCTCTT CAGAAAAGAT  
GGCTCATTT CCCTCAAAAG TTGCCAGGAG CTGCCAAGTA TTCTGCCAAT TCACCCTGGA GCACAATCAA CAAATTCAGC  
CAGAACACAA CTACAGCTAC TATTAGAACT ATTATTATTA ATAAATCTCT CTCCAAATCT AGCCCTTGA CTTGGGATTT  
CAGGATTTCT CCCTCTCTC TAGAACTTG ATAAGTTTCC CGCGTTCCC TTTTCTAAG ACTACATGTT TGTCATCTTA  
TAAAGCAAAG GGGTGAATAA ATGAACCAAA TCAATAACTT CTGGAATATC TGCAACAAAC AATAATATCA GCTATGCCAT  
CTTCACTAT TTAGCCAGT ATCGAGTTGA ATGAACATAG AAAAATACAA AACTGAATTC TTCCCTGTAA ATTCCCGTT  
TTGACGACGC ACTGTAGCC ACGTAGCCAC GCCTACTTAA GACAATTACA AAAGGCGAAG AAGACTGACT CAGGCTTAAG  
CTGCCAGCCA GAGAGGGAGT CATTTCATTG GCGTTGAGT CAGCAAAGGT ATTGCTCTCA CATCTCTGGC TATTAAAGTA  
TTTTCTGTG TTGTTTTCT CTTTGGCTGT TTCTCTCAC ATTGCCTCT CTAAAGCTAC AGTCTCTCT TCTTTCTT  
GTCCCTCCCT GGTTGGTAT GTGACCTAGA ATTACAGTCA GATTTCAGAA AATGATTCTC TCATTTTGCT GATAAGGACT  
GATTCGTTTT ACTGAGGGAC GGCAGAACTA GTTCTCTATG AGGGCATGGG TGAATACAA TGAGGCTTCT CATGGGAGGG  
AATCTCTACT ATCCAAAATT ATTAGGAGAA AATTGAAAAT TTCCAACCT CTCTCTCT TACCTCTGTG TAAGGCAAT  
ACCTTATTCT TGTGGTGTG TTGTAACCTC TTCAAACCTT CATTGATTGA ATGCTGTTC TGGCAATACA TTAGTTGGG  
CACATAAGGA ATACCAACAT AAATAAAACA TTCTAAAAGA AGTTTACGAT CTAATAAAGG AGACAGGTAC ATAGCAAAC  
AATTCAAAGG AGCTAGAAGA TGGAGAAAAT GCTGAATGTG GACTAAGTCA TTCAACAAAG TTTTCAGGAA GCACAAAGAG  
GAGGGGCTCC CTCACAGAT ATCTGGATTA GAGGCTGGCT GAGCTGATGG TGGCTGGTGT TCTCTGTGC AGAAGTCAAG  
ATGGCCAAAG TTCCAGACAT GTTGAAGAC CTGAAGAACT GTTACAGGTA AGGAATAAGA TTTATCTCT GTGATTTAAT  
GAGGTTTCA AGGCTACCA GAATCCAGCT AGGCATAACA GTGGCCAGCA TGGGGGCAGG CCGGCAGAGG TTGTAGAGAT  
GTGTACTAGT CTGAAGTCA GAGCAGTTC AGAGAAGCC CAGAAAAACT AAGCATTGAG CATGTTAAAC TGAGATTACA  
TTGGCAGGGA GACCGCCATT TTAGAAAAAT TATTTTGTAG GTCTGTGAG CCTACATAG ATATCAGCAT CAAGTACAG  
ACAGCCTCTG TTGAGATCAC ATGCCCTGAT ATAAGAATGG GTTTTACTGG TCCATTCTCA GGAAAACTTG ATCTATTCA  
GGAACAGGAA ATGGCTCCAC AGCAAGCTGG GCATGTGAAC TCACATATGC AGGCAATCT CACTCAGATG TAGAAGAAAG  
GTAAATGAAC ACAAAGATAA AATTACGGAA CATATTAAAC TAACATGATG TTTCCATTAT CTGTAGTAAA TACTAACACA  
AATAGGCTG TCAAAATTT GCCTGGATAT TTTACTAAGT ATAAATTATG AAATCTGTT TAGTGAATAC ATGAAAGTAA  
TGTTAATAC ATAACTATT TGGTTAAAT AAAAGGAAG TGCTTCAAAA CCTTCTTTT CTCTAAAGGA GCCTAACATT  
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5'-ACAAACCTTT TCGAGGCAAA AGGCAAAAAA GGCTGCTCTG GGATTCTCTT CAGCCAATCT TCAATGCTCA AGTGTCTGAA GCAGCCATGG CAGAAGTACC TAAGCTCGCC AGTGAAATGA TGGCTTATTA CAGTGGCAAT GAGGATGACT TGTCTTTGA AGCTGATGGC CCTAAACAGA TGAAGTCTC CTCCAGGAC CTGGACCTCT GCCCTCTGGA TGGCGGCATC CAGTACGAA TCTCCGACCA CCACTACAGC AAGGGCTTCA GGCAGGCCGC GTCAGTTGTT GTGGCCATGG ACAAGCTGAG GAAGATGCTG GTTCCCTGCC CACAGACCTT CCAGGAGAAT GACCTGAGCA CCTTCTTTCC CTTCATCTTT GAAGAAGAAC CTATCTTCTT CGACACATGG GATAACGAGG CTTATGTGCA CGATGCACCT GTACGATCAC TGAAGTGCAC GCTCCGGGAC TCACAGCAAA AAAGCTTGGT GATGTCTGGT CCATATGAAC TGAAAGCTCT CCACCTCCAG GGACAGGATA TGGAGCAACA AGTGGTGTTC TCCATGTCTT TTGTACAAGG AGAAGAAAAGT AATGACAAAA TACCTGTGGC CTGCGGCCTC AAGGAAAAAG ATCTGTACCT GTCTGCGTG TTGAAAGATG ATAAGCCCACT TCTACAGCTG GAGAGTGTAG ATCCCAAAAA TTACCCAAAG AAGAAGATGG AAAAGCGATT TGTCTTCAAC AAGATAGAAA TCAATAACAA CTGGAATTT GAGTCTGCC AGTTCCCCAA CTGGTACATC AGCACCTCTC AAGCAGAAAA CATGCCCGTC TTCCTGGGAG GGACCAAAAG CGGCCAGGAT ATAACCTACT TCACATGCA ATTTGTGTCT TCCTAAAGAG AGCTGTACCC AGAGAGTCTT GTGCTGAATG TGGACTCAAT CCCTAGGGCT GGCAGAAAGG GAACAGAAAG GTTTTGTAGT ACGGCTATAG CTTGGACTTT CTGTTGTCT ACACCAATGC CCAACTGCCT GCCTTAGGGT AGTGCTAAGA GGATCTCTG TCCATCAGCC AGGACAGTCA GCTCTCTCT TTCAGGGCCA ATCCAGGCC TTTTGTGAG CCAGGCTCT CTCACCTCTC TACTCACTT AAAGCCCGCC TGACAGAAAC CAGGCCACAT TTTGGTTCTA AGAAACCTC CTCTGTCTT CGTCCACA TTCTGATGAG CAACCGCTT CCTATTATT TATTTATTG TTTGTTGTT TTGATTCATT GGTCTAATTT ATTCAAAGG GGCAAGAAGT AGCAGTGTCT GTAAAAGAGC CTAGTTTTA ATAGCTATGG AATCAATTC AATTTGACTG GTGTGCTCTC TTTAAATCAA GTCTTTAAT TAAGACTGAA AATATATAAG CTCAGATTAT TTAATGGGA ATATTTATAA ATGAGCAAT ATCATACTGT TCAATGGTTC TCAATAAAC TCACT-3' (FRAG. NO.: ) (SEQ. ID NO:2513)

5'-CTGGCAGGAG TAGCAGCTGC CCCTTGGCGC GACTGTGGA GCCGGAAC AGAGAAACAC AGACACGCT CATAGAGCAA CGGCGTCTCT CGGAGCGTGG AGCCCCGCAA GCTCGAGCTG AGCTTTCGCT TGCCGTCCAC CACTGCCAC ACTGTCGTTT GCTGCCATCG CAGACCTGCT GTGACTTCC ATCCCTCTGG ATCCGGCAAG GCCTGCGAT TTTGACAATG TCAAGATTTA CCGTATATCC CTGTTTGT TTGATACACCA GTGACGTCCA CTCTAGAAG ACAAGATTAT ATTACTTAA CAACCAAGA TATGAACTA TCCATGAAGA ACAATATTAT CAATACACAG CAGTCTTTG TAACCATGCC CAATGTGATT GTACCAGATA TTGAAAAGGA AATACGAAGG ATGAAAATG GAGCATGCAG CTCCTTTCT GAGGATGATG ACAGTGCTC TACATCTGAA GAATCAGAGA ATGAAAACCC TCATGCAAGG GGTTCCTTTA GTTATAAGTC ACTCAGAAAG GGAGGACCAT CACAGAGGGA GCAGTACCTG CTTGGTGCCA TTGCCATTTT TAATGTGAAC AACAGCGACA ATAAGGACCA GGAACAGAA GAAAAAAGA AAAAGAAAAA AGAAAAGAAG AGCAAGTCAG ATGATAAAAA CGAAAATAAA AACGACCCAA AGAAGAAGAT GGAAAAGCGA-3' (FRAG. NO.: ) (SEQ. ID NO:2514)

5'-ATGGCCAAAG TTCCAGACAT GTTGAAGAC CTGAAGAACT GTTACAGTGA AAATGAAGAA GACAGTCTT CCATTGATCA TCTGTCTCTG AATCAGAAAT CCTTCTATCA TGTAAGCTAT GGCCCACTCC ATGAAGGCTG CATGGATCAA TCTGTGCTC TGAGTATCTC TGAAACCTCT AAAACATCCA AGCTTACCTT CAAGGAGAGC ATGGTGGTAG TAGCAACCAA CGGGAAGGTT CTGAAGAAGA GACGGTTGAG TTTAAGCCAA TCCATCACTG ATGATGACCT GGAGGCCATC GCCAATGACT CAGAGGAAGA AATCATCAAG CCTAGGTCAG CACCTTTTAG CTCTGAGC AATGTGAAAT ACACTTTAT GAGGATCATC AAATACGAAT TCATCTGAA TGACGCCCTC AATCAAAGTA TAATCGAGC CAATGATCAG TACCTCACGG CTGTGCAAT ACATAATCTG GATGAAGCAG TGAAATTTGA CATGGGTGCT TATAAGTCAT CAAAGGATGA TGCTAAAATT ACCGTGATTC TAAGAATCTC AAAAATCTCA TTGTATGTGA CTGCCAAGA TGAAGACCAA CCAAGTCTGC TGAAGGAGAT GCCTGAGATA CCCAAAACCA TCACAGGTAG TGAGACCAAC CTCCTCTTCT TCTGGGAAAC TCACGGCACT AAGAACTATT TCACATCAGT TGCCCATCCA AACTTGTTTA TTGCCACAAA GCAAGACTAC TGGGTGTGCT TGGCAGGGGG GCCACCTCT ATCACTGACT TTCAGATACT GGAAAACCAG GCGTAGGTCT GGAGTCTCAC TTGTCTCACT TGTGAGTGT TGACAGTTCA TATGTACCAT GTACATGAAG AAGCTAAATC CTTACTGTT AGTCATTTGC TGAGCATGTA CTGAGCCTTG TAATTTCTAAA TGAATGTTA CACTCTTTGT AAGAGTGGAA CCAACACTAA CATATAATGT TGTATTITAA AGAACCCCT ATATTTTGCA TAGTACCAAT CATTTTAATT ATTATTCTTC ATAACAATTT TAGGAGGACC AGAGCTACTG ACTATGGCTA CCAAAAAGAC TCTACCCATA TTACAGATGG GCAAAATTAAG GCATAAGAAA ACTAAGAAAT ATGCACAATA GCAGTTGAAA CAAGAAGCCA CAGACCTAGG ATTTATGAT TCAATTTCAA CTGTTTGCT TCTGCTTTTA AGTTGCTGAT GAACTCTTAA TCAATAGCA TAAGTTTCTG GGACCTCAGT TTTATCATT TCAAAATGGA GGAATAATA CCTAAGCCTT CTGCGCGCAA CAGTTTTTTA TGCTAATCAG GGAGGTCATT TTGGTAAAT ACTTCTCGAA GCCGAGCCTC AAGATGAAG CAAAGCACGA AATGTTATTT TTAATTATT ATTTATATAT GTATTTTATA ATATATTTAA GATAATTATA ATATACTATA TTTATGGGAA CCCCTTCATC CTCTGAGTGT GACCAGGCAT CCTCCACAAT AGCAGACAGT GTTTCTGGG ATAAGTAAGT TTGATTTCAT TAATACAGGG CATTTTGGTC CAAGTTGTGC TTATCCATA GCCAGGAAAC TCTGCATTCT AGTACTTGGG AGACCTGTAA TCATATAATA AATGTACATT AATTACCTTG AGCCAGTAAT TGGTCCGATC TTTGACTCTT TTGCCATTAA ACTTACCTGG GCATTCTTGT TTCATTCAAT TCCACCTGCA ATCAAGTCTT ACAAGCTAAA ATTAGATGAA CTCAACTTG ACAACCATAG ACCACTGTTA TCAAACTTT CTTTTCTGGA ATGTAATCAA TGTCTTCT AGGTTCTAAA AATTGTGATC AGACCATAAT GTTACATTAT TATCAACAAT AGTGATTGAT AGAGTGTTAT CAGTCATAAC TAAATAAAGC TTGCAAGTGA GGGAGTCATT TCATTGGCGT TTGAGTCAGC AAAGAAGTCA AG-3' (FRAG. NO.: ) (SEQ. ID NO:2515)

5'-AGTGCCAGC CAGAGAGGGA GTCATTTTCA TGGCGTTTGA GTCAGCAAAG AAGTCAAGAT GGCCAAAGTT CCAGACATGT TTGAAGACCT GAAGAACTGT TACAGTGAAG ATGAAGAAGA CAGTTCCTCC ATTGATCATC TGTCTCTGAA TCAGAAATCC TTCTATCATG TAAGCTATGG CCCACTCCAT GAAGGCTGCA TGGATCAATC TGTGTCTCTG AGTATCTCTG AAACCTCTAA AACATCCAAG CTACCTTCA AGGAGAGCAT GGTGGTAGTA GCAACCAACG GGAAGGTTCT GAAGAAGAGA CGGTTGAGTT TAAGCCAATC CATCACTGAT GATGACCTGG AGGCCATCG CAATGACTCA GAGGAAGAAA TCATCAAGCC TAGGTCATCA CTTTTTAGCT TCCTGAGCAA TGTGAAATAC AACTTTATGA GGATCATCAA ATACGAATTC ATCTGAATG

ACGCCCTCAA TCAAAGTATA ATTCGAGCCA ATGATCAGTA CCTCACGGCT GCTGCATTAC ATAATCTGGA TGAAGCAGTG  
AAATTTGACA TGGGTGCTTA TAAGTCATCA AAGGATGATG CTAAATTAC CGTGATTCTA AGAATCTCAA AACTCAATT  
GTATGTGACT GCCCAAGATG AAGACCAACC AGTGCTGCTG AAGGAGATGC CTGAGATACC CAAAACCATC ACAGGTAGTG  
AGACCAACCT CCTCTTCTC TGGGAAACTC ACGGCACTAA GAACTATTTC ACATCAGTTG CCCATCCAAA CTGTGTTATT  
GCCACAAAGC AAGACTACTG GGTGTGCTTG GCAGGGGGGC CACCCTCTAT CACTGACTTT CAGATACTGG AAAACCAGGC  
GTAGGTCTGG AGTCTCACTT GTCTCACTTG TGCAGTGTTG ACAGTTCATA TGTACCATGT ACATGAAGAA GCTAAATCCT  
TTACTGTTAG TCATTGCTG AGCATGTACT GAGCCTTGTA ATTCTAAATG AATGTTTACA CTCTTTGTAA GAGTGGAAACC  
AACACTAACA TATAATGTTG TTATTTAAAG AACACCCTAT ATTTGCATA GTACCAATCA TTITAATTAT TATTCTTCAT  
AACAAATTTA GGAGGACCAG AGCTACTGAC TATGGCTACC AAAAAGACTC TACCCATATT ACAGATGGGC AAATTAAGGC  
ATAAGAAAAC TAAGAAATAT GCACAATAGC AGTCGAAACA AGAAGCCACA GACCTAGGAT TTCATGATTT CATTCAACT  
GTTTGCCTTC TGCTTTTAAAG TTGCTGATGA ACTCTTAATC AAATAGCATA AGTTTCTGGG ACCTCAGTTT TATCATTTTC  
AAAATGGAGG GAATAATACC TAAGCCTTCC TGCCGCAACA GTTTTTATG CTAATCAGGG AGGTCATTTT GGTAAAATAC  
TTCTCGAAGC CGAGCCTCAA GATGAAGGCA AAGCACGAAA TGTTATTTTT TAATTATTAT TTATATATGT ATTTATAAAT  
ATATTTAAGA TAATTATAAT ATACTATATT TATGGGAACC CCTTCATCCT CTGAGTGTGA CCAGGCATCC TCCACAATAG  
CAGACAGTGT TTTCTGGGAT AAGTAAGTTT GATTTCATTA ATACAGGGCA TTTTGGTCCA AGTTGTGCTT ATCCCATAGC  
CAGGAAACTC TGCATTCTAG TACTTGGGAG ACCTGTAATC ATATAATAAA TGTACATTAA TTACCTTGAG CCAGTAATTG  
GTCCGATCTT TGACTCTTTT GCCATTAAAC TTACCTGGGC ATTCTTGTTT CATTCAATTC CACCTGCAAT CAAGTCCTAC  
AAGCTAAAAT TAGATGAACT CAACTTTGAC AACCATGAGA CCACTGTTAT CAAAACCTTC TTTTCTGGAA TGTAATCAAT  
GTTTCTTCTA GTTCTAAAA ATTGTGATCA GACCATAATG TTACATTATT ATCAACAATA GTGATTGATA GAGTGTATC  
AGTCATAACT AAATAAGCT TGCAACAAAA TTCTCTG-3' (FRAG. NO: ) (SEQ. ID NO:2516)

**Human Interleukin-1 Receptor (IL-1 R) Nucleic Acids and Anti-sense Oligonucleotide Fragments**

5'-GCCACGTGCT GCTGGGCTC AGTCTCCAC TTCCCGTGTC CTCTGGAAGT TGTGAGGAGC AATGTTGCGC TTGTACGTGT  
TGGTAATGGG AGTTTCTGCC TTCACCCTTC AGCCTGCGG ACACACAGGG GCTGCCAGAA CCTGCCGTT TCGTGGGAGG  
CATTACAAGC GGGAGTTCAG GCTGGAAGGG GAGCCTGTAG CCTGAGGTG CCCCAGGTG CCTACTGGT TGTGGGCTC  
TGTGAGCCCC CGCATCAACC TGACATGGCA TAAAAATGAC TCTGTAGGA CGGTCCCAGG AGAAGAAGAG ACACGGATGT  
GGGCCCAGGA CGGTGCTCTG TGGCTTCTGC CAGCCTTGCA GGAGGACTCT GGCACCTACG TCTGCACTAC TAGAAATGCT  
TCTTACTGTG AAAAAATGTC CATTGAGCTC AGAGTTTTTG AGAATACAGA TGCTTTCCTG CCGTTCATCT CATAACCGCA  
AATTTTAACC TTGTCAACCT CTGGGGTATT AGTATGCCCT GACCTGAGTG AATTCACCCG TGACAAAACT GACGTGAAGA  
TTCAATGGTA CAAGGATTCT CTTCTTTTGG ATAAAGACAA TGAGAAATTT CTAAGTGTGA GGGGGACCAC TCACTTACTC  
GTACACGATG TGGCCTGGA AGATGCTGGC TATTACCGCT GTGTCTGAC ATTTGCCCAT GAAGGCCAGC AATACAACAT  
CACTAGGAGT ATTGAGCTAC GCATCAAGAA AAAAAAGAA GAGACCATTG CTGTGATCAT TTCCCCCTC AAGACCATAT  
CAGCTTCTCT GGGGTCAAGA CTGACAATCC CGTGAAGGT GTTCTGGA ACCGGCACAC CCTTAACCAC CATGCTGTGG  
TGGACGGCCA ATGACACCCA CATAGAGAGC GCCTACCCGG GAGGCGCGT GACCGAGGGG CCACGCCAGG AATATTGAGA  
AAATAATGAG AACTCATTTG AAGTGCCATT GATTTTGTAT CTGTGACAA GAGAGGATTT GCACATGGAT TTAAATGTG  
TTGTCCATAA TACCTGAGT TTTGAGACAC TACGACCAC AGTCAAGGAA GCCTCTCCA CGTTCTCTG GGGCATTGTG  
CTGGCCCCAC TTCACTGGC CTCTTGTT TTGGGGGAA TATGGATGCA CAGACGGTGC AAACACAGAA CTGGAAGAGC  
AGATGGTCTG ACTGTGCTAT GGCCTCATCA TCAAGACTTT CAATCCTATC CCAAGTGAAT TAAATGGAAT GAAATAATC  
AAACACAAAA AAAAAAAAAA AAAAAA GCGGAGCCG ACTCGGAGCG CGCGGCGCG CCGGGAGGAG CCGAGCGCGC  
CGGGCGCGG GTGGGGGCGC CGGCTGCCCC GCGCGCCAG GGAGCGGCAG GAATGTGACA ATCGCGCGCC CGACCGTAG  
CACTCCTCGC TCGGCTCCTA GGGCTCTCGC CCTCTGAGCT GAGCCGGGTT CCGCCCGGGC TGGGATCCCA TCACCCTCCA  
CGGCCGTCCG TCCAGGTAGA CGCACCCTCT GAAGATGGTG ACTCCCTCT GAGAAGCTGG ACCCCTTGGT AAAAGACAAG  
GCCTTCTCCA AGAAGAATAT GAAAGTGTA CTCAGACTTA TTTGTTTCT AGCTTACTG ATTTCTTCT TGGAGCTGA  
TAAATGCAAG GAACGTGAAG AAAAAATAA TTAGTGCTA CTGCAAAATG AAATTGATGT TCGTCCCTGT CCTCTTAACC  
CAAAATGAACA CAAAGGCACT ATAACCTGGT ATAAAGATGA CAGCAAGACA CCGTATCTA CAGAACAAAGC CTCAGGATT  
CATCAACACA AAGAGAACT TTGGTTTGT CTGCTAAGG TGGAGGATTG AGGACATTAC TATTGCGTGG TAAGAAATTC  
ATCTTACTGC CTCAGAATTA AAATAAGTGC AAAATTTGTG GAGAATGAGC CTAACCTATG TTATAATGCA CAAGCCATAT  
TTAAGCAGAA ACTACCCGTT GCAGGAGACG GAGGACTTGT GTGCCCTTAT ATGGAGTTTT TAAAAATGA AAATAATGAG  
TTACCTAAAT TACAGTGGTA TAAGGATTGC AAACCTCTAC TTCTTGACAA TATACACTTT AGTGGAGTCA AAGATAGGCT  
CATCGTATG AATGTGGCTG AAAAGCATAG AGGGAACCTAT ACTGTGATG CATCTACAC ATACTGGGC AAGCAATATC  
CTATTACCCG GGTAATAGAA TTTATTACTC TAGAGGAAAA CAAACCCACA AGGCCTGTGA TTGTGAGCCC AGCTAATGAG  
ACAATGGAAG TAGACTTGGG ATCCAGATA CAATTGATCT GTAATGTCAC CGGCCAGTTG AGTGACATTG CTACTGGAA  
GTGGAATGGG TCAGTAATTG ATGAAGATGA CCCAGTGCTA GGGGAAGACT ATTACAGTGT GGAAATCCT GCAACAAAA  
GAAGGAGTAC CCTCATACA GTGCTTAATA TATCGGAAAT TGAAGATAGA TTTTATAAAC ATCCATTTAC CTGTTTTGCC  
AAGAATACAC ATGGATAGA TGCAGCATAT ATCCAGTTAA TATATCCAGT CACTAATTTT CAGAAGTACA TGATTGGTAT  
ATGTGTCACG TTGACAGTCA TAATTGTGTG TTCTGTTTTT ATCTATAAAA TCTTCAAGAT TGACATTGTG CTTTGGTACA  
GGGATCTCTG CTATGATTTT CTCCAATAA AAGCTTCAGA TGGAAAGACC TATGACGCAT ATATACTGTA TCCAAAGACT  
GTTGGGGAAG GGTCTACCTC TGACTGTGAT ATTTTGTGT TAAAGTCTT GCCTGAGGTC TTGGAAAAAC AGTGTGGATA  
TAAGCTGTTT ATTTATGGAA GGGATGACTA CGTTGGGGAA GACATTGTTG AGGTCATTAA TGAAACGTA AAGAAAAGCA  
GAAGACTGAT TATCATTTTA GTCAGAGAAA CATCAGGCTT CAGCTGGCTG GGTGGTTCAT CTGAAGAGCA AATAGCCATG  
TATAATGCTC TTGTTCAAGG TGGAATTTAA GTTGCTCTG TTGAGCTGGA GAAATCCAA GACTATGAGA AATGCCAGA  
ATCGATTAAA TTCATTAAGC AGAAACATGG GGCTATCCGC TGGTCAGGGG ACTTACACA GGGACCACAG TCTGCAAGA  
CAAGGTTCTG GAAGAATGTC AGGTACCACA TGCCAGTCCA GCGACGGTCA CCTTCATCTA AACACCAGTT ACTGTCACCA  
GCCACTAAGG AGAACTGCA AAGAGAGGCT CAGTGCTCTC TCGGGTAGCA TGGAGAAGTT GCCAAGAGTT CTTTAGGTG  
CTCTCTCTC ATGCTCTGCTC AGCGAGCTT ATGCTGATG CTGACTGCA GACTGATG AATCTAATA TATCATCTT

5'-GCCACGTGCT GCTGGGTCTC AGTCCTCCAC TTCCCGTGTC CTCTGGAAGT TGTCAGGAGC AATGTTGCGC TTGTACGTGT  
TGTAATGGG AGTTTCTGCC TTCACCTTC AGCCTGCGGC ACACACAGGG GCTGCCAGAA GCTGCCGGTT TCGTGGGAGG  
CATTACAAGC GGGAGTTCAG GCTGGAAGGG GAGCTGTAG CCTGAGGTG CCCCAGGTG CCCTACTGGT TGTGGGCTC  
TGTCAGCCCC CGCATCAACC TGACATGGCA TAAAAATGAC TCTGCTAGGA CGGTCCCAGG AGAAGAAGAC ACACGGATGT  
GGGCCAGGA CGGTGCTCTG TGGCTTCTGC CAGCCTTGCA GGAGGACTCT GGCACCTACG TCTGCACTAC TAGAAATGCT  
TCTTACTGTG AAAAAATGTC CATTGAGCTC AGAGTTTTTG AGAATACAGA TGCTTTCCTG CCGTTCATCT CATACCCGCA  
AATTTTAACC TTGTCAACCT CTGGGGTATT AGTATGCCCT GACCTGAGTG AATTCACCCG TGACAAAAT GACGTGAAGA  
TTCAATGGTA CAAGGATTCT CTTCTTTTGG ATAAAGACAA TGAGAAATTT CTAAGTGTGA GGGGGACCAC TCACTTACTC  
GTACACGATG TGGCCCTGGA AGATGCTGGC TATTACCGCT GTGTCCTGAC ATTTGCCCAT GAAGGCCAGC AATACAACAT  
CACTAGGAGT ATTGAGCTAC GCATCAAGAA AAAAAAGAA GAGACCATTG CTGTGATCAT TTCCCCCTC AAGACCATAT  
CAGCTTCTCT GGGGTCAAGA CTGACAATCC CGTGAAGGT GTTCTGGA ACCGGCACAC CCTTAACCAC CATGCTGTGG  
TGGACGGCCA ATGACACCA CATAGAGAGC GCCTACCCGG GAGGCCGCGT GACCGAGGGG CCACGCCAGG AATATTGAGA  
AAATAATGAG AACTACATTG AAGTGCCATT GATTTTGTAT CTGTGCACAA GAGAGGATTT GCACATGGAT TTAAATGTG  
TTGTCCATAA TACCCTGAGT TTTCAGACAC TACGCACCAC AGTCAAGGAA GCCTCCTCCA CGTTCTCTG GGGCATTGTG  
CTGGCCCCAC TTTCAGTGGC CTTCTTGGTT TGGGGGGAA TATGGATGCA CAGACGGTGC AAACACAGAA CTGGAAAAGC  
AGATGGTCTG ACTGTGCTAT GGCCTCATCA TCAAGACTTT CAATCTATC CCAAGTGAAG TAAATGGAAT GAAATAATTC  
AAACACAAAA AAAAAAAAAA AAAAAA-3' (FRAG. NO: 2518) (SEQ. ID NO:2518)

5'-GCCGGAGCCG ACTCGGAGCG CGCGGCGCG CCGGAGGAG CCGAGCGCGC GGGCGCGGC GTGGGGGCGC  
CGGCTGCCCC GCGCGCCCAG GGAGCGGCAG GAATGTGACA ATCGCGCGCC CGCACCGTAG CACTCCTCGC TCGGCTCCTA  
GGGCTCTGCG CCTCTGAGCT GAGCCGGGT CCGCCGGGG TGGGATCCCA TCACCCTCCA CGGCCGTCG TCCAGGTAGA  
CGCACCTCT GAAGATGGTG ACTCCCTCT GAGAAGCTGG ACCCTTGGT AAAAGACAAG GCCTTCTCCA AGAAGAATAT  
GAAAGTGTA CTGAGACTTA TTTGTTTCT AGCTCTACTG ATTTCTTCT TGGAGGCTGA TAAATGCAAG GAACGTGAAG  
AAAAATAAT TTAGTGTCA TCTGCAATG CAATGTATGT TCGTCCTGT CCTTTAACC CAAATGAACA CAAAGGCACT  
ATACTTGGT ATAAAGATGA CAGCAAGACA CCGTATCTA CAGAACAAG CTCCAGGATT CATCAACACA AAGAGAACT  
TTGGTTTGT CTGTCTAAGG TGGAGGATTC AGGACATTAC TATTGCGTGG TAAGAAATTC ATCTTACTGC CTCAGAATTA  
AAATAAGTGC AAAATTTGTG GAGAATGAGC CTAACCTATG TTATAATGCA CAAGCCATAT TTAAGCAGAA ACTACCCGTT  
GCAGGAGACG GAGGACTTGT GTGCCCTTAT ATGGAGTTTT TAAAAATGA AAATAATGAG TTACCTAAAT TACAGTGGTA  
TAAGGATTGC AAACCTCTAC TTCTTGACAA TATACACTT AGTGGAGTCA AAGATAGGCT CATCGTGATG AATGTGGCTG  
AAAAGCATAG AGGGAATAT ACTTGTCATG CATCTACAC ATACTGGGC AAGCAATATC CTATTACCCG GGTAATAGAA  
TTTATTACTC TAGAGGAAAA CAAACCCACA AGCCCTGTGA TTGTGAGCCC AGCTAATGAG ACAATGGAAG TAGACTTGGG  
ATCCAGATA CAATTGATCT GTAATGTAC CGGCCAGTTG AGTGACATTG CTTACTGAA TGGGAATGG TCAGTAATTG  
ATGAAGATGA CCCAGTGCTA GGGGAAGACT ATTACAGTGT GGAAATCCT GCAAACAAAA GAAGGAGTAC CCTCATCACA  
GTGCTTAATA TATCGGAAAT TGAAAGTAGA TTTATAAAC ATCCATTAC CTGTTTTGCC AAGAATACAC ATGGTATAGA  
TGCAGCATAT ATCCAGTTAA TATATCCAGT CACTAATTTC CAGAAGCACA TGATTGGTAT ATGTGTCACG TTGACAGTCA  
TAATTGTGTG TTCTGTTTT CTCTATAAAA TCTTCAAGAT TGACATTGTG CTTTGGTACA GGGATTCCTG CTATGATTTT  
CTCCAATAA AAGCTTCAGA TGGAAAGACC TATGACGAT ATATACTGTA TCCAAAGACT GTTGGGGAAG GGTCTACCTC  
TGACTGTGAT ATTTTGTGT TAAAGTCTT GCCTGAGTTC TTGGAAGAA AGTGTGGATA TAAGCTGTTT ATTTATGGAA  
GGGATGACTA CGTTGGGGAA GACATTGTTG AGGTCATTA TGAAGACGTA AAGAAAGCA GAAGACTGAT TATCATTTA  
GTCAGAGAAA CATCAGGCTT CAGCTGGCTG GGTGGTTCAT CTGAAGAGCA AATAGCCATG TATAATGCTC TTGTTGAGGA  
TGGAAATAAA GTTGTCTGCTG TTGAGCTGGA GAAATCCAA GACTATGAGA AAATGCCAGA ATCGATTAAT TTCAATAGC  
AGAAACATGG GGCTATCCCG TGCTCAGGGG ACTTTACACA GGACCACAG TCTGCAAGA CAAGGTTCTG GAAGAATGTC  
AGGTACCACA TGCCAGTCCA GCGACGGTCA CTTTATCTA AACACCAGT ACTGTACCA GCCACTAAGG AGAACTGCA  
AAGAGAGGCT CACGTGCCTC TCGGGTAGCA TGGAGAAGTT GCCAAGAGTT CTTAGGTGC CTCTGTCTT ATGGCGTTGC  
AGGCCAGGTT ATGCCTCATG CTGACTTGCA GAGTTCATGG AATGTAATA TATCATCCTT TATCCTGAG GTCACCAGGA  
ATCAGG-3' (FRAG. NO: 2519) (SEQ. ID NO:2519)

#### Human Interleukin-8\* Fragments Antisense Oligonucleotide Fragments

5'-GBTGTGTTT BCCBBBGBCT CBBGBBTBGC TTTGCTBTCT BBGBTBCB TTBGBCBTB GBBBBCGCT GTBGGTCBGBB  
BGBTGTGCTT BCCTTCBCBC BGBGCTGCBG BBTBGBBGG CTGCCBBGBBG CCBGCGCCBGC TTGGBGTCTB  
GTTTBCBCB BGTGBGGTGC TCCGGTGGCT TTTGCTGTG GTGCTGCTG GTCTCTG TTC CTCCGGTGG TTCTTCTCTG  
GCTCTGTCC TTCTCTTGG CCCTTGGCCC-3' (FRAG. NO:1834) (SEQ. ID NO:1845)

5'-G CTC CGG-3' (FRAG. NO:1835) (SEQ. ID NO:1846)

5'-CBBGBBTBGC-3' (FRAG. NO:1836) (SEQ. ID NO:1847)

5'-CBCBC BGTGBGGTGC-3' (FRAG. NO:1837) (SEQ. ID NO:1848)

5'-BCCBBBGBCT CBBGBBTBGC-3' (FRAG. NO:1838) (SEQ. ID NO:1849)

5'-GCCBBGBBG CCBGCGCCBGC-3' (FRAG. NO:1839) (SEQ. ID NO:1850)

5'-GTG CTC CGG TGG CTT TTT-3' (FRAG. NO:1289) (SEQ. ID NO:1299)

5'-GCT TGT GTG CTC TGC TGT CTC TG-3' (FRAG. NO:1290) (SEQ. ID NO:1300)

5'-TTC CTT CCG GTG GTT TCT TCC TGG CTC TTG TCC T-3' (FRAG. NO:1291) (SEQ. ID NO:1301)

5'-TTC TCT TGG CCC TTG GCC C-3' (FRAG. NO:1292) (SEQ. ID NO:1302)

5'-GBTGTGTTT BCCBBBGBCT CBBGBBTBGC TTTGCTBTCT BBGBTBCB TTBGBCBTB GBBBBCGCT GTBGGTCBGBB  
BGBTGTGCTT BCCTTCBCBC BGBGCTGCBG BBTBGBBGG CTGCCBBGBBG CCBGCGCCBGC TTGGBGTCTB  
GTTTBCBCB BGTGBGGTGC TCCGGTGGCT TTTGCTGTG-3' (FRAG. NO:1840) (SEQ. ID NO:1851)

#### Human IL-8 Receptor Alpha Antisense Oligonucleotide Fragments

5'-ACAGGGGCTG TAATCTTCATC TGCAGGTGGC ATGCCAGTGA AATTTAGATC ATCAAAATCC CACATCTGTG  
GATCTGTAAT ATTTGACATG TCCTCTTCAG TTTCAGCAAT GGTTTGATCT AACTGAAGCA CCGGCCAGGB CBGGGGCTGT  
BBTCTTCBGC TGCBBGGTGC BTGCCBGTGB BBTBGBTC BTCBBBTCC CBCBTCTGTG GBTCTGTBBT BTTTGBCBTG  
TCCTCTTCB TTTTCBGB TGGTTTGTB TBBCTGBBG BCCGGCCBGG TGGCTCGGTG CTTCTGCCCC TGTGTTGCG  
GCGCTCGGTT GGTGTGGCCC CTGTGGTGCT TCGTTTCCCC CTCTTCTCT TTGTTCCGGG GTTCTGTGG CGGGCTGCTT  
GTCTCGTTCC-3'

EPI-109

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(FRAG. NO:1841) (SEQ. ID NO:1852)

5'-CBGGGGC-3' (FRAG. NO:1842) (SEQ. ID NO:1853)

5'-GCBGGTGGC-3' (FRAG. NO:1843) (SEQ. ID NO:1854)

5'-GCGGCGCTC-3' (FRAG. NO:1844) (SEQ. ID NO:1855)

5'-TGGCTCGGTGCTTCTGCCCC (FRAG. NO:1293)(SEQ. ID NO:1303)

5'-TGTTGTTGCGGCGCTC (FRAG. NO:1294)(SEQ. ID NO:1304)

5'-GGTTGGTGTGGCCCTG (FRAG. NO:1295)(SEQ. ID NO:1305)

5'-TGGTGCTTCGTTTCC (FRAG. NO:1296)(SEQ. ID NO:1306)

5'-CCCTCTTCTCTTTGTTT (FRAG. NO:1297)(SEQ. ID NO:1307)

5'-GGGGTCTTGTGGC (FRAG. NO:1298)(SEQ. ID NO:1308)

5'-GGGCTGCTTGTCTCGTTCC (FRAG. NO:1299)(SEQ. ID NO:1309)

5'-ACAGGGGCTG TAATCTTCATC TGCAGGTGGC ATGCCAGTGA AATTTAGATC ATCAAAATCC CACATCTGTG  
GATCTGTAAT ATTTGACATG TCCTCTTCAG TTTCAGCAAT GGTTCGATCT AACTGAAGCA CCGGCCAGG-3' (FRAG.  
NO:1845) (SEQ. ID NO:1856)

5'-B CBGGGGCTGT BBTCTTCBTC TGCBBGTGGC BTGCCBGTGB BBTTCBGTB BTBBBBBTCC CBCBTCTGTG GBTCTGTBBT  
BTTTGBCTG TCCTCTTCBG TTTCBGCBB TGGTTTGTB TBBCTGBBGC BCCGGCCBGG-3' (FRAG. NO:1846) (SEQ. ID  
NO:1857)

### Interleukin-11 (IL-11) Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GCTCAGGGCA CATGCCTCCC CTCCCAGGC CGCGGCCAG CTGACCCTCG GGGCTCCCC GGCAGCGGAC  
AGGGAAGGGT TAAAGGCCCC CGGCTCCCTG CCCCCTGCCC TGGGGAACCC CTGGCCCTGT GGGGACATGA ACTGTGTTTG  
CCGCCTGGTC CTGGTCGTGC TGAGCCTGTG GCCAGATACA GGTGTCGCCC CTGGGCCACC ACCTGGCCCC CCTCGAGTTT  
CCCCAGACCC TCGGGCCGAG CTGGACAGCA CCGTGCTCCT GACCCGCTCT CTCCTGGCGG ACACGCGGCA GCTGGCTGCA  
CAGCTGAGGG ACAAATTCCT AGCTGACGGG GACCACAACC TGGATTCCCT GCCACCCTG GCCATGAGTG CGGGGGCACT  
GGGAGCTCTA CAGTCCCTAG GTGTGCTGAC AAGGCTGCGA GCGGACCTAC TGTCTACCT GCGGCACGTG CAGTGGCTGC  
GCCGGGCAGG TGGCTCTTCC CTGAAGACCC TGGAGCCCGA GCTGGGCACC CTGCAGGCCC GACTGGACCG GCTGCTGCGC  
CGGCTGCAGC TCCTGATGTC CCGCCTGGCC CTGCCCCAGC CACCCCCGGA CCCGCCGGCG CCCCCTGTGG CCCCCCTC  
CTCAGCCTGG GGGGGCATCA GGGCCGCCCA CGCCATCCTG GGGGGGCTGC ACCTGACACT TGAAGGGCC GTGAGGGGAC  
TGCTGCTGCT GAAGACTCGG CTGTGACCCG GGGCCCAAAG CCACCACCGT CCTTCAAAG CCAGATCTTA TTTATTTATT  
TATTCAGTA CTGGGGGCGA AACAGCCAGG TGATCCCCC GCCATTATCT CCCCCTAGTT AGAGACAGTC CTTCCGTGAG  
GCCTGGGGGA CATCTGTGCC TTATTTATAC TTATTTATT CAGGAGCAGG GGTGGGAGGC AGGTGGACTC CTGGGTCCCC  
GAGGAGGAGG GGAAGGGGT CCCGATTCT TGGGTCTCCA AGAAGTCTGT CCACAGACTT CTGCCCTGGC TCTTCCCCAT  
CTAGGCCTGG GCAGGAACAT ATATTATTA TTTAAGCAAT TACTTTTCAT GTGGGGTGG GGACGGAGGG GAAAGGGAAG  
CCTGGGTTTT TGTACAAAAA TGTGAGAAAC CTTGTGAGA CAGAGAACAG GGAATTAAAT GTGTCATACA TATCC  
CAGCTGCGGC ATCCTCTGTC TCAGAGTCTT GGTGTCTCTG TTCCTTTECC CTCGGGGTCT CCCTGGGTCT CCCAAGTCC  
CTGCTCTCTG CTGCTCTGCG CTGCTCTGATG TGTGACTGG AGAAGCTCTG CTGCTCTCTG CAGGCTCTCG CTTCTGATCG

CTCTCCTCCC TCAGACCCAG GAGGAGTCCA GACCCAGTT CCTCCTCCCT CAGACCCGGG AGTCCAGCCC AGGCCCTCCT  
CTCTCAGACC CGGAGTCCAG CCTGAGCTCT CTGCCCTTATC CTGCCCCCAG GTGTTTGCCG CTGGTCTCTG GTCGTGCTGA  
GCCTGTGGCC AGATACAGCT GTCGCCCCCTG GGCCACCACC TGGCCCCCCT CGAGTTTCCC CAGACCCTCG GGCCGAGCTG  
GACAGCACCG TGCTCCTGAC CCGCTCTCTC CTGGCGGACA CGCGGCAGCT GGCTGCACAG CTGGTAGGAG AGACTGGGCT  
GGGGCCAGCA CAGGAGTGAG AGGCAGAGAG GAACGGAGAG GAGTCTGCGG GCAGCCACTT GGAGGGGTTC TGGGCTCTCA  
GGTGGCAGAG TGAGGGAGGG GAAGAGTTGG GGGCCTGGCG TGGGGATGG AGGGAGCCCC GAGGCTGGGC  
AGGGGCCACC TCACAGCTTT TTTCCCTGCC AGAGGGACAA ATTCCCAGCT GACGGGGACC ACAACCTGGA TTCCCTGCCC  
ACCTGGCCA TGAGTGCAAG GGCAGTGGGA GCTCTACAGG TAAGGGCAAG GGAGTGGGCT GGGGACAAGG TGGGAGGCAG  
GCAGTGAAGG GGGCGGGGAG GATGAGGGGC ACTGCTCGGG GTTCTCTGA TGTCCCGCT CTATCCCCAG CTCCAGGTG  
TGCTGACAAG GCTGCGAGCG GACCTACTGT CCTACCTGCG GCACGTGCAG TGGCTGCGCC GGGCAGGTGG CTCTCCCTG  
AAGACCTGG AGCCCGAGCT GGGCACCTG CAGGCCGAC TGGACGGCT GCTGCGCCGG CTGCAGCTCC TGGTATGTCC  
TGGCCCAAG ACCTGACACC CCAGACCCCC ACCCTGGCC CAAAATCCT GTGGCCTGAG TCCTTGAAGC CTGAGACCCC  
AGACCCGAGT GCAACAGCCC CGCTCTGAGA CCCTGACACC CTAACAGCCC GCTCTGAGAC CCGACACCG TAACAGCCCC  
GCTCTGAGAC CCTGACCCTA ACAGTCTGCG TCTGAGACCC TGACCCTGCA GTCCCAAGAT CCGTGGGCCC TGAGACCCTG  
AGGCCCTAGA CCCCCAAATC CTGCCAGAA ACTTCAAATT CTCACCCAAG ACCCTGAGAC TCCATCATCC ATGACCTCAA  
AGTCCCCAGA TCCCAGCCCC TAAGACCCAA GACCCCATCC TGAAGCCCAA AGCCTTGAGA ATTCAAATCC TCACCTCAAG  
ACTTGGAGAC CCTGGCCCCA TGACATTGAA AACCATGGAC CTGGCCAGGC GTGGTGGCTC ACGCTGTAA TCCCAGCACT  
TTGGGAGGCC GAGGCAAGTG GATCACTGA GGTGCGGAGT TCAAGACCAG CCAGACCAAC ATGGTGAAAC CCTGTCTCTA  
CTAAAAATAC AAAATTAGCC AGGCGTGGTG GTGCATGCTT GTAATCCCAG CTACTTGGGA GGCTGAGGCA GGAGAATCGC  
TTGAACCTGG GAGGCGGAGG TTGAGTGAG CCGAGATCGC ACCATTACAC TCCAGCCTGG GCAACAAGAG CAAAACCTCC  
TCTCTCTCAA AAAAAAAAAA AAAAAAAAAA AAGAAGGAAA AGAAAACCAT GGACCTCCAG ACCCTGAGAC CCCAGGCCCC  
AGCCTGAGA TCCTGACATC TTAAGATCC CAGGCCCTAA GATACAAGAC CTGACCCAA AGCCAGCCTT GGGACCCTGG  
CTGTACAAAC CCAAGACCTC CAGGACCTAG ACCCGAGCC CTGAGGCCCT ATGTCTCACT CCAACATCG AAAACCTGA  
CACCTCAGAT CCTGAGCCTG CGCCTGTACG ACTCCAAGAC CCTCACTTCC AAAGCCAGGC CCAAAGCCTT GAGACCAGAA  
GACTTCAAAC CCTGGTTCTT GGGCCTAACT CCAAAGACCC TGGATCTCAA ATTCCAATT CTAGCTCTGA GACTCCAGCC  
CTCACCATG AGTTCCTGAA CTGAACCCA GAGACCCCAT CTCTAAGACT TCAGCCTTGA GATCCAGGGC CTGACCCTAG  
ACTCGAGCCC ACAGACCTCA GATACTGTCT GTAAAACCCC AGCTCTGGTG GGGAGCAGTG GCTCACTCTT GTAATCCCAA  
GGCAGGGGAG GCCAAGGCAG AAGGACCTCT TGAGGCCATG AGTTTGAGAC AGCCTGGGCA GCATAGCAAG ACTCTGTTT  
TTAATTATTA TTATTATTAT TATTTTTTGG AGACAGAGTC TCGGCTCTG TTGCCAGGC TAGAGTGCAA TGGTGCCATT  
TCGGCTTGCT GGAACCTCCG CCTCCTGGG TCAAGCGATT CTCCTGCTC AGCCTCCTGA GTAGCTGGGA CTTCAGGTGC  
ACACTGCCAC ACCCGGATAA TTTTTTTGTA TTTAGTAGA CACAGGGTTT CACCGTGTG CCCAGGCTGG TCACAACTC  
CTGAGCTCAG GCCATCCGCC CGCCTCGGCC TCCCAAAGCG CTGGGATAAC AGGCGTGACG CCGCGCCTGG CTCTTAATT  
GTTCTAACAG CAGCGACAAC AAAAAAACC CAGCTCTGAG ATTCCAGCCC CGGCGACTCT AACAGTCCCA GGCCGATCC  
CTCACCTAGA ACCGAGATGC CAGCCCTGAC TCCACAGACT TCACCCCAA CCCCACACT CAGCTCTGGA AGCCCGTCT  
GACTCCAGCC TCCATTTTCG GAACCCACA GCCTGAAGAG CTCCCGCCT AAACACTTCA CCCCACGCGC CACAGTCCCC  
CTGTGAATAT GCAGCCCCGA TTCAGCTGCA GCTCCACAGC ACCCTGCCC TGCACCCCC CTGCACCCCC TACCTGTGAC  
TCACCTCTCT CCTCTCCCA CAGATGTCCC GCCTGGCCTT GCCCCAGCCA CCCCAGGACC CGCCGGCGCC CCCGCTGGCG  
CCCCCTCT CAGCCTGGGG GGGCATCAGG GCCGCCACG CCATCCTGGG GGGGCTGCAC CTGACACTTG ACTGGGCGCT  
GAGGGGACTG CTGCTGCTGA AGACTCGGCT GTGACCCGGG GCCCAAAGCC ACCACCGTCC TTCCAAAGCC AGATCTTATT  
TATTTATTA TTTCAGTACT GGGGGCGAAA CAGCCAGGTG ATCCCCCGC CATTATCTCC CCTAGTTAG AGACAGTCT  
TCCGTGAGGC CTGGGGGGCA TCTGTGCTT ATTTATACTT ATTTATTTC GGAGCAGGGG TGGGAGGCAG GTGGACTCT  
GGGTCCCCGA GGAGGAGGGG ACTGGGGTCC CGGATTCTTG GGTCTCCAAG AAGTGTGTC ACAGACTTCT GCCCTGGCTC  
TTCCCCATCT AGGCCTGGGC AGGAACATAT ATTATTTATT TAAGCAATTA CTTTTCATGT TGGGGTGGGG ACGGAGGGGA  
AAGGGAAGCC TGGGTTTTT TACAAAAATG TGAGAAACCT TTGTGAGACA GAGAACAGGG AATTAAATGT GTCATACATA  
TCCACTTGAG GCGGATTTGT CTGAGAGCTG GGGCTGGATG CTGGGTAAC TGGGGCAGGG CAGGTGGAGG GGAGACCTCC  
ATTAGGTGG AGGTCCCAG TGGGCGGGG AGCGACTGGG AGATGGGTG GTCACCCAGA CAGCTCTGTG GAGGCAGGGT  
CTGAGCCTTG CCTGGGGCCC CGCACTGCAT AGGGCCGTTT GTTTGTTTT TGAGATGGAG TCTCGCTCTG TTGCCTAGGC  
TGGAGTGAG TGAGGCAATC TAAGGTCACT GCAACCTCCA CCTCCGGGT TCAAGCAATT CTCCTGCTC AGCCTCCGA  
TTAGCTGGGA TCACAGGTGT GCACCACCAT GCCAGCTAA TTATTTATT CTTTGTATT TTAGTAGAG ACAGGGTTTC  
ACCATGTTGG CCAGGCTGGT TTCGAACCTC TGACCTCAGG TGATCCTCT GCCTCGCCT CCAAAGTGC TGGGATTACA  
GGTGTGAGCC ACCACACCTG ACCCATAGGT CTTCATAAAA TATTTAATGG AAGTTCCAC AAGTCAACCT GTGATCAACA  
GTACCCGTAT GGGACAAAGC TGCAAGGTCA AGATGGTTCA TTATGGCTGT GTTCACCAT GCAAACCTGGA AACAATCTAG  
ATATCCAACA GTGAGGGTTA AGCAACATGG TGCATCTGTG GATAGAAGC CACCCAGCCG CCCGAGCAG GGAAGTGCAT  
TCAGGGAGGC TAAGGAGAGA GGCTTGCTTG GGATATAGAA AGATATCTG ACATTGGCCA GGCATGGTGG CTCACGCTG  
TAATCCTGGC ACTTTGGGAG GACGAAGCGA GTGGATCACT GAAGTCCAAG AGTTTGAGAC CGGCTGCGA GACATGGCAA  
AACCTGTCT CAAAAAAGAA AGAATGATGT CTGACATGA AACAGCAGGC TACAAAACCA CTGCATGCTG TGATCCCAAT  
TTTGTGTTTT TCTTTCTATA TATGGATTAA AAAAAAATC TAAAGGGAA ATACGCCAAA ATGTTGACAA TGACTGTCTC  
CAGGTCAAAG GAGAGAGGTG GGATTGTGGG TGACTTTTAA TGTGTATGAT TGTCTGTATT TTACAGAATT TCTGCCATGA  
CTGTGTATT TGCATGACAC ATTTAAAAA TAATAAACAC TATTTTATA ATAACAGAAT ATCAGCCTCC TCCTCTCAA



AAATAAGCCC TCAGGAGGGG ACAAAGTTGA CCGCTGATTG AGCCTGTCAG GGCTGTGCAC-3' (FRAG. NO: )SEQ. ID NO:2523)

5'-GCTCAGGGCA CATGCCTCCC CTCCCAGGC CGCGGCCAG CTGACCCTCG GGGCTCCCC GGCAGCGGAC  
AGGGAAGGGT TAAAGGCCCC CGGCTCCCTG CCCCCTGCCC TGGGGAACCC CTGGCCCTGT GGGGACATGA ACTGTGTTG  
CCGCCTGGTC CTGGTCGTGC TGAGCCTGTG GCCAGATACA GCTGTGCCCC CTGGGCCACC ACCTGGCCCC CCTCGAGTTT  
CCCCAGACCC TCGGGCCGAG CTGGACAGCA CCGTGCTCT GACCCGCTCT CTCTGGCGG ACACGCGGCA GCTGGCTGCA  
CAGCTGAGGG ACAAATTTCC AGCTGACGGG GACCACAACC TGGATTCCCT GCCACCCTG GCCATGAGTG CGGGGGCACT  
GGGAGCTCTA CAGTCCAG GTGTGCTGAC AAGGCTGCGA GCGGACCTAC TGTCTACCT GCGGCACGTG CAGTGGCTGC  
GCCGGGCAGG TGGCTCTTCC CTGAAGACCC TGGAGCCGA GCTGGGCACC CTGCAGGCC GACTGGACCG GCTGCTGCGC  
CGGCTGCAGC TCCTGATGTC CCGCTGGCC CTGCCCCAGC CACCCCCGGA CCGCGCGCG CCCCCGCTGG CGCCCCCTC  
CTCAGCCTGG GGGGGCATCA GGGCCGCCA CGCCATCTG GGGGGGCTG ACCTGACACT TGA CTGGGGC GTGAGGGGAC  
TGCTGCTGCT GAAGACTCGG CTGTGACCCG GGGCCAAAG CCACCACCGT CCTTCCAAAG CCAGATCTTA TTTATTATT  
TATTTAGTA CTGGGGCGA AACAGCCAGG TGATCCCCC GCCATTATCT CCCCCTAGTT AGAGACAGTC CTTCCTGAG  
GCCTGGGGGA CATCTGTGCC TTATTTATAC TTATTTATT CAGGAGCAGG GGTGGGAGG AGTGGA CTGGGTCCCC  
GAGGAGGAG GACTGGGGT CCGGATTCT TGGGTCTCA AGAAGTCTGT CCACAGACTT CTGCCCTGGC TCTTCCCAT  
CTAGGCCTGG GCAGGAACAT ATATTATTA TTTAAGCAAT TACTTTTCAT GTTGGGGTGG GGACGGAGGG GAAAGGGAAG  
CCTGGGTTTT TGTACAAAAA TGTGAGAAAC CTTGTGAGA CAGAGAACAG GGAATTAAAT GTGTCATACA TATCC-3'  
(FRAG. NO: )SEQ. ID NO:2521)

5'-CAGCTGCGGC ATCCTCTGTC TCAGAGTCTT GGTGTCTCTG TTCCTTTCCC CTCGGGGTCT CCCTGGGTCT CCCCAGTCC  
CTCTGCTGT CTCTCCCG CTCTCTGATC TCTGACTCCC AGAACCTCTC CCTCTGTCTC CAGGGCTGCC CCTCTGATCC  
TCTTTGCTTC TCTGGTGTGT CTCTCTGGCT GCCTCCATCT CTGTGGATCT CCGTCTCCCT GTCTCTGTCT CAGTCTGTCC  
TTCACTCTGT GTGTGTGTGT GTCTCTCTCT CTCTCTCTCC TTCCCTTCCA CTCCCTCTC CTCTGCTC CACCTCTCCA  
GGCCCTGTC TTGTCCCTCC GTCCGGCCTT TCTGTGCTT TCCGTCTCC TGCTCCCCA TCTCTCTCTG CTAGTCTGT  
CCAGCCGGAC CCCCACCAC AGTCGGGCCC CAGCGCTTGA GCCTGAGTGT CTGCTCCGGC CCGTGGAGGT GGAGGGAGGG  
GACGCCAATG ACCTACCAG CCCCTCTCCG ACCACCCCC CTTTCCCTT TTCAACTTTT CCAACTTTT CTCTCGTGCC  
CTCTCCGAG CGCGGGCGG TGAGCCCTGC AAGGCAGCCG CTCCGTCTGA ATGGAAAAGG CAGGCAGGGA GGGTGAGTCA  
GGATGTGTCA GGCGGGCCCT CCCCTGCCG CTGCCCCCG CCGCCCCG CCAGGCCCC TATATAACC CCCAGGCGTC  
CACACTCCCT CACTGCCGCG GGCCCTGCTG CTCAGGGCAC ATGCCTCCCC TCCCCAGCCG CGGGCCAGC TGACCCTCGG  
GGCTCCCCCG GCAGCGGACA GGAAGGGTT AAAGGCCCC GGCTCCCTGC CCCCTGCCCT GGGGAACCCC TGGCCCTGTG  
GGGACATGAA CTGTAAGTTG GTTCATGGG AGGTGGAGG GGACAGGGAG GCAGGGAGGA GAGGGACCA  
CGGCGGGGGT GGGAGCAGAC CCGCTGAGT CGCACAGAGA GGGACCCGA GACAGGCAGC CGGGGAGGAG  
AGCAGTTCTG GAGACAGGAG GCGGCGGAGG AGATGGGCAG AGAGAGACAC AGACAGGAGC GGATGGAGGC  
AGCCAATCAG AGGCGCCGA GGAGGGACGG GCCAGACAGG GCCGAGAGG AGCGAGACGC GAGACCGAGC  
AGGGGAGGG ACGCAGGGAC TGGTGCCGG AGGGAGGTGA CCCCCATCGA CCCAGGCCCC AGGGAGCCCC CGGGGACCGG  
GAGACTCCCT GGGATTCCGG CAGAGAGGCT CCGGAGGGA ACTGAGGCAG GGTCCGCGGA GAGCGGAGCA AGCCAGGGAG  
TAGCGACCCC AGCCGGGGG AGGAGAGAGA CTGGGCGCG GGGGAAAGCG GGGAGAGCCG GGCAGATGCG  
GCCGACGGAG GCGCGGACAG ACCGACGGT GCGGGCCCC GGGGGCGGC TGGGGGTGTG CGAGGCGCGG  
GCGGCCGGG AGCGCTGATT GGCTGGCGG TGGCGGGTG GCGGGGCGG CCGGGGTGG CTGCGGGAG CGAGCTCCG  
ACCCCGCGC CCGGGCGCC CCGCGGCC CCGCGGCCA GCTCTCCCG TCCGCGCGC CGGCGGGCC ATGGCTCTG  
CCCTCTCCG CCAGGTGCG TGCGGCCCG GCTTCTGCC CACCCCGG GGGCTCCTG GAGGGGTCT AAGGGGTCT  
CCGTGGGAGA GTCCGTGTC TCCGGACTC CGTCTGGG TTTTGGCTC TCCCTGCT CCCAGCCAGC TCGGGCTCC  
GCGGCCGGG GAGGGGGCAG GTTCTGGCT GTGCTCCCC CACCATCCG CCCCCGGG CCAGATTCCG GCGTCCGGG  
GCGGACGGGA GACGCCCCG CCGCTCTG TCCGACGGG GGGGAGCCA GAGCCAGGA GGGAGAGGA AGCCGCCTG  
GCCCTGCGAC CTGCCCCGG GCGTCCACC CTGGGACTTA AGACCTCCAG CTCCATCTC CTAAGGCGG GGAGTCCAG  
CCCCAGACC TCCTCCCCGA GACCCAGGAG TCCAGACCC AGGCCTTCT CCTCAGACC TAGGAGTCCA GGGCCAGC  
CTCTCTCC TCAGACCCAG GAGGAGTCCA GACCCAGTT CCTCTCCT CAGACCCGG AGTCCAGCC AGGCCTCT  
CTCTCAGAC CGAGTCCAG CTGAGCTCT CTGCTTATC CTGCCCCAG GTGTTGCGC CTGGTCTG GTCGTGCTG  
GCCTGTGGC AGATACAGT GTCGCCCTG GGCCACCAC TGGCCCCCT CGAGTTTCC CAGACCTCG GCGGAGCTG  
GACAGCACG TGCTCTGAC CCGCTCTCT CTGGCGGACA CGCGGAGCT GGCTGCACAG CTGGTAGGAG AGACTGGCT  
GGGGCAGCA CAGGAGTGA AGGCAGAGAG GAACGAGAG GAGTCTGCG GCAGCCACTT GGAGGGGTT TGGGCTCTCA

CACCTCAGAT CTTGAGCCTG CGCTGTACG ACTCCAAGAC CCTCACTTCC AAAGCCAGGC CCAAAGCCCT GAGACCAGAA  
 GACTTCAAAC CTTGGTCTT GGGCCTAACT CCAAAGACCC TGGATCTCAA ATTCCAACCT CTAGCTCTGA GACTCCAGCC  
 CTCACCCATG AGTTCCTGAA CTGGAACCCA GAGACCCAT CTCTAAGACT TCAGCCTTGA GATCCAGGGC CTGACCCATG  
 ACTCGAGCCC ACAGACCTCA GATACTGTCT GTAAACCCCT AGCTCTGGTG GGGAGCAGTG GCTCACTCT GTAACTCCAA  
 GGCAGGGGAG GCCAAGGCAG AAGGACCTCT TGAGGCCATG AGTTTGAGAC AGCCTGGGCA GCATAGCAAG ACTCTGTTTC  
 TTAATTATTA TTATTATTAT TATTTTGTG AGACAGAGTC TCGCGCTCTG TTGCCAGGC TAGAGTGCAA TGGTGCCATT  
 TCGGCTTGCT GGAACCTCCG CCTCCTGGGC TCAAGCGATT CTCTGCCTC AGCCTCTGA GTAGCTGGGA CTTCAGGTGC  
 AACTGCCAC ACCCGGATAA TTTTGTGTA TTTAGTAGA CACAGGGTTT CACCGTGTG CCCAGGCTGG TCACAACTC  
 CTGAGCTCAG GCCATCCGCC CGCTCGGCC TCCCAAAGCG CTGGGATAAC AGGCGTGACG CCGCGCCTGG CTCTTAATT  
 GTTCTAACAG CAGCGACAAC AACAAAAACC CAGCTCTGAG ATTCCAGCCC CGGCGACTCT AACAGTCCCA GGCCCGATCC  
 CTCACCTAGA ACCGAGATGC CAGCCCTGAC TCCACAGACT TCACCCCAA CCCCACACT CAGCTCTGGA AGCCCGCTCT  
 GACTCCAGCC TCCATTTTCG GAACCCACA CCGTGAAGAG CTCCCGGCTT AAACACTTCA CCCCACGGC CACAGTCCCC  
 CTGTGAATAT GCAGCCCGA TTCAGCTGCA GCTCCACAGC ACCCTGCCC TGACCCCCG CTGCACCCC TACCTGTGAC  
 TCACCTCTCT CCTCECCCA CAGATGTCCC GCCTGGCCCT GCCCCAGCCA CCCCAGGACC CGCCGGCGCC CCCGCTGGCG  
 CCCCCTCTCT CAGCTGGGG GGGCATCAGG GCGCCACAG CCATCCTGGG GGGGCTGCAC CTGACACTTG ACTGGGCCGT  
 GAGGGGACTG CTGCTGCTGA AGACTCGGT GTGACCCGGG GCCCAAAGCC ACCACCGTCC TTCAAAGCC AGATCTTATT  
 TATTTATTA TTTCAGTACT GGGGGCGAAA CAGCCAGGTG ATCCCCCGC CATTATCTCC CCTAGTTAG AGACAGTCTT  
 TCCGTGAGCA TGGGGGGGA TCTGTGCTT ATTTATCTT ATTTATTTA GGAGCAGGGG TGGGAGGGAG GTGGACTCCT  
 GGGTCCCCG CGAGGAGGGG ACTGGGTCTT CGGATTCTTG GGTCTCCAAG AAGTCTGTCC ACAGACTTCT GCCTGGCTC  
 TTCCCATCT AGGCTGGGC AGGAACATAT ATTATTATT TAAGCAATTA CTTTTCATGT TGGGGTGGG ACGGAGGGGA  
 AAGGGAAGCC TGGGTTTTG TACAAAAATG TGAGAACTT TGTGAGACA GAGAACAGGG AATTAATGT GTCATACATA  
 TCCACTTGAG GCGGATTGT CTGAGAGCTG GGGCTGGATG CTTGGGTAAC TGGGGCAGGG CAGGTGGAGG GGAGACCTCC  
 ATTCAGGTGG AGGTCCCGAG TGGCGGGGG AGCGACTGGG AGATGGGTG GTCAACCGA CAGCTCTGTG GAGGCAGGT  
 CTGAGCCTTG CTTGGGGCCC CGCACTGCAT AGGGCGGTT GTTTGTTTT TGAGATGGAG TCTCGCTCTG TTGCTTAGG  
 TGGAGTGCA TGAGGCAATC TAAGGTACT GCAACCTCCA CACTCCGGT TCAAGCAATT CTCTGCCTC AGCTCCCGA  
 TTAGCTGGGA TCACAGGTGT GCACCATCAT GCCAGCTAA TTATTATT CTTTGTATT TTTAGTAGAG ACAGGGTTTC  
 ACCATGTTGG CCAGGCTGGT TTCGAACCTC TGACCTCAGG TGATCCTCT GCCTCGGCT CCAAAGTGC TGGGATTACA  
 GGTGTGAGCC ACCACACCTG ACCCATAGGT CTTCAATAAA TATTAATGG AAGGTCCAC AAGTCACCCT GTGATCAACA  
 GTACCCGTAT GGGACAAAGC TGCAAGGTCA AGATGGTTCA TTATGGCTGT GTTACCATTA GCAAACCTGGA ACAAATCTAG  
 ATATCCAACA GTGAGGGTTA AGCAACATGG TGCATCTGTG GATAGAAGCG CACCCAGCCG CCGGAGCAG GGAAGTCTAT  
 TCAGGGAGGC TAAGGAGAGA GGCTTGCTTG GGATATAGAA AGATATCCTG ACATTGGCCA GGCATGGTGG CTACGCCTG  
 TAATCCTGGC ACTTTGGGAG GACGAAGCGA TGGATACCT CAGTCCAAG AGTTTGAGAC CGGCTCGGA GACATGGCAA  
 AACCTGTCT CAAAAAGAA AGAATGATGT CCGACATGA AACAGCAGGC TACAAAACCA CTGCATGCTG TGATCCCAAT  
 TTTGTGTTT TCTTCTATA TATGGATTAA ACAAATAAT CTAAGGGAA ATACGCCAAA ATGTTGACAA TGACTGTCTC  
 CAGGTCAAAG GAGAGAGGTG GGATTGTGG TGACTTTTAA TGTGTATGAT TGTCTGATT TTACAGAATT TCTGCCATGA  
 CTGTGATT TGCATGACAC ATTTAAAAA TAATAAACAC TATTTTAGA ATAACAGAAT ATCAGCCTCC TCTCTCAA  
 AAATAAGCCC TCAGGAGGGG ACAAAGTTGA CCGCTGATTG AGCCTGTGAG GGCTGTGCAC-3' (FRAG. NO. ) (SEQ.  
 ID NO: 2522)

#### Human GM-CSF Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CTTGBGCBGG BBGCTCTGGG GCBGGGBGCT GCBGGGGCC BGGGGGGTGG CTTCCTGCBG TGTCCBGBGT GCBCTGTGCC  
 BCBGCBGBG CTGCBGGGCC BTGCBGCTCB TGGGGCTCTG GGTGGCBGGT CCBGCCBTGG GTCTGGGTGG GGCTGGGCTG  
 CBGGCTCCGG GCGGTCCBGGCBTGGGTCTG GGGGCTGGG CTGCBGGCTC CGGGCGGGCG GGTGCGGGCT GCGTGTGGG  
 GGCTGCCCCG CAGGCCCTGC GGTCCBGGCB TGGGTCTGGG GGCTGGGCTG CBGGCTCCGG GCGGGCGGGT GCGGCTGCG  
 TGCTGGGGG TGCCCCGAG GCCCTGC-3' (FRAG. NO:1847) (SEQ. ID NO: 1858)  
 5'-GBGCBGG BBG-3' (FRAG. NO:1848) (SEQ. ID NO: 1859)  
 5'-GCCBGBGCBGCBG-3' (FRAG. NO:1849) (SEQ. ID NO: 1860)  
 5'-GGG TGC GGG C-3' (FRAG. NO:1850) (SEQ. ID NO: 1861)  
 5'-GGT CCB GCC BTG GGT CTG GG-3' (FRAG. NO:1300)(SEQ. ID NO:1310)  
 5'-GGC TGG GCT GCB GGC TCC GG-3' (FRAG. NO:1301)(SEQ. ID NO:1311)  
 5'-GCG GGC GGG TGC GGG CTG CGT GCT GGG-3' (FRAG. NO:1302)(SEQ. ID NO:1312)  
 5'-GGC TGC CCC GCA GGC CCT GC-3' (FRAG. NO:1303)(SEQ. ID NO:1313)  
 5'-CTTGBGCBGG BBGCTCTGGG GCBGGGBGCT GCBGGGGCC BGGGGGGTGG CTTCCTGCBG TGTCCBGBGT GCBCTGTGCC  
 BCBGCBGBG CTGCBGGGCC BTGCBGCTCB TGGGGCTCTG GGTGGCBGGT CCBGCCBTGG GTCTGGGTGG GGCTGGGCTG  
 CBGGCTCCGG GC-3' (FRAG. NO:1851) (SEQ. ID NO: 1862)

#### Human Tumor Necrosis Factor " Antisense Oligonucleotide Fragments

5'-GCBCCGCTG GBGCCCTGGG GCCCCCTGT CTCTTGGGG BGGCCTCTC CGGCCBGTG CCGTCCCG BTCTGCTTT  
 CBGTGCTBT GGTGTCCTTT CCBGGGBGB GBGGGGCTGG TCCTCTGCTG TCCTGCTGG TGCTBTGGT GTCCTTCCG  
 CCCTGGGGCC CCCTGTCTT CTGGGGCTT CTCCCTCTG GGGGCGTCT CTCTCCCTCT CTTCGCTCT TCTTTCTC  
 TCTCTCTT CCCCCTTCCC GCTCTTCTG TCTCGGTGTC TGGTTTTCT TCTCGCTGG CTGCCTGTCT GGCCTGCGCT  
 CTGGGCTGT GCTGTTCTC CTCCGGTTC TGCTCTCT GCTGTGCG CCCTCTGGG TCTCCCTCT GGTGTGGTC  
 TTGTTGCTG GGCTGGGCTC CGTGTCTCB GTGCTBTGG TGTCGCTGB GGBGCGTCT GCTGGGCTG GTCCTCTGCTGTC  
 CTGCTGGTG CTBTGGTGT CTTTCCGCC CTGGGGCCCC CTGTCTTCT TGGGCTCT TCCCTCTGG GGCCGTCTC  
 TCTCCCTCT TGCGTCTCT CTCTTCTCT CTCTCTCT CCCCCTCCG CTCTTCTGT CTGGTGTCT GGTCTTCTCT  
 CTCCGCTGG TGCTGTCTG CCCTGCGCTC TTGGCTGTG CTGTTCTCC TCCGGTCTCT GTCCTCTCTG TGTGCGCC  
 CCTCTGGGT CTCCCTCTG CGTGGTGTG TTGTTGCTG GGCTGGGCTC CGTGTCTCB GTGCTBTGG TGTCGCTGB  
 GGBGCGTCT GCTGGC-3' (FRAG. NO:1852) (SEQ. ID NO:1863)  
 5'-GGGGCCCCC-3' (FRAG. NO:1853) (SEQ. ID NO:1864)

5'- GGG GGC CG TCT-3' (FRAG. NO:1854) (SEQ. ID NO:1865)

5'-CCBGGGGBGB GBGGGGCTGG-3' (FRAG. NO:1855) (SEQ. ID NO:1866)

5'-

GCBCCGCTGGBGCCCTGGGCCCCCTGTCTTCTTGGGGBGCGCCTCCTCGGCCBGTCCBCGTCCCGGBTCBTGCTTCBGTGC  
TCBTGGTGTCTTTCCBGGGGBGBGGG-3' (FRAG. NO:1304) (SEQ. ID NO:1314)

5'-GCT GGT CCT CTG CTG TCC TTG CTG GTG CTC BTG GTG TCC TTT CC GCC CTG GGG CCC CCC TGT CTT CTT GGG G  
CCT CTT CCC TCT GGG GGC CG TCT CTC TCC CTC TCT TGC GTC TCT C TCT TTC TCT CTC TCT CTT CCC C TTT CCC GCT  
CTT TCT GTC TC GGT GTC TGG TTT TCT CTC TCC GCT GGC TGC CTG TCT GGC CTG CGC TCT T GGC CTG TGC TGT TCC  
TCC TCC GGT TCC TGT CCT CTC TGT CTG TC GCC CCC TCT GGG GTC TCC CTC TGG C GTG GTG GTC TTG TTG CTT GGG  
CTG GGC TCC GTG TCT C CBG TGC TCB TGG TGT CC-3' (FRAG. NO:1305) (SEQ. ID NO:1315)

5'-GCT GBG GGB GCG TCT GCT GGC GCT GGT CCT CTG CTG TCC TTG CTG GTG CTC BTG GTG TCC TTT CC GCC CTG  
GGG CCC CCC TGT CTT CTT GGG G CCT CTT CCC TCT GGG GGC CG TCT CTC TCC CTC TCT TGC GTC TCT C TCT TTC  
TCT CTC TCT CTT CCC C TTT CCC GCT CTT TCT GTC TC GGT GTC TGG TTT TCT CTC TCC GCT GGC TGC CTG TCT GGC  
CTG CGC TCT T GGC CTG TGC TGT TCC TCC TCC GGT TCC TGT CCT CTC TGT CTG TC GCC CCC TCT GGG GTC TCC CTC  
TGG C GTG GTG GTC TTG TTG CTT GGG CTG GGC TCC GTG TCT C CBG TGC TCB TGG TGT CC GCT GBG GGB GCG TCT  
GCT GGC-3'

(FRAG. NO:1306) (SEQ. ID NO:1316)

5'-GCT GGT CCT CTG CTG TCC TTG CTG-3' (FRAG. NO:1655) (SEQ. ID NO:1665)

5'-GTG CTC BTG GTG TCC TTT CC-3' (FRAG. NO:1656) (SEQ. ID NO:1666)

5'-GCC CTG GGG CCC CCC TGT CTT CTT GGG G-3' (FRAG. NO:1657) (SEQ. ID NO:1667)

5'-CCT CTT CCC TCT GGG GGC CG-3' (FRAG. NO:1658) (SEQ. ID NO:1668)

5'-TCT CTC TCC CTC TCT TGC GTC TCT C-3' (FRAG. NO:1659) (SEQ. ID NO:1669)

5'-TCT TTC TCT CTC TCT CTT CCC C-3' (FRAG. NO:1660) (SEQ. ID NO:1670)

5'-TTT CCC GCT CTT TCT GTC TC-3' (FRAG. NO:1661) (SEQ. ID NO:1671)

5'-GGT GTC TGG TTT TCT CTC TCC-3' (FRAG. NO:1662) (SEQ. ID NO:1672)

5'-GCT GGC TGC CTG TCT GGC CTG CGC TCT T-3' (FRAG. NO:1663) (SEQ. ID NO:1673)

5'-GGC CTG TGC TGT TCC TCC-3' (FRAG. NO:1664) (SEQ. ID NO:1673)

5'-TCC GGT TCC TGT CCT CTC TGT CTG TC-3' (FRAG. NO:1665) (SEQ. ID NO:1675)

5'-GCC CCC TCT GGG GTC TCC CTC TGG C-3' (FRAG. NO:1666) (SEQ. ID NO:1676)

5'-GTG GTG GTC TTG TTG CTT-3' (FRAG. NO:1667) (SEQ. ID NO:1677)

5'-GGG CTG GGC TCC GTG TCT C-3' (FRAG. NO:1668) (SEQ. ID NO:1678)

5'-CBG TGC TCB TGG TGT CC-3' (FRAG. NO:1669) (SEQ. ID NO:1679)

5'-GCT GBG GGB GCG TCT GCT GGC-3' (FRAG. NO:1670) (SEQ. ID NO:1680)

#### Human Leukotriene C4 Synthase Nucleic Acids and Antisense Oligonucleotide Fragments

5'-CTCGGTBGB C GCGCTCBB C TCGGGTGGG C CGGTGGTGBG CGGCGGCB C CGCGGBBGG C CCTGCGCGCC  
GBGBTCBCCTG CBGGGBBBG TBGGCTTGC B GCBGBBCTCC CBGGBGGGTG BCBGCBGCCB GTBGBGCTBC CTCGTCTTC  
BTGGTBCCGT CGGTGTGGTG GCBGGGCTG TGTGTBBGG CGBGCTGGG C CCGTCTGCT GCTCCTCGT CCGCCTCGTC  
CTTCA TGG TA CCGTCGGTGT GGTGGCCTCG GGTGGGCGG TGGTGGGGCG CGCGCGCTCG CGTGGCTCCG GCTCTTCTT  
CCCGGCTCCG CGGCCGGGG GCCTTGGTCT CCCTCGTCT TCBTGGTBCC G-3' (FRAG. NO:1856) (SEQ ID NO: 1867)

5'-GCB GCBGGBC-3' (FRAG. NO:1857) (SEQ ID NO: 1868)

5'-CCCGGCTCCG-3' (FRAG. NO:1858) (SEQ ID NO: 1869)

5'-CGGCCCGGG GCC-3' (FRAG. NO:1859) (SEQ ID NO: 1870)

5'-CB CGCGG-3' (FRAG. NO:1860) (SEQ ID NO: 1871)

5'-GCC CCG TCT GCT GCT CCT CGT GCC G-3' (FRAG. NO:1307) (SEQ. ID NO:1317)

5'-CCT CGT TCT TCA TGG TAC CGT CGG TGT GGT GGC-3' (FRAG. NO:1308) (SEQ. ID NO:1318)

5'-CTC GGG TGG GCC GGT GGT G-3' (FRAG. NO:1309) (SEQ. ID NO:1319)

5'-GGG CGC GCG CGC TCG CGT-3' (FRAG. NO:1310) (SEQ. ID NO:1320)

5'-GGC TCC GGC TCT TCT TTC CCG GCT CCG TCG GCC CGG GGG CCT TGG TCT C-3' (FRAG. NO:1311) (SEQ. ID NO:1321)

5'-CCT CGT CCT TCB TGG TBC CG-3' (FRAG. NO:1312) (SEQ. ID NO:1322)

5'-CTCGGTBGB C GCGCTCBB C TCGGGTGGG C CGGTGGTGBG CGGCGGCB C CGCGGBBGG C CCTGCGCGCC  
GBGBTCBCCTG CBGGGBBBG TBGGCTTGC B GCBGBBCTCC CBGGBGGGTG BCBGCBGCCB GTBGBGCTBC CTCGTCTTC  
BTGGTBCCGT CGGTGTGGTG GCBGGGCTG TGTGTBBGG CGBGCTGG-3' (FRAG. NO:1861) (SEQ ID NO: 1872)

#### Human Endothelin-1 Nucleic Acids and Antisense Oligonucleotide Fragments

5'-BCCGGCGBG CCGCCBGGGT GGBCTGGGBG TGGGTTTCTC CCCGCCGTT CCBCCBCCG CGTGGBGCTC BGCGCCTBBG  
BCTGCTGTT CTGGBGCTCC TTGGCBGGC BCBBCBGB C GBGBBBBBB CBTGBGCB B TBTCBTT C TGBBBBBBBG  
GGBTCBBBB C CTTCCGTT C CCGTTCCG C TGGCGCGCG TCGGGGTT C TCGTGGGTT CTTCCCGCGG TTTCTCCGTC  
TGTTGCCTT GTGGGCTTCT TGCTTTTTC GCTGTTCTT TCTGCTTG C GTCTTTTTC TTCTTTTG C CTGGTTTG  
GGTCCGCTG TCTTTGCC TGTGTGTTT TGTGCTGCT TCGCTGCGG CCGCTGCGG GTTCTCTG C GTTTCTCCC  
CGCGTTTCT CCGTCTGTTG CTTTGTGGG CTCTGTGCT TTGTGCTGT TCTTTCTG CTTGCGCTT TTTCTTTCT  
TTGTGCTCG TTGTGGGTCC GCTGGTCTT TGCCCTGTG GTTTCTGCTG-3' (FRAG. NO:1862) (SEQ. ID NO:1873)

5'-CCGGCGBG CCGCCBGGGT GGB C-3' (FRAG. NO:1863) (SEQ. ID NO:1874)

5'-CCGCCBGGG-3' (FRAG. NO:1864) (SEQ. ID NO:1875)

5'-GGCGCGCGC-3' (FRAG. NO:1865) (SEQ. ID NO:1876)

5'-GTGGGTCCGC-3' (FRAG. NO:1866) (SEQ. ID NO:1877)

5'-CCCGTTCGCTGGCGC-3' (FRAG. NO:1313) (SEQ. ID NO:1323)

5'-GCGCTCGGGTTCTCTC-3' (FRAG. NO:1314) (SEQ. ID NO:1324)

5'-GTGGGTTTCTCCCCCGGTTCTC-3' (FRAG. NO:1315) (SEQ. ID NO:1325)

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5'-CTTCTGTCTTTTGGCT-3' (FRAG. NO:1317)(SEQ. ID NO:1327)  
5'-GTTCTTTCTGCTTGGC-3' (FRAG. NO:1318)(SEQ. ID NO:1328)  
5'-GTCTTTTCTTTCTT-3' (FRAG. NO:1319)(SEQ. ID NO:1329)  
5'-TGTGCTCGGTTGTGGGTC-3' (FRAG. NO:1320)(SEQ. ID NO:1330)  
5'-CGCTGGTCTTTGCC-3' (FRAG. NO:1321)(SEQ. ID NO:1331)  
5'-CTGTGTGTTTCTGCTG-3' (FRAG. NO:1322)(SEQ. ID NO:1332)  
5'-CCCCTTCGCTGGCGC-3' (FRAG. NO:1323)(SEQ. ID NO:1333)  
5'-GCGCTCGGGTTCCTC-3' (FRAG. NO:1324)(SEQ. ID NO:1334)  
5'-GTGGGTTTCTCCCGCCGTTCTC-3' (FRAG. NO:1325)(SEQ. ID NO:1335)  
5'-CGGTCTGTTCCTTTGTGGG-3' (FRAG. NO:1326)(SEQ. ID NO:1336)  
5'-CTTCTGTCTTTTGGCT-3' (FRAG. NO:1327)(SEQ. ID NO:1337)  
5'-GTTCTTTCTGCTTGGC-3' (FRAG. NO:1328)(SEQ. ID NO:1338)  
5'-GTCTTTTCTTTCTT-3' (FRAG. NO:1329)(SEQ. ID NO:1339)  
5'-TGTGCTCGGTTGTGGGTC-3' (FRAG. NO:1330)(SEQ. ID NO:1340)  
5'-CGCTGGTCTTTGCC-3' (FRAG. NO:1331)(SEQ. ID NO:1341)  
5'-CTGTGTGTTTCTGCTG-3' (FRAG. NO:1332)(SEQ. ID NO:1342)

**Endothelin Receptor ET-B Nucleic Acids and Antisense Oligonucleotide Fragments**

5'-GCCCTGTCGG GCGGGAAGCC TCTCTCTCT CCCAGATC CGCGACAGGC CGCAGGCAAG AACCAGCGCA ACCAGGGCGC  
GTCCGCACAG ACTTGGAGGC GGCTGCATGC TGCTACCTGC TCCAGAAGCG TCCGGTGGCC GCCGCGCC CTGTGGGGCG  
GGBBGCTCT CTCCTCTCC CBGTCCGCG BCBGGCCGCB GGCBBGBBCC BCGCBBCB GGGCGCTCC GCBCBGBCTT  
GGBGGCGGCT GCBTGTGCT BCCTGCTCGGGCG GGBBGCTCCG GTGGCCGCG CGCGTCCGGT GCCCGCCGCG  
CCTCTCTCT CTCCTCGTG CCCTGTCGGG CGGTCTGTC CGTCTGTCT CTTTTCTTT TGCTGTCTTG TCTCCCGTC  
TCTGCTT-3' (FRAG. NO: 1867) (SEQ. ID NO: 1878)  
5'-CGGGCG GBBGCC-3' (FRAG. NO: 1868) (SEQ. ID NO: 1879)  
5'-CGGGCGGG-3' (FRAG. NO: 1869) (SEQ. ID NO: 1880)  
5'-CCGCBGBBC-3' (FRAG. NO: 1870) (SEQ. ID NO: 1881)  
5'-GCGTCCGGTGGCCGCCG-3' (FRAG. NO:1333)(SEQ. ID NO:1343)  
5'-GCCTCTCTCTCTCCC-3' (FRAG. NO:1334)(SEQ. ID NO:1344)  
5'-GTGGCCCTGTGGGGCGG-3' (FRAG. NO:1335)(SEQ. ID NO:1345)  
5'-TCCTGCCGTCTGTCTCCTT-3' (FRAG. NO:1336)(SEQ. ID NO:1346)  
5'-TCTTTTGTCTGTGT-3' (FRAG. NO:1337)(SEQ. ID NO:1347)  
5'-CTTCCCGTCTGTCTT-3' (FRAG. NO:1338)(SEQ. ID NO:1348)  
5'-GCCCTGTCGG GCGGGAAGCC TCTCTCTCT CCCAGATC CGCGACAGGC CGCAGGCAAG AACCAGCGCA ACCAGGGCGC  
GTCCGCACAG ACTTGGAGGC GGCTGCATGC TGCTACCTGC TCCAGAAGCG TCCGGTGGCC GCCGC-3' (FRAG. NO: 1871)  
(SEQ. ID NO: 1882)  
5'-GCCCTGTCGG GCGGGBBGC TCTCTCTCT CCCBGTCC GCGBCBGGCC GCBGGCBGB BCCBGCGB BCCBGGGCGC  
GTCCGCBGB BCTTGBBGC GGCTGCTGC TGCTBCTGC TCCBGBBGC TCCGGTGGCC GCCGC-3' (FRAG. NO: 1872)  
(SEQ. ID NO: 1883)

**Endothelin ETA Receptor Nucleic Acids and Antisense Oligonucleotide Fragments**

5'-GTCTGTCTC CCCGTCTCT CCCACTGCT CTCCTGGGGG CTCCCGGGC TTCGGGTGGC CGGTGTCCCG GGCTCCGGCG  
CGGCGGGCG TTCGGTGGC GGTGGGTGGC GCGGGCTGCC GGGTCCGCGC GCGCCTGGG CCTTGTGCT GCTTTTGTCT  
TGTTCCGTT TGGTGTCTC GGTCTGTGT GTGGTGTGT TGTCTCTCT TGGGTGTGG CCTTGGGTT TTGGCTGTGG  
GCCCTTGGG GCCTTGGCT CTGGCTGTC TGCTCTCCC GTCTCTCCC ACTGCTTCT CCCGGGGGCT TCCCCGGCT  
CGGGTGGCG GTGTCCCGG CTCGGGCGG GCGGCGGCT CGGTGCGGG TGGGTGGCG GGGTGGCGG GTCCGCGCGG  
CGCTGGGC CTGTGTCTG TTTTGTCTG TTCCTTCTG GCTGTCCCG TCTGTGTGT GGTGTTTTG TTTCTCTTG  
GTGTGGGC TTGCGTTT GGCTGTGGG CTGTGGGC CTGTCTCT GGTCTCAT CCACATGATT GCTTAGATT  
GTGCTGTAT TCTCAGGATT ATCACTGATT ACACATCAA CCAGTGCCAG CCAAAGGAT GCCCTGAGGC AAAGGGTTTC  
CATCTGAGG CAAATTGAG GACBTCCBC BTGTTGCTT BGTGTTGTG TGTCTCTC BGGTTTCTB CTGTTTBCB  
BTCCBCCBG TGCCBCCBB BBGGTGTCCC TGBGGCBGB GGTTCBCT TTGBGGCB TTTGBGB-3' (FRAG. NO:1873)  
(SEQ. ID NO: 1884)  
5'-GBGGCBGBGG-3' (FRAG. NO:1874) (SEQ. ID NO: 1885)  
5'-GCCBGCBB BBGB-3' (FRAG. NO:1875) (SEQ. ID NO: 1886)  
5'-CGCCTGGGCC C-3' (FRAG. NO:1876) (SEQ. ID NO: 1887)  
5'-GTCTGTCTCCCCGTCTCTCCC-3' (FRAG. NO:1339)(SEQ. ID NO:1349)  
5'-ACTGCTTCTCCCGGG-3' (FRAG. NO:1340)(SEQ. ID NO:1350)  
5'-GCTTCCCGGCTTC-3' (FRAG. NO:1341)(SEQ. ID NO:1351)  
5'-GGGTGGCCGTGTCCCGGGCTCCGCGCGGCGGC-3' (FRAG. NO:1342)(SEQ. ID NO:1352)  
5'-GGCTTCGGCTGC-3' (FRAG. NO:1343)(SEQ. ID NO:1353)  
5'-GGGTGGGTGGCGGG-3' (FRAG. NO:1344)(SEQ. ID NO:1354)  
5'-GCTGCGGGTCCGCGCGGCGCTGGCC-3' (FRAG. NO:1345)(SEQ. ID NO:1355)  
5'-CTTGTGCTCTTT-3' (FRAG. NO:1346)(SEQ. ID NO:1356)  
5'-TGCTTGTTCGTT-3' (FRAG. NO:1347)(SEQ. ID NO:1357)  
5'-TGGCTGCTCCGGTCTGTGTGTGTTGTTT-3' (FRAG. NO:1348)(SEQ. ID NO:1358)  
5'-TTTCTCTTGGGTGTGG-3' (FRAG. NO:1349)(SEQ. ID NO:1359)  
5'-CCTTGGCGTTTGG-3' (FRAG. NO:1350)(SEQ. ID NO:1360)  
5'-CTGTGGGCCCTTTG-3' (FRAG. NO:1351)(SEQ. ID NO:1361)  
5'-GGGCTTGGCTTCTGGCTC-3' (FRAG. NO:1352)(SEQ. ID NO:1362)  
5'-CATCCACATG ATTGCTAGA TTTGTGCTGT ATCTCTCAGG ATTACTG ATTACATC CAACAGTGC CAGCCAAAAG  
GATGCCCTGA GGCAAAGGT TTCCATCTTG AGGCAATT GAGGA-3' (FRAG. NO:1353)(SEQ. ID NO:1363)

5'-CBTCCBCBTG BTTGCTTBGB TTTGTGCTGT BTCTCTCBGG BTTBTCBCTG BTTBCBCBTC CBCCCBGTGC CBGCCBBBGG  
GBTGCCCTGB GGCBBBGGGT TTCCBTCTTG BGGCBBBTTT GBGG-3' (FRAG. NO:1354)(SEQ. ID NO:1364)

**Endothelin Receptor A Nucleic Acid and Antisense Oligonucleotide Fragments**

5'-GCCACCATGG AAACCTTTG CCTCAGGGCA TCCTTTTGGC TGGCACTGGT TGGATGTGTA ATCAGTGATA ATCCTGAGAG  
ATACAGCACA AATCTAAGCA ATCATGTGGA TGATTTCACC ACTTTTCGTG GCACAGAGCT CAGCTTCCTG GTTACCACTC  
ATCAACCCAC TAATTTGGTC CTACCCAGCA ATGGCTCAAT GCACAACTAT TGCCACAGC AGACTAAAAT TACTTCAGCT  
TTCAAATACA TTAACACTGT GATATCTTGT ACTATTTTCA TCGTGGGAAT GGTGGGGAAT GCAACTCTGC TCAGGATCAT  
TTACCAGAAC AAATGTATGA GGAATGGCCC CAACGCGCTG ATAGCCAGTC TTGCCCTTGG AGACCTTATC TATGTGGTCA  
TTGATCTCCC TATCAATGTA TGGCTGGGCG CTGGCCTTTT GATCACAATG ACTTTGGCGT ATTTCTTTGC AAGCTGTTCC  
CCTTTTGTGA GAAGTCCTCG GTGGGGATCA CCGTCCTCAA CCTCTGCGCT CTTAGTGTTG ACAGGTACAG AGCAGTTGCC  
TCCTGGAGTC GTGTTCAAGG AATTGGGATT CCTTTGGTAA CTGCCATTGA AATTGCCTCC ATCTGGATCC TGTCTTTAT  
CCTGGCCATT CTGAAGCGA TTGGCTTCGT CATGGTACCC TTTGAATATA GGGGTGGACA GCATAAAACC TGTATGCTCA  
ATGCCACATC AAAATTCATG GAGTTCTACC AAGATGTAAA GGACTGGTGG CTCTTCGGGT TCTATTTCTG TATGCCCTTG  
GTGTGCACTG CGATCTTCTA CACCCTCATG ACTGGTGAGA TGTGAACAG AAGGAATGGC AGCTTGAGAA TTGCCCTCAG  
TGAACATCTT AAGCAGCGTC GAGAAAGTGGC AAAAACAGTT TTCTGCTTGG TTGTAATTTT TGCTCTTTGC TGGTCCCTC  
TTCATTTAAG CCGTATATTG AAGAAACTG TGTATAACGA GATGGACAAG AACCAGATGTG AATTACTTAG TTTCTTACTG  
CTCATGGATT ACATCGGTAT TAACTTGGCA ACCATGAATT CATGTATAAA CCCCATAGCT CTGTATTTTG TGAGCAAGAA  
ATTTAAAAAT TGTTCCAGT CATGCCTCTG CTGCTGCTGT TACCAGTCCA AAAGTCTGAT GACCTCGGTC CCCATGAACG  
GAACAAGCAT CCAAGTGAAG AACCACGATC AAAACAACCA CAACACAGAC CGGAGCAGCC ATAAGGACAG CATGAACTGA  
CCACCCTTAG AAGCACTCCT GAATTCGGGA AAAAGTGAAG GTGTAAAAGC AGCACAAGTG CAATAAGAGA TATTTCTCA  
AATTTGCCCTC AAGATGGAAA CCCTTGGCT CAGGGCATCC TTTTGGCTGG CACTGGTTGG ATGTGTAATC AGTGATAATC  
CTGAGAGATA CAGCACAAT CTAAGCAATC ATGTGGATGA TTTCACTACT TTTCTGTTGCA CAGAGCTCAG CTCTCTGGTT  
ACCACTCATC AACCCACTAA TTTGGTCCTA CCCAGCAATG GCTCAATGCA CAACTATTGC CCACAGCAGA CTAATAATTAC  
TTCAGCTTTC AAATACATTA AACTGTGAT ATCTTGTAAT ATTTTCATCG TGGGAATGGT GGGGAATGCA ACTCTGCTCA  
GGATCATTTA CCAGAACAAA TGTATGAGGA ATGGCCCCAA CGCGCTGATA GCCAGTCTTG CCCTTGGAGA CCTTATCTAT  
GTGGTCATTG ATCTCCCTAT CAATGTATTT AAGCTGCTGG CTGGGCGCTG GCCTTTTGAT CACAATGACT TTGGCGTATT  
TCTTTGCAAG CTGTTCCCT TTTGCGAGAA GTCTCTGGTG GGGATCACCG TCCTCAACCT CTGCGCTCTT AGTGTGACA  
GGTACAGAGC AGTTGCCTCC TGGAGTCGTG TTCAGGGAAT TGGGATTCTT TTGGTAACTG CCATTGAAAT TGTCTCCATC  
TGGATCCTGT CCTTATCCT GGCCATTCTT GAAGCGATTG GCTTCGTCAT GGTACCTTTT GAATATAGGG GTGAACAGCA  
TAAACCTGT ATGCTCAATG CCACATCAA ATTCATGGAG TTCTACCAAG ATGTAAAGGA CTGGTGGCTC TTCGGTTCT  
ATTTCTGTAT GCCCTTGGTG TGCACTGCGA TCTTCTACAC CCTCATGACT TGTGAGATGT TGAACAGAAG GAATGGCAGC  
TTGAGAATTG CCTCAGTGA ACATCTTAAG CAGCGTCGAG AAGTGGCAA AACAGTTTTC TGCTTGGTTG TAATTTTTCG  
TCTTTGCTGG TTCCCTCTTC ATTTAAGCCG TATATTGAAG AAACTGTGT ATAACGAGAT GGACAAGAAC CGATGTGAAT  
TACTTAGTTT CTTACTGCTC ATGGATTACA TCGGTATTA CTGGCAACC ATGAATTCAT GTATAAACCC CATAGCTCTG  
TATTTTGTGA GCAAGAAATT TAAAAATTGT TTCCAGTCAT GCCTCTGCTG CTGCTGTTAC CAGTCCAAAA GTCTGATGAC  
CTCGGTCCCC ATGAACGGAA CAAGCATCCA GTGGAAGAAC CACGATCAA ACAACCACAA CACAGACCGG AGCAGCCATA  
AGGACAGCAT GAACTGACCA CCCTTAGAAG CACTCCTCGG TACTCCATA ATCCTCTCGG AGAAAAAAT CACAAGGCAA  
CTGTGAGTCC GGAATCTCT TCTCTGATCC TTCTTCTTA ATCACTCCC ACACCAAGA AGAAATGCTT TCCAAAACCG  
CAAGGGTAGA CTGGTTTATC CACCCACAAC ATCTACGAAT CGTACTTCTT TAATTGATCT AATTACATA TTCTGCGTGT  
TGTATTCAGC ACTAAAAAT GGTGGGAGCT GGGGGAGAAT GAAGACTGTT AAATGAAACC AGAAGGATAT TTAATACTTT  
TGCATGAAAA TAGAGCTTTC AAGTACATGG CTAGCTTTTA TGGCAGTTCT GGTGAATGTT CAATGGGAAC TGGTCACCAT  
GAACTTTAG AGATTAACGA CAAGATTTTC TACTTTTTT AAGTGATTTT TTTGCTCTC AGCCAAACAC AATATGGCT  
CAAGTCACTT TTATTTGAAA TGTCAATTTG TGCCAGTATC CCGAATTC GAATTCGGGA AAAAGTGAAG GTGTAAAAGC  
AGCACAAGTG CAATAAGAGA TATTTCTCA AATTTGCCCTC AAGATGGAAA CCCTTGGCT CAGGGCATCC TTTTGGCTGG  
CACTGGTTGG ATGTGTAATC AGTGATAATC CTGAGAGATA CAGCACAAT CTAAGCAATC ATGTGGATGA TTTCACTACT  
TTTCGTGGCA CAGAGCTCAG CTCTCTGGTT ACCACTCATC AACCCACTAA TTTGGTCCTA CCCAGCAATG GCTCAATGCA  
CAACTATTGC CCACAGCAGA CTAATAATTAC TTCAGCTTTC AAATACATTA AACTGTGAT ATCTTGTAAT ATTTTCATCG  
TGGGAATGGT GGGGAATGCA ACTCTGCTCA GGATCATTTA CCAGAACAAA TGTATGAGGA ATGGCCCCAA CGCGCTGATA  
GCCAGTCTTG CCCTTGGAGA CCTTATCTAT GTGGTCATTG ATCTCCCTAT CAATGTATTT AAGCTGCTGG CTGGGCGCTG  
GCCTTTTGAT CACAATGACT TTGGCGTATT TCTTTGCAAG CTGTTCCCT TTTGCGAGAA GTCTCTGGTG GGGATCACCG  
TCCTCAACCT CTGCGCTCTT AGTGTGACA GGTACAGAGC AGTTGCCTCC TGGAGTCGTG TTCAGGGAAT TGGGATTCTT  
TTGGTAACTG CCATTGAAAT TGTCTCCATC TGGATCCTGT CCTTATCCT GGCCATTCTT GAAGCGATTG GCTTCGTCAT  
GGTACCTTTT CAATATACCG CTGAACACCA TAAACCTCT ATCTCAATC CCACATCAA ATTCATCCAG TTCTACCAAC

CAGCACAAAT CTAAGCAATC ATGTGGATGA TTTCACCACT TTTCGTGGCA CAGAGCTCAG CTTCCTGGTT ACCACTCATC  
AACCCACTAA TTGGTCTTA CCCAGCAATG GCTCAATGCA CAACTATTGC CCACAGCAGA CTAATAATTAC TTCAGCTTTC  
AAATACATTA AACTGTGTAT ATCTTGACT ATTTTCATCG TGGGAATGGT GGGGAATGCA ACTCTGCTCA GGATCATTTA  
CCAGAACAAA TGTATGAGGA ATGGCCCCAA CGCGCTGATA GCCAGTCTTG CCCTTGGAGA CTTATCTAT GTGGTCATTG  
ATCTCCCTAT CAATGTATTT AAGCTGCTGG CTGGGCGCTG GCCTTTTGAT CACAATGACT TTGGCGTATT TCTTTGCAAG  
CTGTTCCCTT TTTTGCAGAA GTCTCGGTG GGGATCACCG TCCTCAACCT CTGCGCTCTT AGTGTGACA GGTACAGAGC  
AGTTGCCTCC TGGAGTCGTG TTCAGGGAAT TGGGATTCCT TTGGTAACTG CCATTGAAAT TGTCTCCATC TGGATCCTGT  
CCTTTATCCT GGCCATTCTT GAAGCGATTG GCTTCGTAT GGTACCTTTT GAATATAGGG GTGAACAGCA TAAACCTGT  
ATGCTCAATG CCACATCAAA ATTCATGGAG TTCTACCAAG ATGTAAAGGA CTGGTGGCTC TTCGGGTTCT ATTTCTGTAT  
GCCCTTGGTG TGCATGCGA TCTTCTACAC CCTCATGACT TGTGAGATGT TGAACAGAAG GAATGGCAGC TTGAGAATTG  
CCCTCAGTGA ACATCTTAAG CAGCGTCGAG AAGTGGCAAA AACAGTTTTC TGCTTGGTTG TAATTTTTCG TCTTTGCTGG  
TTCCCTCTTC ATTTAAGCCG TATATTGAAG AAAACTGTGT ATAACGAGAT GGACAAGAAC CGATGTGAAT TACTTAGTTT  
CTTACTGCTC ATGGATTACA TCGGTATTAA CTGGCAACC ATGAATTCAT GTATAAACCC CATAGCTCTG TATTTTGTGA  
GCAAGAAAT TAAAAATTGT TTCCAGTCAT GCCTCTGCTG CTGCTGTAC CAGTCCAAAA GTCTGATGAC CTCGGTCCCC  
ATGAACGGAA CAAGCATCCA GTGGAAGAAC CACGATCAAA ACAACCACAA CACAGACCG AGCAGCCATA AGGACAGCAT  
GAACTGACCA CCCTAGAAG CACTCCTCGG TACTCCATA ATCCTCTCGG AGAAAAAAT CACAAGGCAA CTGTAGTCC  
GGGAATCTCT TCTCTGATCC TTCTCCTTA ATTCATCCC ACACCAAGA AGAAATGCTT TCCAAAACCG CAAGGGTAGA  
CTGGTTTATC CACCCACAAC ATCTACGAAT CGTACTTCTT TAATTGATCT AATTACATA TTCTGCGTGT TGTATTGAGC  
ACTAAAAAAT GGTGGGAGCT GGGGGAGAAT GAAGACTGTT AAATGAAACC AGAAGGATAT TACTACTTT TGCATGAAAA  
TAGAGCTTTC AAGTACATGG CTAGCTTTTA TGGCAGTTCT GGTGAATGTT CAATGGGAAC TGGTACCAT GAAACTTTAG  
AGATTAACGA CAAGATTTTC TACTTTTTT AAGTGATTIT TTTGCTCTC AGCCAAACAC AATATGGGCT CAAGTCACTT  
TTATTGAAA TGTCAATTGG TGCCAGTATC CCGAATTC-3' (FRAG. NO: 2482) (SEQ ID NO: 2482)

5'-GAATTCGGGA AAAAGTGAAG GTGTAAGAGC AGCACAAGT CAATAAGAGA TATTTCTCA AATTTGCCTC  
AAGATGGAAG CCCTTGCCT CAGGGCATCC TTTGGCTGG CACTGGTTGG ATGTGTAAT AGTGATAATC CTGAGAGATA  
CAGCACAAT CTAAGCAATC ATGTGGATGA TTTCACCACT TTTCGTGGCA CAGAGCTCAG CTTCCTGGTT ACCACTATC  
AACCCACTAA TTGGTCTTA CCCAGCAATG GCTCAATGCA CAACTATTGC CCACAGCAGA CTAATAATTAC TTCAGCTTTC  
AAATACATTA AACTGTGTAT ATCTTGACT ATTTTCATCG TGGGAATGGT GGGGAATGCA ACTCTGCTCA GGATCATTTA  
CCAGAACAAA TGTATGAGGA ATGGCCCCAA CGCGCTGATA GCCAGTCTTG CCCTTGGAGA CTTATCTAT GTGGTCATTG  
ATCTCCCTAT CAATGTATTT AAGCTGCTGG CTGGGCGCTG GCCTTTTGAT CACAATGACT TTGGCGTATT TCTTTGCAAG  
CTGTTCCCTT TTTTGCAGAA GTCTCGGTG GGGATCACCG TCCTCAACCT CTGCGCTCTT AGTGTGACA GGTACAGAGC  
AGTTGCCTCC TGGAGTCGTG TTCAGGGAAT TGGGATTCCT TTGGTAACTG CCATTGAAAT TGTCTCCATC TGGATCTGT  
CCTTTATCCT GGCCATTCTT GAAGCGATTG GCTTCGTAT GGTACCTTTT GAATATAGGG GTGAACAGCA TAAACCTGT  
ATGCTCAATG CCACATCAAA ATTCATGGAG TTCTACCAAG ATGTAAAGGA CTGGTGGCTC TTCGGGTTCT ATTTCTGTAT  
GCCCTTGGTG TGCATGCGA TCTTCTACAC CCTCATGACT TGTGAGATGT TGAACAGAAG GAATGGCAGC TTGAGAATTG  
CCCTCAGTGA ACATCTTAAG CAGCGTCGAG AAGTGGCAAA AACAGTTTTC TGCTTGGTTG TAATTTTTCG TCTTTGCTGG  
TTCCCTCTTC ATTTAAGCCG TATATTGAAG AAAACTGTGT ATAACGAGAT GGACAAGAAC CGATGTGAAT TACTTAGTTT  
CTTACTGCTC ATGGATTACA TCGGTATTAA CTGGCAACC ATGAATTCAT GTATAAACCC CATAGCTCTG TATTTTGTGA  
GCAAGAAAT TAAAAATTGT TTCCAGTCAT GCCTCTGCTG CTGCTGTAC CAGTCCAAAA GTCTGATGAC CTCGGTCCCC  
ATGAACGGAA CAAGCATCCA GTGGAAGAAC CACGATCAAA ACAACCACAA CACAGACCG AGCAGCCATA AGGACAGCAT  
GAACTGACCA CCCTAGAAG CACTCCTCGG TACTCCATA ATCCTCTCGG AGAAAAAAT CACAAGGCAA CTGTAGTCC  
GGGAATCTCT TCTCTGATCC TTCTCCTTA ATTCATCCC ACACCAAGA AGAAATGCTT TCCAAAACCG CAAGGGTAGA  
CTGGTTTATC CACCCACAAC ATCTACGAAT CGTACTTCTT TAATTGATCT AATTACATA TTCTGCGTGT TGTATTGAGC  
ACTAAAAAAT GGTGGGAGCT GGGGGAGAAT GAAGACTGTT AAATGAAACC AGAAGGATAT TACTACTTT TGCATGAAAA  
TAGAGCTTTC AAGTACATGG CTAGCTTTTA TGGCAGTTCT GGTGAATGTT CAATGGGAAC TGGTACCAT GAAACTTTAG  
AGATTAACGA CAAGATTTTC TACTTTTTT AAGTGATTIT TTTGCTCTC AGCCAAACAC AATATGGGCT CAAGTCACTT  
TTATTGAAA TGTCAATTGG TGCCAGTATC CCGAATTC-3' (FRAG. NO: 2470) (SEQ ID NO: 2470)

5'-GCCACCATGG AAACCTTTG CCTCAGGGCA TCCTTTTGGC TGGCACTGGT TGGATGTGA ATCAGTGATA ATCCTGAGAG  
ATACAGACA AATCTAAGCA ATCATGTGGA TGATTTCACC ACTTTTCGTG GCACAGAGCT CAGCTTCTG GTTACCCTC  
ATCAACCCAC TAATTTGGTC CTACCCAGCA ATGGCTCAAT GCACAACATAT TGCCACAGC AGACTAAAAAT TACTTCAGCT  
TTCAAATACA TTAACACTGT GATATCTTG ACTATTTTCA TCGTGGGAAT GGTGGGGAAT GCAACTCTGC TCAGGATCAT  
TTACCAAGAA AAGTGTATGA GGAATGGCCC CAACGCGCTG ATAGCCAGTC TTGCCCTTGG AGACCTTATC TATGTGGTCA  
TTGATCTCCC TATCAATGTA TGGCTGGGCG CTGGCCTTTT ATGACAAATG ACTTTGGCGT ATTTCTTTGC AAGCTGTTCC  
CCTTTTGTGA GAAGTCTCTG GTGGGGATCA CCGTCTCAA CCTCTGCGCT CTTAGTGTG ACAGGTACAG AGCAGTTGCC  
TCCTGGAGTC GTGTCAGGG AATTGGGATT CCTTTGGTAA CTGCCATTGA AATTGCCTCC ATCTGGATCC TGTCTTTAT  
CCTGGCCATT CTGAAGCGA TTGGCTTCGT CATGGTACCC TTGAATATA GGGGTGGACA GCATAAAACC TGTATGCTCA  
ATGCCACATC AAAATTCATG GAGTTCTACC AAGATGTAAA GGAATGGTGG CTCTCGGGT TCTATTCTG TATGCCCTTG  
GTGTGCACTG CGATCTTCTA CACCCTCATG ACTGGTGAGA TGTGAACAG AAGGAATGGC AGCTTGAGAA TTGCCCTCAG  
TGAACATCTT AAGCAGCTC GAGAAGTGGC AAAAAAGTT TCTGTCTGG TTGTAATTTT TGCTCTTTCG TGGTTCCCTC  
TTCAATTAAG CGGTATATTG AAGAAAACTG TGTATAACGA GATGGACAG AACCAGTGTG AATTACTTAG TTCTTACTG  
CTCATGGATT ACATCGGTAT TAACTTGGCA ACCATGAATT CATGTATAAA CCCCATAGCT CTGTATTTTG TGAGCAAGAA  
ATTTAAAAAT TGTTCCAGT CATGCCCTG CTGCTGCTGT TACCAGTCCA AAAGTCTGAT GACCTCGGTC CCCATGAACG  
GAACAAGCAT CCAGTGAAG AACCACGATC AAAACAACCA CAACACAGAC CGGAGCAGCC ATAAGGACAG CATGAACGA  
CCACCCTTAG AAGCACTCT-3' (FRAG. NO: 2469) (SEQ ID NO: 2469)

**Substance P Antisense Nucleic Acids and Oligonucleotide Antisense Oligonucleotide Fragments**

5'-CTGCTGBGGC TTGGTCTCC GGGGCBTCT CTGCBGBBGB TGCTCBBGG GCTCCGGCBG TTCTCCTTG BTCTGGTCGCT  
GTCGTBCCBG TCGGBCCBG BTTCBGBTC BTCTTGGCT CCTBTCTT CTGCBBCBG CTGBGTGGBG BCBBGBBBB  
BGBCTGCCB GGCCBCBGG BTTCBGTG TGGTTTTC GBCGGBCBGT CCCGCGGGT GCTGAGTTT TCTGGTCTC  
CCGBGCCBC GTGTCGCTC CGCTTTCTC TGTTTCTCC GGTCCGCGG GGTGCTGTCT GGTGCTGTC GTGGCTGGG  
TCTCCGGGCG GTTCTCTCC TTTCCGC-3' (FRAG. NO:1877) (SEQ ID NO: 1888)



5'-CTCC GGGCGB-3' (FRAG. NO:1878) (SEQ ID NO: 1889)  
5'-GGCCBCGBGG-3' (FRAG. NO:1879) (SEQ ID NO: 1890)  
5'-GGGTCTCCGGGCG-3' (FRAG. NO:1880) (SEQ ID NO: 1891)  
5'-GGG TCTCCGGGCG G-3' (FRAG. NO:1881) (SEQ ID NO:1892)  
5'-CGTGGTCTCCGCG-3' (FRAG. NO:1355)(SEQ. ID NO:1365)  
5'-GTTTCTCTGTTCTCCG-3' (FRAG. NO:1356)(SEQ. ID NO:1366)  
5'-GTCCCGCGGGGTGCTG-3' (FRAG. NO:1357)(SEQ. ID NO:1367)  
5'-TCTGGTCTGCTGCTG-3' (FRAG. NO:1358)(SEQ. ID NO:1368)  
5'-GGCTTGGTCTCCGGGCG-3' (FRAG. NO:1359)(SEQ. ID NO:1369)  
5'-GTTTCTTCTTTTCCGCG-3' (FRAG. NO:1360)(SEQ. ID NO:1370)  
5'-CTGCTBGGC TTGGTCTCC GGGCBBTCT CTGCBGBBGB TGCTCBBGG GCTCCGGCBG TTCCTCCTTG BTCTGGTCTGCT  
GTCGTBCCBG TCGGBCCBG BTTCBGBTC BTCBTGGCT CCTBTCTT CTGCBBCBG CTGBGTGGBG BCBBGBBBB  
BGBCTGCCBB GGCCBCGBGG BTTCBTGT TGGTCTTGC GBCGBCBG CCCCGGGGT GCTGAGTTC TCTGTTCT  
CCGBGCGCB-3' (FRAG. NO:1882) (SEQ ID NO: 1893)

Substance P Receptor Nucleic Acids and Antisense Oligonucleotide Fragments

5'-GGGCTBBGT GBTCCBCBT BCTCCBCGT TGCCBCCBC BGBGGTCBC BCBBTGBCCG TGTBGGCBGC TGCCBBBGG  
BCBBTTTGCC BGGCTGGTG CBCGBBCTGB TTGGGTTCCG BGGTGTBGT GGBGTGTTT GGGGBBGGT CTBGTCCBC  
CGGBBGGBCG TBTCCBTTT CBBGCTBGG CGGTBBBCCC CTBCTBTCTG TBCBCBCCC CCTCTGCBG CBGBGTCTG  
TCGTGGGCC TGGGGCTCBG GTCCGGGC TAAGATGATC CACATCACTA CCAGTTGCC CACCACAGAG GTCACCACAA  
TGACCGTGA GGCAGCTGCC CAAAGGACAA TTTGCCAGGC TGGTGCACG AACTGATTGG GTTCCGAGGT GTTAGTGGAG  
ATGTTGGGG AGAGGTCTGA GTCCACCGG AGGACGTTAT CCATTTCAA GCTAGCGGT AAAGCCCTAC TATCTGTACA  
CAACCCCTT CTGACGAGA GTCTGTCTG GCGCCTGGG GCTCAGGGTC GTCTCTGTCG TGGCGCCTGG GGCTCTTCT  
TTGTGGGCTC TTTGGTGGCT GTGGCTGTGG TCTCTGTGTG TGCTGCCCTG GGTCTGGGGG TGTGGCCTG GGGCCGCTC  
CTGGCTCCTC CTCGTGGGCC CCC-3' (FRAG. NO:1883) (SEQ. ID NO:1894)  
5'-GGGBGGBCG-3' (FRAG. NO:1884) (SEQ. ID NO:1895)  
5'-GGGTC CG-3' (FRAG. NO:1885) (SEQ. ID NO:1896)  
5'-GGGCC CCC-3' (FRAG. NO:1886) (SEQ. ID NO:1897)  
5'-GTCCTGCTGGCGCCTGGGGCTC-3' (FRAG. NO:1361)(SEQ. ID NO:1371)  
5'-TTCTTTTGGGGCT-3' (FRAG. NO:1362)(SEQ. ID NO:1372)  
5'-CTTTGGTGGCTGTGGCTG-3' (FRAG. NO:1363)(SEQ. ID NO:1373)  
5'-TGGTCTGTGTTG-3' (FRAG. NO:1364)(SEQ. ID NO:1374)  
5'-CTGCCCTGGTCTGG-3' (FRAG. NO:1365)(SEQ. ID NO:1375)  
5'-GGGTGTGGCCTTGGGGCCGTCCTGCTCCTCCTGTTGGCCCCC (FRAG. NO:1366)(SEQ. ID NO:1376)  
5'-GGGCTAAGAT GATCCACATC ACTACCAGT TGCCACCAC AGAGGTCACC ACAATGACCG TGTAGGCAGC  
TGCCCAAAGG ACAATTGCC AGGCTGGTG CACGAAGTGA TTGGGTTCCG AGGTGTTAGT GGAGATGTTT GGGGAGAGGT  
CTGAGTCCAC CGGGAGGACG TTATCCATTTC GAAGCTAGGC GGTAAAGCCC TACTATCTGA CACAACCCCT  
CTCTGCAGCA GAGTCTGTC GTGGCGCTG GGGCTCAGGGTCC-3' (FRAG. NO:1367)(SEQ. ID NO:1377)  
5'-GGGCTBBGT GBTCCBCBT BCTCCBCGT TGCCBCCBC BGBGGTCBC BCBBTGBCCG TGTBGGCBGC TGCCBBBGG  
BCBBTTTGCC BGGCTGGTG CBCGBBCTGB TTGGGTTCCG BGGTGTBGT GGBGTGTTT GGGGBBGGTCT TGBGTCCBC  
GGGBGGBCGT TBTCCBTTT GBBGCTBGG GGTBBBCCCC TBCTBTCTGTB CBCBCCCCC CTCTGCBGB GBGTCTGTC  
GTGGCGCCTG GGGCTCBGGG TCC-3' (FRAG. NO:1368) (SEQ. ID NO:1378)

Chymase Antisense Nucleic Acids and Oligonucleotides Antisense Oligonucleotide Fragments

5'-GGBGCTGBTB CTGCBGATTT CBGBGGBBG BBCCCTGBTB CTCBCCGCT TCBGCTCTGG BGCBCBBBG BBBGBGCBG  
BGGGGGBBG GBBGBBGBG CBTCTCCCB GBGBGGCTGC CTGBGCBBT GCTGGTTTC CTTCCBGTCT TGGGTTTTB  
TBBCTCCCBG BBGGCBBG BGGGGCBGG CGTTTTCTT TCTCGCTGT TTTCTTTCC TGGCAGTGG TGGGGTGGG  
GGTGGGGTGG CTTCTTGT CTTGGGGGTG TCCTCTGTCT CTGGGCTTTT CTTCCCTTT CTTCTCTGTC TGTCTCTG  
GGGCTCTCT CTGTCTGT GTCTTGCC TGGCCCTCTT CCTCTCTG TCTCTGTCC CTGTGTTCC CGGCTCTCC  
CTCTCTGAC CTTCTTTCC TGGCTCTCT GGGGCTCTG CTGTTCTG CTCTCTGGT TGGGGTTTT TCTGTGTGTC

AGAAAGACAC AGTCATTACT CAGAGAATAA TAAACAGCCT GGCAGCACAT GAATGAATAG AAAAAAGATG TTACATGCAA  
AGCATGAAAT AACCAAATTC CATAACAGAT GTTAATCTGT AATGTGTTA GGAGAATTTA GAGGAAGTAT AAGATTATT  
CTTTCATCAA AAAAATTATA GCCAATGAGG ATATATCTAT CAATTATCCA TCAAGTGGTG ATATGGCAGC ACAAGGTA  
ACACAAAGGA ATAAAACCAA CGTTTATTAA GAACCAATCA TGTGGCATTT CACATTGAGC ATCATATTTA ATTCTGAAAA  
AAATCCTTGT ACTGTATCAT TCTTCATATT TTATGGATGC AGTAACTAAG GCTGAGAACT TAAAAATTTT TCCTAAGTTC  
AGACACATAG CTAAGTGGCA GAACCAAGAT TCAAACCTAC CCCATCTAAC TGCAGAGCAA ACTGCATGCC TTAAATGTCA  
AAGTGAATAC TAGCACAGTT AATACAATGT TTGGAAACTC AGAGAAGGAA TGATCCCTCT GCATTATAGT TACTAAGGAA  
TCATTGCCAT TATTTAAATG CCAGTGCTTC TACATCAGGC CCAAATTTTC TGTCTACTA ACTGTGAATC AAGACTTGAT  
TCAACCTCTA CTTGAGTATC TGCCGCAATG AGAAATCACT TACCTCCACT AACCAACAT TTATTTTATA ACAACAGATT  
GTTAGTAAGT CTTTCTTAT ACATACTCAA CAGCTGCTC CCAAGATGCT GTAGGATTAT GTCTAGAGTC AAACAGCCA  
GAAGCAATGT CCAAAATACA CCATAACACT GTGCAGCAA GGTCTACTA CCACTTGTTT GGCCCAACA TTCTAGGCAG  
CACTGGATAT CTGAATCATC AATTATTTCC ACAAACACTG ACCCTCTAC CAGTACCCT CACTAGAAGA ATTAATCCA  
CATGATAATA GCTCCCTCAT GTTACTCCCT TCTAAGTCAA ATTGTACACC CCTTATCTG ATTAACAGAG TCTAAGTCAC  
ATGACCTAAA TGCAAGAGAA CTGGGAATGG ACGTTTGTGG ATTCTACCTT AGTAAGGCAA AGTTATCATT GGGAAATCCT  
CTAATACAGG AAGGGTGTTC CAGAGACATT AAGGAGCCAT ATAAATGGAA AATGTCCACT ACAATCCATC ACTTGGTTGC  
CCCACATCAA CATTCACTCT TTTGCCACAC TTAAGTTTC CAAGAACAAA AATTATCCCA CTGAACATCA TCTTTACTAT  
CTTTTATATA AAGGAAAATT AGACTTGACT CAGCAGAACT GAAAGATGCT GTAGGATTAT GTCTAGAGTC AAACAGGATT  
GTACTGTGTC TCTAGGTGAT ACCTGCTCCA ACAATAGTTT GGTCACTTT TCAATTTGAT ATTCTAGT CTCCCACTT  
GATAACTGTA CCCTAAACCA TAAAGTTCAC TACCAACATG CTATATATAA AATAACCAA GGGGGAAGAA GAAAGAGAAA  
AAGGAAATCT CTAAAATAC ACAGGTATAC ATATGACAAA GCAAAGAAAG AAATGTGAGC AGATAGTGCA GTCCTCGTTT  
CTGAAATGG TCCCTGACT GGGGCTATAC CTATTCCATT TCCTACCCT CAGCCAGGCA GGTGGAGCAA AAACCTAAGT  
CTTGGTGGAT CTGAATCTTG ATGCTGTGGA GCTGTCTTAC TAGCCCAAGA CTACCTGCCT CTCATTTCT AATTATCA  
GTGAAGCAA ACAGCTTTGA TTTGTTTAA GCTCTGATT TTTGGTCTAA CTGATGTAAG ACCAAGGA CAAGAGTTCT  
CCAGCTCCG GTTCTCTTCT GTTCTGTTAA TGGTGAATG CCGAGAGAA GAGTTGCCAA CTTTGGCAA TAAAAATAC  
AGGATTCCAG TTAATTTCAA ATTTAGATAA ACAACAATTT TTAGTATTA GTGTGTCCA TTCAATATT GGACATACTT  
AACTAAAAA TGATTTGTTG TTCATCTGAA ATACAATTT AACTGGGCAT TCTGAATATT CTCTGGCAAC CCCCAGAGA  
GTGAAGAAAG TGGTACAAGG AACTTAAGA AGACCAGATT TGAAGAGACA TTACGGATGT GTTAAATGT CTTATTCTAG  
AGAGAGTTAG AGCTGTAGGT AGAATTTGGG AAATTAAGTT AAAAGCAGAC ACAGAGACCT GGCCAATATA TACTAAGGAG  
TGGACTACT TGGTCAAG CCCAACCCTA GACCAAGGCG ATAGTGAGAT GATTTGGGAA AGGCACCTAT ACACACTCA  
TCCCCTCTT TGAATAAAT GCCTTATAA TCTCAAGAG AATGACAGT CCACCATGTG GACTGCTTC TGTAAGTCCA  
GGGAAAAATAA AAGCTATGTG CTGAAACCC ACTTCTGATA TTATAAGGTG TGTGATCTT GTCATGTTAA TGGGTCTGAG  
TATCAATTCT ACAATTGTAA AGTGACAGTA ATGGTGTGTC CCCAGGTTGT TGTGGAAAGC TTGATTCTTA ATGCAACAGT  
AGGAAACCCC AGCCTCTCTG GAGCAAACAC CTTCTACAT CTTTACTTCC CTGACATTT GGCAGGACTC TATTCCTCTA  
TTTCTCTCTA GTGCTAGAGC AGAAAGGGAC CTTGATTTGA TATCAGGAAA ATCTATTTCT GAACCATAAG CTATGATAGC  
TGATTTAAAA AATTGACTAT CATGACATGA TAATGATCAT AATGGTAATA CATATTGATA GGGTGGCGT GAAAGTAATA  
ATATATCTAA GAGTTGTGAC AATATATGAT ACGCTAGAC TCTCAGAAA TGTCAATTCC AATCCCAATT GCTCTTGTGA  
TAAAGTTCTG TCCTAGGGTC GTTCTTTTC CCACATCTAC CCTCTTGGG TCTCTTCT GTCTTTTCA TGTGGTTCAG  
AGGAGGAGAG AGATCCAGGT CAATGTTTTT CAAATTACAA GGAATTATCA TTAAATGGG GAAGAAGCTC AAGTTTGTAC  
GTGTAGTGGG ATTTGAGTGG AGTGGAGTGG AATGGAACT AACAGGAAGA CACTGCACAT GGTAAAGATA AAGATTGTTT  
CCTGAAACCT TTAATTTGTG CTTACATACT CACACATACA TATGTGCATG CACTGGGACT CTGCAATATG CATTCTGAC  
TATGGAACAT AGCCATAAAA GTCTTTGCAC TGAACGTTCA GTGGGCCCTT CACAAGCTGC CTAATTTGGG AAAGAAAAAC  
ATGGTCCCTC CATTTCTCTG CCCCACCTCC AGAAAAGTCA CCATAGTTGA GGTACATCT GAGAAGCCAG CACTTGGGAG  
TTCAGGGCTC AAGTTCTTTT CTAGAAAAAC ACTGGGTGAT TCTAGGGGAA CTTCCGATCA GAAACAGCCA ATTCAGAGTG  
AGAGAGAAA ACGTGACCAT GCAGTTCCTG TGGTTACCAG CTTGCCCT CTCTGCTT CTGGGAGTTA TAAACCCAA  
GACTGGAAAG GAAACACAGC ATTTGCTCAG GCAGCCTCTC TGGGAAGATG CTGCTTCTC CTCTCCCCCT GCTGCTCTT  
CTCTGTGCT CCAGAGCTGA AGCTGGTGAG TATCAGGTTT CTTCCCTCTG AATCTGACAG TATCAGCTCC TGAAACAAAG  
ATGTTTAGTC TGAAATAGCT GACTCCTAAA CAGGGTTCCA AGATCTCTCT TCAAGAGTCC CACAGAGGAA ATTTCCACTT  
GGGATGTGTG CCACCCCAAC CCCACCCCA CCACTGCCA TTCTCTACAG CTTAGGACAC CCCCAGGAAC AAGGAATTTT  
ACCTCAATTG TAGAAAAGCC CAGAGCAAGT GGAAGGAAAA GGGGTATCCC CAGGAAAAA GACATGCTCT CTTAATCTT  
TGAGCATGAG GGCTACCAT TACTTTGTGA CTTTCTCAT CTGTGACCAT GCTCAAGAGC TATGGAGAAA TCTAAACAG  
GAACCTGGAC AGTGGGTCCT ACACAGAGAC AGAGGAGAGT GGGCCAGGGC AAGGTGGGAG TGGGAGAAAGT  
CTGAGATGAA AACATCAGAA TGGAGCAGAG GCAAGAATGA GATTTACCT GGGAGGTTAT GGGTGGGAA AGATACGAAA  
TACAGGAGAC AGGAGAGGGA AGATGGGCGG AACACAGGGT GAGAATGAGA TTCCAGGGAA GCCTAGCTCA GCTTTAACCC  
AATTTGTCCA TTCAATGGAG AGAGTATCTA TGGCCGTGTT CAAACCCTGG GGTGCTCTGT TCCAGGGGAG ATCATCGGGG  
GCACAGAATG CAAGCCACAT TCCCGCCCT ACATGGCTA CTTGGAATTT GTAACCTTCA ACGTCCCTC AAAATTTTGT  
GGTGGTTTCC TTATAAGAGC GAACCTTTGTG CTGACGGCTC CTTACTGTG AGGAAGGTGA GAAACAGGGT TCTATTATC  
TCCAAATGGG AGATGAACAA CCAGAGTAGC ATCCAGGAAT ACACCTGCAC TGGGGACTGA AGAGGGGGTC CTGGGTCTTG  
TCAACTTTCA GGAGAGGGAA GACTTTGGGC TGAAGAGACT TAGTCTGTGT TTGAATAGTT CCTTGAGCCT CAGTCACTGA  
GCTAAGCTCC CTTGGGAGGA AAAGGAGGTC CTGTCCGAAG GTCCCTCTTG TTGCAGTAGC ACCCTCACC CTTACCCAAC  
TCAAGACACA CGGCTCACTT TTCAGGGCCC CACCCAGTCT CAGGGCCACT TCCTCTATGG CTTTTCAG AACACTGGCT  
CTAGTTCTCA GGGTCTGAA CCCATCATT TATGGGAGCA GAGAACAGGT CTACATAAGA CCCCACCTT CCCGTTTAA  
CTGATATCTC CTGCTTCAGG GGCTGGCCCT CATGCAGGGT TCCCTGAATT AGGAAGTGTG AACCTGTCC CTTGAGTCT  
CCCTGGCCTG TTCAGTCCCC AGCAATTCCA GGGGTCTGAT AAATGTGTG TGTTCCTGA GAAAGCTCT TCAATGTTA  
AGCCTGAGCC CTCAAATGCC ACAAGTGGCC CATAAAAGG GAGATGGGTA GAGTCCGGCN ACCAGGTGAC AGAGTTTGT  
CCTCTTTCT CAGAATGAGC TCACCTCAGA AGAAACCCCA AGCCATCACT GTCGCTCTCT TTTCTTCTCT TCTCTCTAC  
AGCAGGTCTA TAACAGTCAC CTTGGAGCC CATAACATAA CAGAGGAAGA AGACACATGG CAGAAGCTTG AGGTTATAAA  
GCAATTCGT CATCCAAAT ATAACACTT TACTCTTAC CAGGATATCA TGTACTAAA GGTGACAACA CCTCTCTCT  
CCCTTTCAC TTCCCATCT CTAAGCTTCT TCCTCAGGT CCTCATGCC CTGAATTTT CTTAGGACTT GGCTATAACA  
TGAAGCTACT CACCCTGTCC CTCCTGATC ACCTCCAAC GTCCAGAGCC CATTTCGAGG ACTGACAGTC CTTCAATCCC

TTACAGTTG AAGGAGAAAG CCAGCCTGAC CTTGGCTGTG GGGACACTCC CTTTCCCAC ACAATTCAAC TTTGTCCCAC  
CTGGGAGAAT GTGCCGGTG GCTGGCTGGG GAAGAACAGG TGTGTTGAAG CCGGGCTCAG AACTCTGCA AGAGGTGAAG  
CTGAGACTCA TGGATCCCCA GGCCTGCAGC CACTTCAGAG ACTTTGACCA CAATCTTCAG CTGTGTGTGG GCAATCCCAG  
GAAGACAAAA TCTGCATTGA AGGTGATCCT CCACTAGGT TTCCTCTCCA AAACCTACTG TTCAGGGACC TGAATGCTCT  
TAGAAGGAGA TGGGGTCAGC AGGTGTGTCAG TCAGGTGACA GGGTGAGCAT CACAGGAATT GCTGTCTCTC CTGGGTCCAA  
GACAGCCTCT GACCATCCAT TCCAGTCTAC TGCCTGGGG GCATGGGGTG ACTGTGGAGA ATGTGGATGA CGGTCCCAAG  
AAAGGAAGAA GGGGCATCAG AACTAGATGT ATAAGTGAGG AGCTCCACCT CTTGGGTCTG ACTTTAGGTC TCACTGTGAC  
TCCAAGCTGG CTGGCAGACA GGAGTGGAGG ACTCCCGGG CTCACCTTCT TCTCTCTCTC CTCCCTTAC AGGGAGACTC  
TGGGGGCCCT CTCTGTGTG CTGGGGTGGC CCAGGGCAGC GTATCCTATG GACGGTCGGA TGCAAGCCCC CTTGTGTCT  
TCACCCGAAT CTCCATTAC CGGCCCTGGA TCAACCAGAT CTGCAGGCA AATTAATCCT GGATCTGAG CCAGCCTGAA  
GGGAAGCTGG AACTGGACCT TAGCAGCAAA GTGTGTGCAA CTCATTCTGG TTCTACCTT GGTTCCTCA GCCACAACCC  
TAAGCCTCCA AGAGGTCTCC TACAGTAAC AGAATTTC AATAACTTCA GTGAAGACAC AGCTTCTAGT CGTGAGTGTG  
TGTCCTCTC TGCTGTCTC TTCTCTGCA CATGTGACCT GATTCACAGC CCAAGCACA AGGA ATCATCGGGG  
GCACAGAATC CAAGCCACAT TCCCGCCCT ACATGGCCTA CTTGGAAATT GTAATTCCA ACGGTCCCTC AAAATTTGT  
GGTGGTTTCC TTATAAGACG GAACCTTTGT CTGACGGCTG CTCATTGTGC AGGAAGGTCT ATAACAGTCA CCGTTGGAGC  
CCATAACATA ACAGAGGAAG AAGACACATG GCAGAAGCTT GAGGTTATAA AGCAATTCCG TCATCCAAAA TATAACTT  
CTACTCTTCA CCACGATATC ATGTTACTAA AGTTGAAGGA GAAAGCCAGC CTGACCCTGG CTGTGGGGAC ACTCCCTTC  
CCATCACAAT TCAACTTTGT CCCACCTGGG AGAATGTGCC GGGTGGCTGG CTGGGGAAGA ACAGGTGTGT TGAAGCCGGG  
CTCAGACACT CTGCAAGAGG TGAAGCTGAG ACTCATGGAT CCCAGGCCT GCAGCCACTT CAGAGACTTT GACCACAATC  
TTCAGCTGTG TGTGGGCAAT CCCAGGAAGA CAAATCTGC ATTTAAGGA GACTCTGGG GCCCTCTTCT GTGTGTGGG  
GTGGCCCAAG GCATCGTATC CTATGGACGG TCGGATGCAA AGCCCTCTGC TGTCTTCAAC CGAATCTCCC ATTACCGGCC  
CTGGATCAAC CAGATCTCTG AGGCAAAATTA A-3' (FRAG. NO:1887) (SEQ. ID NO:1898)

5'-ATCATCGGGG GCACAGAATC CAAGCCACAT TCCCGCCCT ACATGGCCTA CTTGGAAATT GTAATTCCA ACGGTCCCTC  
AAAATTTGT GGTGGTTTCC TTATAAGACG GAACCTTTGT CTGACGGCTG CTCATTGTGC AGGAAGGTCT ATAACAGTCA  
CCCTTGGAGC CCATAACATA ACAGAGGAAG AAGACACATG GCAGAAGCTT GAGGTTATAA AGCAATTCCG TCATCCAAAA  
TATAACACTT CTACTCTTCA CCACGATATC ATGTTACTAA AGTTGAAGGA GAAAGCCAGC CTGACCCTGG CTGTGGGGAC  
ACTCCCTTC CCATCACAAT TCAACTTTGT CCCACCTGGG AGAATGTGCC GGGTGGCTGG CTGGGGAAGA ACAGGTGTGT  
TGAAGCCGGG CTCAGACACT CTGCAAGAGG TGAAGCTGAG ACTCATGGAT CCCAGGCCT GCAGCCACTT CAGAGACTTT  
GACCACAATC TTCAGCTGTG TGTGGGCAAT CCCAGGAAGA CAAATCTGC ATTTAAGGA GACTCTGGG GCCCTCTTCT  
GTGTGTGGG GTGGCCCAAG GCATCGTATC CTATGGACGG TCGGATGCAA AGCCCTCTGC TGTCTTCAAC CGAATCTCCC  
ATTACCGGCC CTGGATCAAC CAGATCTCTG AGGCAAAATTA A-3' (FRAG. NO:) (SEQ. ID NO:2467)

5'-TCCAGTTAA TACATAATCA ATATGCAATT TATTAATACA TCTCTCATG TCCACTCCCC CTGTATCTTG CCATTCTTGA  
CCTGCATTTC CATCTCTCTT ACCTTCCCTA GAGGCCAACT CATTTCTTT GAAAAACCTG GCATTTCCTA GAAAAAAG  
TGAAGGGCTG GGAGCTGTCC GTTGTCTCTG TTTGCTCTCT CTGCCCTTG TCCAAATGT GGTGGAAAG AAGCACTATT  
GAAAAATCCC TAAAGCCACC CTTGACGGGT TGTGCTTACC CTGATGCCAT GGACACATGC TGTGATACC ACTGCCTCA  
TGAGTCTCAC ATAATTGCC CTTCACACT ATCTACCCA TCAGCCTTAC CAAAACATA CTTGCATCCT GGGCAGCATC  
TGCCCTTCAA GAGACTAAGG AATCTCCTT CAACCAAGAA TGACTAGACC AATGAGACAC CCTTAAAGG CCCAGCACA  
TATAGAAATC CCACAATATG GTAATCCCAG TAAGGAGCTA TCAAGCCATT GCAGGACCAT CTAGAATACA ACTAGAGTAT  
AGTTCCTTTC AATCCAGGAA CTATACTTA ACAGCTTGGC TCACAGGAAC CAGAAGTGA GATGATGAGG ATCAGGGCTG  
AGCCTGTGAG CACCAGTCC ACCACTGACA CCAACCACAG ATTAACAAG CATCTTGTGG ACCCTGGGA TGGAAGAAT  
AGTTGTGGC TTATCAACCT CCCCCACAGC CCACACAGAA AAGATAAAAT CATCATGGT ACAGTGTAC AGAAGATGAT  
GACCAAGGA GTAGCCTGC CTGAGTGAAT GCTGAGATG ATAATGGAG CAGTAGCATC CAGCAGATA CAGCAGAAC  
CATCCACATA AAGAGCTTTG CCAAACTTA TGATAAAGG CACCCTCAGA GACTCTCCT ACTTTAATAT TAGCCATTG  
CAGAAATGGT GAGTGGAAAG AGAAATCTTA GGAAGAACC CTAAAAAAG CAAATGCTT TTAGGTTTG TGCTGAAGAG  
CCTGGAAGG AAATAAGGAC ACACACGCTG AGAATCTTC CTCTGCCCC AACACTGGGA TAATCTCAA GGATCTCTCC  
ATATCTCATT CTCTGGATA CACTGTCCAC TCAGAAATAT TGTGCAGAGT GCAGTAATC AAAAGTGAGC TATTGTGTTA  
GGAGTGAAGG CAAGAGTATC GTAAATATA TCAAAATTTGA AATGAATTCT CTAAATTTG TTTATAGATG TTTAATGTAA  
GCCAGCAGT ATTAACAGT AAACCTTAAA TTCGAGAAA ACTTGGTAT TCAGAACTA TAGAAACAGG CAGGACTTAT  
TGCGAGGGCA AACACAGAGT GAGCTCCAGC GTCTTCAAG AAAATCTGCC AGTGCCATGA AGGATGTACT CTGTCTGCTC  
CACTGCACTA CTGCTCAGTA TGAGCCCATG CCATCAGCTG TCCCTGACCC ACAGGAGTTC TTTAGAAGAG ACTGGTCAAC  
AAAAGTTCT AGGGTGTCTT ATACCTGCCA ACTCGAGGT TAAACAAGT TGCATAGAAA TGCTCAATCA AGAAAGACAC  
AGTCATTACT CAGAGAATAA TAAACAGCCT GGCAGCATAT GAATGAATAG AAAAAGATG TTACATGCAA AGCATGAAAT  
AACCAATTC CATAACAGAT GTTAATCTGT AATGTGTTA GGAGAATTA GAGGAAGTAT AAGATTTATT CTTTATCAA  
AAAAATTATA GCCAATGAGG ATATATCTAT CAATTATCCA TCAAGTGGT ATATGGCAGC ACAAGGTAAA ACACAAAGGA  
ATAAAACCA CGTTTATTA GAACCAATCA TTGGCATT CATCTGAGC ATCATATTTA ATTTGAAAA AAATCTTGT  
ACTGTATCAT TTTTATATTT TATGGATGC AGTAACTAAG CTGAGAACT TAAAAATTT TCTTAAGTGC AGACACATAG  
CTAAGTGGCA GAACCAAGAT TCAAACTCAC CCCATCTAAC TGCAGAGCAA ACTGCATGCC TTAATGTCA AAGTGAATAC  
TAGCAGAGTT AATACAATGT TTGGAACCTC AGAGAAGGAA TGATCCCTCT GCATTATAGT TACTAAGGAA TCATTGCCAT  
TATTTAAATG CCAGTGCTTC TACATCAGGC CCAAAATTTT TGTCTACTA ACTGTGAATC AAGACTGTAT TCAACCTCTA  
CTTGAGTATC TGCCGCAATG AGAAATCACT TACCTCACT AACACACAT TTATTTTATA ACAACAGATT GTTAGTAAAT  
CCTTTCTTAT ACATACTCAA CAGCTGCTTC CCAAGATGCT GTAGGATTAT GTCTAGAGTC AAAGTGGCA GAAGCAATGT  
CCAAAATACA CCATAACAT GTGCAGCAAA GGTCTACTA CCATTGTTT GGCCCAACA TTCTAGGCAG CACTGGATAT  
CTGAATCAT AATTATTTCC ACAAACACTG ACCCTCTAC CAGTACCCT CACTAGAAGA ATTAATCCA CATGATAATA  
GCTCCCTCT GTTACTCCCT TCTAAGTCAA ATTGTACCC CTTTATCTG ATTAACAGAG TTAAGTCTAC ATGACATAA  
TGCAAGAGAA CTGGGAATGG ACGTTTGTGG ATTCTACCTT AGTAAGGCAA AGTTATCATT GGAATTCCT CTAATACAGG  
AAGGGTGTTC CAGAGACATT AAGGAGCCAT ATAAATGGAA AATGTCCACT ACAATCCATC ACTTGGTTGC CCCACATCAA  
CATTCATTCT TTTGCCACAC TTAAGTTTC CAAGAACAAA AATTATCCCA CTGAACATAA TCTTACTAT CTTTATATA  
AAGGAAATTT AGACTTGAAT CAGCAGAACT GAAATAACCC AGCTCTAACA GTTACTGCTT TTAACCTCAA GTACTGTGC  
TCTAGGTGAT ACCTGTCCA ACAATAGTTT GGTACATTT TCAATTTGAT ATTCTTAGT CTCCCACTT GATAACTGTA

CCCTAAACCA TAAAGTTCAC TACCAACATG CTATATATAA AATAACCAAA GGGGGAAGAA GAAAGAGAAA AAGGAAATCT  
CTTAAATAC ACAGGTATAC ATATGACAAA GCAAAGAAAG AAATGTGAGC AGATAGTGCA GTCCTCGTTT CTGAAATGGG  
TCCCCTGACT GGGGCTATAC CTATTCCATT TCCTCACCCT CAGCCAGGCA GGTGGAGCAA AAACCTAAGT CTGGTGGAT  
CTGAATCTTG ATGCTGTGGA GCTGTCTTAC TAGCCCCAGA CTACCTGCCT CTCAATTTCT AATTATATCA GTGAAAGCAA  
ACAGCTTTGA TTTGTTTAAG CCTCTGATT TTTGGTCTAA CTGATGTAAG ACCACAAGGA CAAGAGTTCT CCAGCTCCGG  
ATTCTCTTCT GTTCTGTAA TGGTGAAATG CCCGAGAGAA GAGTGGCCAA CTTTGGCAAA TAAAAATAC AGGATTCCAG  
TTAAATTCAA ATTTAGATAA ACAACAATT TTTAGTATTA GTGTGTCCCA TTCAATATT GGACATACTT AACTAAAAAA  
TGATTTGTG TTCATCTGAA ATACAAATTT AACTGGGCAT TCTGAATATT CTCTGCAAC CCCCAGAGA GTGAAGAAAG  
TGGTACAAGG AACTTAAGA AGACCAGATT TGAAGAGACA TTACGGATGT GTTAAATGT CTATTCTAG AGAGAGTTAG  
AGCTGATGGT AGAAGTTGGG AAATTAAGTT AAAAGCAGAC ACAGAGACCT GGCCAATATA TACTAAGGAG TGGATCACT  
TGCTCACAAG CCCAACCTGA GACCAAGGGC ATAGTGAGAT GATTGGGAA AGGCACTTAT ACTACTCA TCCCCGCTCT  
TGAATAAAT GCCTATAAA TCTCAAGAG AAATGACAGT CCACCATGTG GACTGCTTTC TGTAAGTCCA GGGAAATAA  
AAGCTATGTG CTGAAACCC ACTTCTGATA TTATAAGGTG TGTGATCTT GTCATGTAA TGGGTCTGAG TATCAATTCT  
ACAATTGTAA AGTGACAGTA ATGGTGTGTC CCCAGGTTGT TGTGGAAGC TTGATTCTTA ATGCAACAGT AGGAAACCCC  
AGCCTCTCTG GAGCAACAC CTTCTACAT CTTTACTTCC CCGCACATT GGCAGGACTC TATTCCTCTA TTCTCTCTA  
GTGCTAGAGC AGAAGGGGAC CTGATTGTA TATCAGGAAA ATCTATTCT GAACCATAAG CTATGATAGC TGATTTAAAA  
AATTGACTAT CATGACATGA TAATGATCAT AATGGTAATA CATATTGATA GGGTTGCCGT GAAAGTAATA ATATATCTAA  
GAGTTGTGAC AATATATGAT ACGCCTAGAC TCTCAGAAAA TGCTAATTCC AATCCCAATT GCTCTTTGCA TAAAGTTCTG  
TCCTAGGGTC TGTCTTTT CCACATCTAC CCTCCTTGA TCTCTTCT GTCTTTTCA TGTGGTTCAG AGGAGGAGAG  
AGATCCAGGT CAATGTTTT CAAATTACAA GGAATTATCA TTAAATGGG GAAGAAGCTC AAGTTTGTAC GTGTAGTGGA  
ATTGGAGTGG AGTGGAGTGG AATGGAACT AACAGGAAGA CACTGCACAT GGTTAAGATA AAGATTGTTT CCTGAAACCT  
TTAATTTGTG CTACATACT CACACATACA TATGTGCATG CACTGGGACT CTGCAATATG CATTCTGAC TATGGAACAT  
AGCCATAAAA GTCTTGTGAC TGAACGTTA GTGGGCTTT CACTAGCTGC CCTAATTGGG AAAGAAAAAC ATGGTCCCTC  
CATTTCTGTC CCCCACTCC AGAAAAGTCA CCATAGTTGA GGGTACATCT GAGAAGCCAG CACTGGGAG TTCAGGGCTC  
AAGTTCTTT CTAGAAAAAC ACTGGGTGAT TCTAGGGGAA CTCCGATCA GAAACAGCCA ATTCAGAGTG AGAGAAGAAA  
ACGTGACCAT GCAGTTCCTG TGGTTACCAG CCTTGGCCCT CTCTGCCTT CTGGGAGTTA TAAACCCAA GACTGGAAAG  
GAAACCAGC ATTTGCTCAG GCAGCCTCTC TGGGAAGATG CTGCTCTTC CTCTCCCCT GCTGCTCTT CTCTGTGCT  
CCAGAGCTGA AGCTGGTGAG TATCAGGGT CTCCCTCTG AAATCTGCAG TATCAGCTCC TGAACAAAAG ATGTTTAGTC  
TGAAATAGCT GACTCTAAA CAGGGTTCCA AGATCTCTCT TCAAGAGTCC CACAGAGGAA ATTTCCACTT GGGATGTGTG  
CCACCCACAT CCCACCCCA CCCACTGCCA TTCTTACAG CCTAGGACAC CCCAGGAA AAGGAATTC ACCTCAATTG  
TAGAAAAGCC CAGAGCAAGT GGAAGGAAAA GGGGTATCCC CAGGAAAAACA GACATGTCCT GTTAATCTTC TGAGCATCAG  
GGCTACCCAT TACTTTGTGA CTTTCTACT CTGTGACCAT GCTCAAGAGC TATGGAGAAA TCTAAACAG GAACCTGGAC  
AGTGGGCTCT ACACAGAGAC AGAGGAGAGT GGGCCAGGGC AAGGTGGGAG TGGGAGAAGT CTGAGATGAA  
AACATCAGAA TGGAGCAGAG GCAAGAATGA GATTTCACCT GGGAGGTTAT GGGTGGGGAA AGATACGAAA TACAGGAGAC  
AGGAGAGGGA AGATGGGCGG AACACAGGGT GAGAATGAGA TTCCAGGGAA GCCTAGCTCA GCTTTAACCC AATTTGTCCA  
TTAATTTGAG AGATATCTA TGGCCGTGT CAAACCTGG GGTGCTCTGT TCCAGGGGAG ATCATCGGGG GCACAGTAATG  
CAAGCCACAT TCCCGCCCT ACATGGCTA CTTGGAATT GTAACCTTCCA ACGTCCCTC AAAATTTGT GGTGGTTTCC  
TTATAAGACG GAACTTTGTG CTGACGGCTG CTCATTGTG AGGAAGGTGA GACAACAGGG TCTATTTATC TCCAAATGGG  
AGATGAACAA CCAGAGTAGC ATCCAGGAAT ACACCTGCAC TGGGGACTGA AGAGGGGGTC CTGGGTCTTG TCAACTTTCA  
GGAGAGGGAA GACTTTGGG TGAAGACTT TAGTCTGTG TTGAATAGT CTTGAGCCT CAGTACTGA GCTAAGCTCC  
CTTCGGAGGA AAAGGAGGTC CTGTCCGAAG GTCCCTCTTG TTGCAGTAGC ACCCTCACC CCTACCCAAC TCAAGACACA  
CGGCTCACTT TTCAGGGCCC CACCCAGTCT CAGGGCCACT TCCTCTATGG CTTTTCAG AACACTGGCT CTAGTTCTCA  
GGTCTCTGAA CCCATCATTT TATGGGAGCA GAGAAGAGT CTACATAAG CCCCCTTTT CCCGTTTTAA CTGATATCTC  
CTGCTTCAGG GGCTGGCCCT CATGCAGGT TCCTGCAATT AGGAAGTGTG AACCTGTCC CTGAGTCTCT CCCTGGCCTG  
TTCAGTCCC AGCAATTCCA GGGGTCTGAG AAATTGTGTC GTTTCTCTGA GAAAGCTCT TCATGAGTTA AGCCTGAGCC  
CTCAAATGCC ACAAGTGGC CATGAAAAGG GAGATGGGT GAGTCCGGC ACCCAGTGAC AGAGTTAGT CCTCTTTCT  
CAGAATGAGC TCACCTCAGA AGAAACCCCA AGCCATCACT GTCGCTCTT TTTCTTCTCT TCTCTCTAC AGCAGGTCTA  
TAACAGTCAC CTTGGAGCC CATAACATAA CAGAGGAAGA AGACACATGG CAGAAGCTTG AGGTATATAA GCAATTCCGT  
CATCCAAAAT ATAACACTT TACTCTTAC CACGATATCA TGTTACTAAA GGTGACAACA CCTCTCTCT CCCTTTCCAC  
TTCCATTTCT CTAAGCTTC TCCTCAGGT CTTCTAGGCT CTGAATTTT CTAGGACTT GGCTATAACA TGAAGTACT  
CACCTGTCC CTCCTGATC ACCTCCAAT GTCCAGGACC CATTCGAGG ACTGACAGTC CTTCACTCCC TTCACAGTTG  
AAGGAGAAAG CCAGCTGAC CTGGCTGTG GGGACACTCC CCTTCCATC ACAATTCAAC TTTGTCCCAC CTGGGAGAAT  
GTGCCGGGTG GCTGGCTGGG GAAGAACAGG TGTGTTGAAG CCGGGCTCAG AACTCTGCA AGAGGTGAAG CTGAGACTCA  
TGGATCCCCA GGCTGCAGC CACTTCAGAG ACTTTGACCA CAATCTTCAG CTGTGTGTGG GCAATCCAG GAAGACAAA  
TCTGCATTA AGGTGATCCT CCAACTAGGT TTCTCTCCA AAATCACTG TTCAGGGACC TGAATGCTCT TAGAAGGAGA  
TGGGGTCAGC AGTTGTCTAG TCAGGTGACA GGGTGAGCAT CACAGGAATT GCTGTCTCTC CGTGGTCCA GACAGCCTCT  
GACCATCAT TCCAGTCTAC TGCACTGGG GCATGGGGT ACTGTGGAGA ATGTGGATGA CGGTCCCAAG AAAGGAAGAA  
GGGGCATCAG AACTAGATGT ATAAGTGAG AGTCCACCT CTGGGTCTG ACTTTAGGTC TACTGTGAC TCCAAGTGG  
CTGGCAGACA GGAGTGGAGG ACTTCCGGG CTCACCTCT TCTCTCTCT CTCCCCCTAC AGGGAGACTC TGGGGGCCCT  
CTTCTGTGTG CTGGGGTGGC CCAGGGCATC GTATCCTATG GACGGTCCGA TGCAAGGCC CCTGTGTCT TCACCCGAAT  
CTCCATTAC CGGCCCTGGA TCAACAGAT CTGACAGGCA AATTAATCCT GGATCCTGAG CCAGCCTGAA GGAAGCTGG  
AACTGGACCT TAGCAGCAAA GTGTGTGCAA CTCATTCTGG TTCTACCTT GGTTCCTCA GCCACAACCC TAAGCCTCCA  
AGAGGTCTCC TACAGGTAAC AGAATTTCA ATAACTTCA GTGAAGACAC AGCTTCTAGT CGTGAGTGTG TGTCCTCTC  
TGCTGCTCTC TTCTCTGCA CATGTGACCT GATTCCAGC CCAAGCACCA AGGA-3' (FRAG. NO:) (SEQ. ID NO:2467)

5'-GGBGCBBCB-3' (FRAG. NO:1888) (SEQ. ID NO:1899)

5'-GGBGCBGC-3' (FRAG. NO:1889) (SEQ. ID NO:1900)

5'-GGGGCBGG CG-3' (FRAG. NO:1890) (SEQ. ID NO:1901)

5'-CGTTTTCTTCTCTC-3' (FRAG. NO:1369) (SEQ. ID NO:1379)

5'-GCTGTTTTCTTTCC-3' (FRAG. NO:1370) (SEQ. ID NO:1380)

5'-TGGCAGTGGGTGGGGGTGGGGGTGGGGTGGC-3' (FRAG. NO:1371)(SEQ. ID NO:1381)  
5'-TTCCTTGTTCCTGGGGGTGTCCT-3' (FRAG. NO:1372)(SEQ. ID NO:1382)  
5'-CTTGCTCTGGGCTTTTCT-3' (FRAG. NO:1373)(SEQ. ID NO:1383)  
5'-CCCCCTTTCTCC-3' (FRAG. NO:1374)(SEQ. ID NO:1384)  
5'-TGCTCTGTTTCTCTGGGG-3' (FRAG. NO:1375)(SEQ. ID NO:1385)  
5'-CTCTCTCTGTCTCTGTGT-3' (FRAG. NO:1376)(SEQ. ID NO:1386)  
5'-CCTTGGCCCTGGCCC-3' (FRAG. NO:1377)(SEQ. ID NO:1387)  
5'-TCTTCCCTCTCTGTCTCCTGT-3' (FRAG. NO:1378)(SEQ. ID NO:1388)  
5'-CCCTGTGTTCCGCCC-3' (FRAG. NO:1379)(SEQ. ID NO:1389)  
5'-GTCTTCCCTCTCTG-3' (FRAG. NO:1380)(SEQ. ID NO:1390)  
5'-ACCTCCTTTCTCTCCG-3' (FRAG. NO:1381)(SEQ. ID NO:1391)  
5'-CTGGGTGGGGCCCTG-3' (FRAG. NO:1382)(SEQ. ID NO:1392)  
5'-CCTGTCTCTGCTCCC-3' (FRAG. NO:1383)(SEQ. ID NO:1393)  
5'-TGGCTTGGGGTTTCTTCTG-3' (FRAG. NO:1384)(SEQ. ID NO:1394)  
5'-TGTGTCTTCTCTCTGT-3' (FRAG. NO:1385)(SEQ. ID NO:1395)  
5'-GGCTGGCTTCTCCTTC-3' (FRAG. NO:1386)(SEQ. ID NO:1396)  
5'-TTTTGTCTCTGGG-3' (FRAG. NO:1387)(SEQ. ID NO:1397)  
5'-TGCCCCCTTCTCTTCTGGG-3' (FRAG. NO:1388)(SEQ. ID NO:1398)  
5'-TCCTTGGTGCTGGGCTGGG-3' (FRAG. NO:1389)(SEQ. ID NO:1399)  
5'-GGBGCTGBTB CTGCBGATTT CBGBGGBBG BBCCCTGBTB CTCBCCBGCT TCBGCTCTGG BGCBCBBGBG BBBGBGCBGC  
BGGGGGBGBG GBBGBBGBG CBTCTCCCB GBBGGGCTGC CTGBGCBBBT GCTGGTTTTC CTTCCBGTG TTGGGTTTTB  
TBBCTCCCBG BBGGCBGBG BGGGCBGBG-3' (FRAG. NO:1891) (SEQ. ID NO:1902)

**Endothelial Nitric Oxide Synthase Nucleic Acids and Antisense Oligonucleotide Fragments**

5'-GCGTCTTGGG GTGCBGGGCC CBTCTGCTG CGCTGGGCG CTGCTGTGCG TCCGCTGCT GGGGGGCCGG GGTGGCTGGG  
CCCTGCTTGC CGCACGACCC CGGCGCGACC CGAGGCTCG GGGGCTGTGT TCTGGCGCTG GTGGGCTTGG GCCCTCTGG  
GGGCTGGGT TCCTGCTGCG CCTGGGCGCT GCGCTCTTG GGTGCGGGCC CGGGGGCCG GGGGGCCGCT GTTCTGGGG  
CTGGGGGTGC CTGTGGCTGC CGGTGCCCC GGTGGTGGC GCGCTCTGC TGCCGTCGT TGGCTGGGTG CCCCCCCCC  
TTCTCTGGG TCCGCTGGG GTGCTCCGT TCCTCGTGC GCTGCTGCT TGTCTTCCG GCGGTGGCG CGTGTGGTC  
CGCCCCCTT GGCCTTCTG TCGGGGTCT GCTGTTGCC GGTGCCCTG GCGGCGGTCT TCTCTGCTT GGCTCTGGG  
CCGGCCGGTC TCGGGCGTCT CGTGTTCGCT CTGTGCTGT TCGGGCCGCT CCTTCTCTT CCGCCGCCGC CGTCCCCCG  
CCGCTCTGC CCCTGGCCCC GCCTCTCTT GCGCGTGTG TCGGGCGGG GCCTTGGCG TCCGTTTGGG GCTGCTCTG  
GCGCTTCCG CCCTCGGCT GGGCGCTCT TCCGCGTGT TGGGTGGCC CTGCTGGGC CCTCTGGC TCCGGTGTCT  
TGTGTGTCG CGGCTGGTGG CCGGGCCGCT TGGGCGGGCG GGGGCGCCG CGGGTCTCT GGGTGCCTT TCTCCGCCG  
GGGTCCCGG CTCTGCTGT TCCCTGGGT CTCTGCTCT TCTCTGGGT GGGTGTGGG TGCCGGGGT TCCGGGCTT  
CCCCCGCTG CTGGGCGTTC TGCGGTCTT GGGTGTCTG TGGCCCCGT CGTGTGCGCC TCCGTGCGCC GTCGCCGGC  
TCGTCCCCC CTGGGTGCG GCGGGGCTG TCCTGGCGT TTGCTCTTC CTGGGCGTCT TGGGTGCBG GCGCCCTCT  
GCTGCGCTG GCGCTGCTG TGCTCCGTG TGCTGGGGG CCGGGGTGG TGGGCGCTG TTGCCGACG ACCCGGGGC  
GACCCGAGC TCGGGGGGCT GTGTCTGGC GCTGGTGGC TTGGGCCCC CTGGGGGCTG GGTTCCTGC TGCGCTGGG  
CGCTGGGCTG TTGGGTGGC GGGCCGGGG GCGGGGGGG CGCTGTCTG GGGCTGGGG GTGCTGTGG CTGCCGTTG  
CCCCGGTTG TGGCGCGTC CTGCTGCCG TCGTTGGCTG GGTCCCCCG CCCGTTTCT GGGGTCCGC TGGGTGCTC  
CGGTCTCTG TGCCGTGCT GCCTGTCTT TCCGCGGTG GCGCGTGGT GGTCCGCCC CCTGGCCTT CTGCTCGGG  
TCTGGCTGT TGCGCGGCT GTCTCTTCC TCTTCTTCC TGTGCTCTG GGGCCCGCC GGTCTCGGC GTCTCGTGT  
CGCTCTGTG CTGTCCGGC CGCTCTTCC TCTTCCGCG CCGCGCTCC CCGCCGCTC GTCGCCCTG CCGGCTCTC  
TCCTGGCGG TGTCTCGGC GCGGCTTTC GCGTCCGT TGGGGCTGC TCTGGCGCT CCGGCTCTG GCCTGGGCG  
TCTTCTCGC CTGTGCTGT GCGCTCTG GCGGCTCTT GCGCTCCGT GTCTGTGGT CCGGCGCTG GTGGCGGGC  
CGGTGGGGG GCGTGGGGC CCGGCGGTC CTCGGGCTG CCTTCTCCG CCGGGGTTC CGGCTCTG CTGTTCCCTG  
GGCTCTTCT CTTCTCTCT GGGTGGGTG TGGGTGCCG GGTCTCCGG CTGCCCCG GCTGCTGGG GTTCTGCGGT  
CTTGGGGTTG TGTGTGGCC CGCTCGTGT GCGCTCCGT CCGGCTGCC GCGCTCGTC CCTCTGGGT GCGCGCGGG  
CTGGTCTTG CGTTTGTCT CTTCTGG-3' (FRAG. NO:1892) (SEQ. ID NO: 1903)  
5'-GCGGGGCCG-3' (FRAG. NO:1893) (SEQ. ID NO: 1904)  
5'-CGGGGGCG-3' (FRAG. NO:1894) (SEQ. ID NO: 1905)  
5'-GCGCGGGCGG-3' (FRAG. NO:1895) (SEQ. ID NO: 1906)  
5'-CTGTGCGTCCGTCTGCTGG (FRAG. NO:1390)(SEQ. ID NO:1400)  
GGGGCCGGGGTGGCTGGGCCCTGCTTGCCG (FRAG. NO:1391)(SEQ. ID NO:1401)  
ACGACCCCGGGCCGACCCGAG (FRAG. NO:1392)(SEQ. ID NO:1402)  
GCTCGGGGGCTGTGTTCTGGCGCTGGTGGG (FRAG. NO:1393)(SEQ. ID NO:1403)  
CTTGGGCCCCCTGGGGGGCTGGGT (FRAG. NO:1394)(SEQ. ID NO:1404)  
TCCTGCTGCGCTGGGCGCTG (FRAG. NO:1395)(SEQ. ID NO:1405)  
GCGTCTTGGGGTGC (FRAG. NO:1396)(SEQ. ID NO:1406)  
GGGGCCGGGGGCGGGGG (FRAG. NO:1397)(SEQ. ID NO:1407)  
GCGGCTGTTCTGGGCGCTGGG (FRAG. NO:1398)(SEQ. ID NO:1408)  
GGTGCCTGTGGCTGCC (FRAG. NO:1399)(SEQ. ID NO:1409)  
GGTGGCCCCGTTGGTGGC (FRAG. NO:1400)(SEQ. ID NO:1410)  
GCGTCTGCTGCGGGT (FRAG. NO:1401)(SEQ. ID NO:1411)  
CGTTGGCTGGGTCCCCCGC (FRAG. NO:1402)(SEQ. ID NO:1412)  
CCGTTTCTGGGGTCC (FRAG. NO:1403)(SEQ. ID NO:1413)  
GCGTGGGGTGTCC (FRAG. NO:1404)(SEQ. ID NO:1414)  
GGTCTCTGTCGGC (FRAG. NO:1405)(SEQ. ID NO:1415)  
CTGCTCTGCTGCTGGG (FRAG. NO:1406)(SEQ. ID NO:1416)

GGCCGTGGCGGCGTGGTGGTCC (FRAG. NO:1407)(SEQ. ID NO:1417)  
GCCCCCCTGGCCTTCTGCTC (FRAG. NO:1408)(SEQ. ID NO:1418)  
GGGGTCTGGCTGGT (FRAG. NO:1409)(SEQ. ID NO:1419)  
TGCCGGTGCCCTTGGCGGC (FRAG. NO:1410)(SEQ. ID NO:1420)  
GGTCTTCTCCTGGTG (FRAG. NO:1411)(SEQ. ID NO:1421)  
GCTCTGGGCGCGCGGTCTCGG (FRAG. NO:1412)(SEQ. ID NO:1422)  
GCGTCTCGTGTTCG (FRAG. NO:1413)(SEQ. ID NO:1423)  
CTCTTGCTGTTCGGCCG (FRAG. NO:1414)(SEQ. ID NO:1424)  
CTCCTTCTCTCCGCCGCC (FRAG. NO:1415)(SEQ. ID NO:1425)  
GCCGCTCCCCGCC (FRAG. NO:1416)(SEQ. ID NO:1426)  
GCTCGTCGCCCTGGCCC (FRAG. NO:1417)(SEQ. ID NO:1427)  
GGCCTCTCTGGCCGC (FRAG. NO:1418)(SEQ. ID NO:1428)  
TGTCGCGGCGCGCGCCTTGGC (FRAG. NO:1419)(SEQ. ID NO:1429)  
GCTCCGTTGGGGCTG (FRAG. NO:1420)(SEQ. ID NO:1430)  
CCTCTGGCGCTTCC (FRAG. NO:1421)(SEQ. ID NO:1431)  
GGCCCTCGGCCTGGCGCTC (FRAG. NO:1422)(SEQ. ID NO:1432)  
TCTTCCGCTGTGC (FRAG. NO:1423)(SEQ. ID NO:1433)  
TGGTGGCCCTCGTGG (FRAG. NO:1424)(SEQ. ID NO:1434)  
GCCCTCCTGGCCTCCGGTGTCC (FRAG. NO:1425)(SEQ. ID NO:1435)  
TGTCGTCCCCCGCTGGT (FRAG. NO:1426)(SEQ. ID NO:1436)  
GGCCGGGCGGTTGGGCGGGC (FRAG. NO:1427)(SEQ. ID NO:1437)  
GTGGGCGCGGCGGGTCTCC (FRAG. NO:1428)(SEQ. ID NO:1438)  
GGGCTGCCCTTCTCC (FRAG. NO:1429)(SEQ. ID NO:1439)  
GCCGGGGTCCCGC (FRAG. NO:1430)(SEQ. ID NO:1440)  
GCTCCTGCTGTCCCTGGGCTCTTCTGCC (FRAG. NO:1431)(SEQ. ID NO:1441)  
TCTCTCTGGGTGGGTGCTGGGTGCCG (FRAG. NO:1432)(SEQ. ID NO:1442)  
GGGTCTCGGGGCTTG (FRAG. NO:1433)(SEQ. ID NO:1443)  
CCCCGCGCTGTGGGCGTTCTGC (FRAG. NO:1434)(SEQ. ID NO:1444)  
GGTCTTGGGGTTGTC (FRAG. NO:1435)(SEQ. ID NO:1445)  
TGTGCCCCGCTCG (FRAG. NO:1436)(SEQ. ID NO:1446)  
TGTCGCCCTCCGTCGCC (FRAG. NO:1437)(SEQ. ID NO:1447)  
CGTCGCGGCGCTCGTCC (FRAG. NO:1438)(SEQ. ID NO:1448)  
CCTCTGGGTGCCG (FRAG. NO:1439)(SEQ. ID NO:1449)  
GGCGGGCTGGTCTC (FRAG. NO:1440)(SEQ. ID NO:1450)  
GGCGTTTGTCTCTTCTGG (FRAG. NO:1441)(SEQ. ID NO:1451)  
5'-GCGTCTTGGGGTGCBGGGCCBCTCTGCTGCGCCTGGGCGCTG-3' (FRAG. NO:1896) (SEQ. ID NO: 1907)

**Inducible Nitric Oxide Synthase Nucleic Acids and Antisense Oligonucleotide Fragments**

5'-CTGCCCCBGT TTTTGTCTT CBCBTGCCGT GGGGBGBCB BTGGCTGCCT CCCCAGGGTT TCTGCTGCTT GCTGCTTCTT  
TCCCGTCTCC CTTCTTCCC GTCTCCTTTT TGCTCTTTG GGTTCTGTT GTTTCTGGCC TGCTTGGTGG CGGCTTGTGC  
GTTCTCTCTC TCTTCTTTG GGTCTCCGT TCTCTCTCTG CTTTCTCTG TCTCTGTCG CCGTTCCTC CTCCGGCGTC  
CTCTGCCCT GTGCTGTTG CTEGGGTGG TCGGGTCCC GGTGCTCCC CGGCGGGCG GCTGGTTGCC TGGGCTGTG  
TGGTGGGGTG TGGGCGCGT GGGTTGGGG TGTGGTGGC TCTTCTGTG CTTGTGGGC TGTGGTGTG TCTGTGGCG  
TGTGCTGGT CTTGGGGCT CTTCCCTGT GCTGGGTGG GCCTCCCCG CCCCCTCTG GGCCGGTGG CTGGCTCCT  
GTGGGCGCT CTGGCTCTG CCCTGTCTT CTTCGCTCG TGCTGCTGG GCTGC CATATGTATG GGAATACTGT  
ATTTCAGGCA TTATAAGGAA TGAATTATA GGCCGGGCAT TGTGGCTAAC CCTTGTATC CTAGCACTTT  
GAGAGGCTGA AGTGGGCAGA TCACTTGAGC TTCAGAGTTC GAGACCAGCA TGGACAACAT GGTGAAACCC  
AGTCTCTACC AAAACACAA AAATATTAGC TGGGTGTGGT GGTGCATGCC TGTAGTCCCA GCTACTCAGG  
AGGCTGAGGT GGGAGGATCG CTTGAGCCTG GGAGGCAGAA GTTGCAATGA GCAGAGATCG TGCCACTCCG  
CTCCAGTCTT GGTGACAGAA TGAGACTCCA TCTCAAAAT AAATAAATAA ATAAATAAAA TAAATGAAAT  
GAAATTATAA GAAATTACCA CTTTTTCATG TAAGAAGTGA TCATTTCAT TATAAGGGAA GGAATTTAAT  
CCTACCTGCC ATTCCACCAA AGCTTACCTA GTGCTAAAGG ATGAGGTGTT AGTAAGACCA ACATCTCAGA  
GGCCTCTCTG TGCCAATAGC CTTCTTCTC TTCCCTTCCA AAAACCTCAA GTGACTAGTT CAGAGGCGCTG  
TCTGGAATAA TGGCATCATC TAATATCACT GGCCTTCTGG AACCTGGGCA TTTTCCAGTG TGTTCATAC  
TGTCATATTT CCCCAGCTT CCTGGACTCC TGTCACAAGC TGGAAAAGTG AGAGGATGGA CAGGGATTA  
CCAGAGAGCT CCCTGCTGAG GAAAAAATCT CCCAGATGCT GAAAGTGAGG CCATGTGGCT TGGCCAAATA  
AAACCTGGCT CCGTGGTGCC TCTGTCTTAG CAGCCACCCT GCTGATGAAC TGCCACCTTG GACTTGGGAC  
CAGAAAGAGG TGGGTGGGT GAAGAGGCAC CACACAGAGT GATGTAACAG CAAGATCAGG TCACCCACAG  
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CAGCAGGATG GGCCCTGCAC CCAAGACGC TGCCTGGGCT CCTGGTATT TCCAGGAAA CTACAGGGCC GGCCCTCCC  
CGGCCCCCGG GCCCCTGAGC AGCTGCTGAG TCAGGCCCCG GACTTCATCA ACCAGTACTA CAGCTCCATT AAGAGGAGCG  
GCTCCAGGC CCACGAACAG CGGCTTCAAG AGGTGGAAGC CGAGGTGGCA GCCACAGGCA CCTACCAGCT TAGGGAGAGC  
GAGCTGGTGT TCGGGGCTAA GCAGGCCTGG CGCAACGCTC CCCGCTGCGT GGGCCGGATC CAGTGGGGGA AGTGCAGGT  
GTTGATGCC CGGGACTGCA GGTCTGCACA GGAATGTTT ACCTACATCT GCAACCAT CATAGTATGCC ACCAACGGG  
GCAACCTTC CTGGCCATC ACAGTGTTC CGCAGCGCTG CCCTGGCCGA GGAGACTTC GAATCTGGAA CAGCCAGCTG  
GTGCGCTACG CGGGTACCG GCAGCAGGAC GGCTCTGTG GGGGGGACCC AGCCAACGTG GAGATCACCG AGCTGTGCAT  
TCAGCACGGC TGGACCCAG GAAACGGTGC CTTGACGTG CTGCCCCG TGCTGCAGGC CCCAGATGAG CCCCAGAAC  
TCTTCTTCT GCCCCCGAG CTGGTCTTG AGGTGCCCC GTAGCACCCC ACGTGGAGT GGTTCGAGC CTTGGGCTG  
CGCTGGTACG CCCTCCCGG AGTGTCCAAC ATGCTGCTG AAATTGGGG CTTGGAGTTC CCCGAGCCC CTTCACTG  
CTGGTACATG AGCACTGAGA TCGGCACGAG GAACCTGTGT GACCTCAC GCTACAACAT CTTGGAGGAT GTGGCTGTCT  
GATGAGCTT GCAATAGGCG AGCACTGCT CTTCTGCA AGACAAGCA GCACTGCA TCAACGTGGC GTGCTGCAC

GGCATCACCA GGAAGAAGAC CTTTAAAGAA GTGGCCAACG CCGTGAAGAT CTCGCGCTCG CTCATGGGCA-CGGTGATGGC  
GAAGCGAGTG AAGGCGACAA TCCTGTATGG CTCCGAGACC GGCCGGGCCC AGAGCTACGC ACAGCAGCTG GGGAGACTCT  
TCCGGAAGGC TTTTGATCCC CGGGTCCTGT GTATGGATGA GTATGACGTG GTGTCCCTCG AACACGAGAC GCTGGTGCTG  
GTGGTAACCA GCACATTTGG GAATGGGGAT CCCCCGGAGA ATGGAGAGAG CTTTGCAGCT GCCCTGATGG AGATGTCCGG  
CCCCTACAAC AGCTCCCCCTC GGCCGGAACA GCACAAGAGT TATAAGATCC GCTTCAACAG CATCTCCTGC TCAGACCCAC  
TGGTGTCTCT TTGGCGGCGG AAGAGGAAGG AGTCCAGTAA CACAGACAGT GCAGGGGGCCC TGGGCACCCT CAGGTTCTGT  
GTGTTCCGGC TCGGCTCCCG GGCATACCCC CACTTCTGCG CCGTTGCTCG TGCCGTGGAC ACACGGCTGG AGGAACCTGGG  
CGGGGAGCGG CTGCTGCAGC TGGGCCAGGG CGACGAGCTG TGGCGCCAGG AGGAGGCCTT CCGAGGCTGG GCCCAGGCTG  
CCTTCCAGGC CGCCTGTGAG ACCTTCTGTG TGGGAGAGGA TGCCAAGGCC GCGGCCGAG ACATCTTCAG CCCCCAACGG  
AGCTGGAAGC GCCAGAGGTA CCGGCTGAGC GCCCAGGCCG AGGGCCTGCA GTTGCTGCCA GGTCTGATCC ACGTGACAG  
GCGGAAGATG TTCCAGGCTA CAATCCGCTC AGTGGAAGAAC CTGCAAGCA GCAAGTCCAC GAGGGGCCACC ATCTGGTGC  
GCCTGGACAC CGGAGGCCAG GAGGGGCTGC AGTACCAGCC GGGGGACCAC ATAGGTGTCT GCCCGCCCAA CCGGCCCGGC  
CTTGTTGAGG CGCTGCTGAG CCGCGTGGAG GACCCGCGG CGCCCACTGA GCCCGTGGA GTAGAGCAGC TGGAGAAGGG  
CAGCCCTGGT GCGCCTCCCC CCGGCTGGGT GCGGAGCCCC CGCTGCCCC CGTGACGCT GCGCCAGGCT CTCACCTTCT  
TCCTGGACAT CACCTCCCCA CCCAGCCCTC AGCTCTTGGC GCTGCTCAGC ACCTTGGCAG AAGAGCCCCA GGAACAGCAG  
GAGCTGGAGG CCCTCAGCCA GGATCCCCGA CGTACGAGG AGTGGAAGTG GTTCCGCTGC CCCACGCTGC TGGAGGTGCT  
GGAGCAGTTC CCGTCGGTGG CGCTGCCTGC CCCACTGCTC CTCACCCAGC TGCTCTGTCT CCAGCCCCGG TACTACTCAG  
TCAGCTCGGC ACCCAGCACC CACCAGGAG AGATCCACCT CACTGTAGCT GTGCTGGCAT ACAGGACTCA GGATGGGCTG  
GGCCCCCTGC ACTATGGAGT CTGCTCCACG TGGCTAAGCC AGCTCAAGCC CGGAGACCCT GTGCCCTGCT TCATCCGGGG  
GGCTCCCTCC TTCCGGCTGC CACCCGATCC CAGCTTGCCC TGCATCTGG TGGGTCCAGG CACTGGCATT GCCCCTTCC  
GGGGATTCTG CGAGGAGCGG CTGCATGACA TTGAGAGCAA AGGGTGCAG CCCACTCCCA TGACTTTGGT TTTCGGCTGC  
CGATGCTCCC AACTTGACCA TCTTACCGC GACGAGGTGC AGAACGCCCC GCAGCGCGGG GTGTTTGGCC GAGTCTCAC  
CGCCTTCTCC CGGGAACCTG ACAACCCCAA GACCTACGTG CAGGACATCC TGAGGACGGA GCTGGCTGCG GAGGTGCACC  
GCGTCTGTG CCTCGAGCGG GGCCACATGT TTGTCTGCG CGATGTTACC ATGGCAACCA ACGTCTGCA GACCGTGCAG  
CGCATCTGG CGACGGAGGG CGACATGGAG CTGGACGAG CCGGCGACGT CATCGGCGTG CTGCGGGATC AGCAACGCTA  
CCACGAAGAC ATTTTCGGGC TCACGCTGCG CACCCAGGAG GTGACAAGCC GCATACGCAC CCAGAGCTTT TCCTTGACGG  
AGCGTCAGTT GCGGGGCGCA GTGCCCTGGG CGTTCGACCC TCCCGGCTCA GACACCAACA GCCCTGAGA GCCGCTGGC  
TTCCCTTCC AGTTCGCGGA GAGCGGCTGC CCGACTCAGG TCCGCCCCGAC CAGGATCAGC CCCGCTCTC CCCTCTGAG  
GTGGTGCTT CTCACATCTG TCCAGAGGCT GCAAGGATTC AGCATTATTC CTCCAGGAAG GAGCAAAAGC CCTCTTTTCC  
CTCTTAGGC CTGTTGCCCTC GGGCCTGGGT CCGCCTTAAT CTGGAAGGCC CCTCCAGCA GCGGTACCC AGGGCCTACT  
GCCACCCGCT TCCTGTTTCT TAGTCCGAAT GTTAGATTCC TCTTGCTCT CTCAGGAGTA TCTTACCTGT AAAGTCTAAT  
CTCTAAATCA AGTATTATT ATTGAAGATT TACCATAAGG GACTGTGCCA GATGTTAGGA GAACTACTAA AGTGCCCTACC  
CCAGCTC-3' (FRAG. NO: ) (SEQ. ID NO: 2508)

5'-CCCCGGGG-3' (FRAG. NO:1898) (SEQ. ID NO: 1909)

5'-GGGGCCGCTGGG-3' (FRAG. NO:1899) (SEQ. ID NO:1910)

5'-GGGGGTGTGG-3' (FRAG. NO:1900) (SEQ. ID NO: 1911)

5'-CTGCTCCCCGGGGT-3' (FRAG. NO:1442) (SEQ. ID NO:1452)

5'-TTCTGTGCTTGCTG-3' (FRAG. NO:1443) (SEQ. ID NO:1453)

5'-CTTCTTTCCGCTCC-3' (FRAG. NO:1444) (SEQ. ID NO:1454)

5'-CTTCTTTCCGCTCC-3' (FRAG. NO:1445) (SEQ. ID NO:1455)

5'-TTTGTGCTCTTG-3' (FRAG. NO:1446) (SEQ. ID NO:1456)

5'-GGTTCCTGTTTCT-3' (FRAG. NO:1447) (SEQ. ID NO:1457)

5'-GGCCTGCTGGTGGCG-3' (FRAG. NO:1448) (SEQ. ID NO:1458)

5'-GCTTGTGCGTTCC-3' (FRAG. NO:1449) (SEQ. ID NO:1459)

5'-TCTCTTCTCTTGGGTCTCCGCTTCTCGTCTGCC-3' (FRAG. NO:1450) (SEQ. ID NO:1460)

5'-TTTTCTGTCTGTGCG-3' (FRAG. NO:1451) (SEQ. ID NO:1461)

5'-GCCGTTCTCTCC-3' (FRAG. NO:1452) (SEQ. ID NO:1462)

5'-GGCGTCTCTGCC-3' (FRAG. NO:1453) (SEQ. ID NO:1463)

5'-TGTGCTGTTGCTCGG-3' (FRAG. NO:1454) (SEQ. ID NO:1464)

5'-GTGGTGCGGGTCCC-3' (FRAG. NO:1455) (SEQ. ID NO:1465)

5'-GGTGCTCCCCGGC-3' (FRAG. NO:1456) (SEQ. ID NO:1466)

5'-GGGCCGGCTGGTGCCTGGGC-3' (FRAG. NO:1457) (SEQ. ID NO:1467)

5'-CTGCTGGTGGGGTGTGGGGCC-3' (FRAG. NO:1458) (SEQ. ID NO:1468)

5'-CTGGGGTGGGGGTGTGGTG-3' (FRAG. NO:1459) (SEQ. ID NO:1469)

5'-GGCTCTTCTGTGGCC-3' (FRAG. NO:1460) (SEQ. ID NO:1470)

5'-TGTGGGGCTGTGGTG-3' (FRAG. NO:1461) (SEQ. ID NO:1471)

5'-TCTCTGTTGGGCTGTG-3' (FRAG. NO:1462) (SEQ. ID NO:1472)

5'-CTGGGTCTGGGGCTTC-3' (FRAG. NO:1463) (SEQ. ID NO:1473)

5'-CTCCCTGTGCTGGG-3' (FRAG. NO:1464) (SEQ. ID NO:1474)

5'-TGCGGCTCCCCGC-3' (FRAG. NO:1465) (SEQ. ID NO:1475)

5'-CCCCCTTCTGGGC-3' (FRAG. NO:1466) (SEQ. ID NO:1476)

5'-GGTGGCCTGGCTCCTTGTGG-3' (FRAG. NO:1467) (SEQ. ID NO:1477)

5'-GCGCTTCTGGCTCTTG-3' (FRAG. NO:1468) (SEQ. ID NO:1478)

5'-CCCTGTCTTCTCGCTCGT-3' (FRAG. NO:1469) (SEQ. ID NO:1479)

5'-GGCTGCTGGGCTGC-3' (FRAG. NO:1470) (SEQ. ID NO:1480)

5'-CTGCCCCGTTTTTGTBCTCCTCCTGCGCTGGGGGGBGBCTGG-3' (FRAG. NO:1901) (SEQ. ID NO: 1912)

#### **NF-kB Nucleic Acids and Antisense Oligonucleotide Fragments**

5'-CGGCCCTTCT CACTGGAGGC ACCGGGCAGT CCTCCATGGG AGGGTTGGGC TTGGCCGGGG CTGCCCGGTG CCTCCTCTTG  
GCTGGTCCCT CGTTGTCCTT GGGCCCCGC TCCGCTGCT CCGCCTCCGT GTTCTTTGGC CTCTTGCTCC GCCTGCTGC

TTGTCCCGTC CCCTCCCGC TTGCGTTTCC CTCTCTCTG TCTTCCAGGC CTTCCTCCG TCCTCGTCT GGGGCCCGCG  
CCGGGGGGGG GCTCGGCTCC GCGGCTTCT CCCCAGGCTGG GGGGCTCTGG TCTCCGGGGC CTGCGGCTCG CGGGCTCGGG  
CTGCGTGGC CCGCGCGCGG CGTCCGCGGT GGGTGGCGCT GTCCCGCGT GGTGTGTCTC CTTCTCTGTC GTGCGCCGT  
CTGTCTGCC CGTGGGGTCC TGGGCGTGGT GGGGGGCGTC TGGTGCCTCG TCTGCCCCGT GGGGCTTCGG GCTCGGGGT  
GTTCTGCCCC CTTGCCGCTC TGTGGCCTCC GGGGCTCCTC GTTTCTGCTG CTTCGGGTGT CCTTCTCGGC GTGTGGCCCC  
GGGTCCCGGC CTTGCTGGG TGGGCGGGT CGTGCCTG GGTCTCTGG CCGTCTGTT GTCTGTGGT GCTGTCTCG  
GGTTCTGCG CTCTGTCTG GCGCTTCTC TGCTCTCTG TCCGCCCTC TGGTGGCTCG GCTGGGGGTG CCCGTGCGGG  
GGTGGGTGTG GGTGTTTTC GGGGTCTCC CTTCCC-3' (FRAG. NO:1902) (SEQ. ID NO:1913)

5'-GGGCGGGTCCG-3' (FRAG. NO:1903) (SEQ. ID NO:1914)

5'-GCGCCGTCC-3' (FRAG. NO:1904) (SEQ. ID NO:1915)

5'-GGGCGTGGTGG-3' (FRAG. NO:1905) (SEQ. ID NO:1916)

5'-GTTGGGCTTGGCCGGGG-3' (FRAG. NO:1471)(SEQ. ID NO:1481)

5'-CTGCCCCGTGCTCC-3' (FRAG. NO:1472)(SEQ. ID NO:1482)

5'-TCTTGGCTGGTCCCTCGT-3' (FRAG. NO:1473)(SEQ. ID NO:1483)

5'-TGTCCTTGGGCCCC-3' (FRAG. NO:1474)(SEQ. ID NO:1484)

5'-GCTCCCGCTGCTCGGCTCCGT-3' (FRAG. NO:1475)(SEQ. ID NO:1485)

5'-GTTCTTTGGCCTTTGCTCC-3' (FRAG. NO:1476)(SEQ. ID NO:1486)

5'-GCCTGCTGTCTTGTCC-3' (FRAG. NO:1477)(SEQ. ID NO:1487)

5'-CGTCCCTCTCGCTTGCCTTC-3' (FRAG. NO:1478)(SEQ. ID NO:1488)

5'-CCTCTCTTGTCTTCCA-3' (FRAG. NO:1479)(SEQ. ID NO:1489)

5'-GGCCTTCTCCGCTTCCGCTGC-3' (FRAG. NO:1480)(SEQ. ID NO:1490)

5'-TGGGGCCCGCGCCGG-3' (FRAG. NO:1481)(SEQ. ID NO:1491)

5'-GGGGGCGCTCGGCTCCGCGCTTCTCCCGG-3' (FRAG. NO:1482)(SEQ. ID NO:1492)

5'-CTGGGGGCTCCTGG-3' (FRAG. NO:1483)(SEQ. ID NO:1493)

5'-TCTCCGGGCTCGGCTCGC-3' (FRAG. NO:1484)(SEQ. ID NO:1494)

5'-GGGCTCGGGGCTGCGTGCGCC-3' (FRAG. NO:1485)(SEQ. ID NO:1495)

5'-GCGCGCGCGTCCGCGGTG-3' (FRAG. NO:1486)(SEQ. ID NO:1496)

5'-GGTGGCGCTGTCGCC-3' (FRAG. NO:1487)(SEQ. ID NO:1497)

5'-GTGGTGTGTCTCGTTCTGCTCGCGCTC-3' (FRAG. NO:1488)(SEQ. ID NO:1498)

5'-CTGGTCTGCCCCTGG-3' (FRAG. NO:1489)(SEQ. ID NO:1499)

5'-GGTCTGGGCGTGGTGG-3' (FRAG. NO:1490)(SEQ. ID NO:1500)

5'-GGGGCGCTGCTGGTGC-3' (FRAG. NO:1491)(SEQ. ID NO:1501)

5'-CTCGCTGCCCCGTG-3' (FRAG. NO:1492)(SEQ. ID NO:1502)

5'-GGGCTTCGGGCTCGG-3' (FRAG. NO:1493)(SEQ. ID NO:1503)

5'-GGCTGTTCGTCCCCCTGCCCTCTGTGGCTCC-3' (FRAG. NO:1494)(SEQ. ID NO:1504)

5'-GGGGCTCTCGTTTTC-3' (FRAG. NO:1495)(SEQ. ID NO:1505)

5'-GCTGCTCGGGTGTCTTCTC-3' (FRAG. NO:1496)(SEQ. ID NO:1506)

5'-GGCGTGTGGCCCCCG-3' (FRAG. NO:1497)(SEQ. ID NO:1507)

5'-GTCCCGGCCCTGTTGGGCTGGCGGGGTC-3' (FRAG. NO:1498)(SEQ. ID NO:1508)

5'-GTGCGCTGGGCTTCTGGCCGTCT-3' (FRAG. NO:1499)(SEQ. ID NO:1509)

5'-GGTTGTCTGTGGT-3' (FRAG. NO:1500)(SEQ. ID NO:1510)

5'-GCTTGTCTCGGGTTTCTGG-3' (FRAG. NO:1501)(SEQ. ID NO:1511)

5'-CCTCTGTGCTGGG-3' (FRAG. NO:1502)(SEQ. ID NO:1512)

5'-GCTTCTGCTCCTGCTCC-3' (FRAG. NO:1503)(SEQ. ID NO:1513)

5'-GCCCTCCTGGTGGCTC-3' (FRAG. NO:1504)(SEQ. ID NO:1514)

5'-GGCTGGGGGTGCCGTGCG-3' (FRAG. NO:1505)(SEQ. ID NO:1515)

5'-GGGGTGGGTGTGGGGTGT-3' (FRAG. NO:1506)(SEQ. ID NO:1516)

5'-TTCGGGCTCTCCCTTCC-3' (FRAG. NO:1507)(SEQ. ID NO:1517)

5'-CGGCCCTTCTCACTGGAGGACCGGGCAGTCTCCATGGGAGG-3' (FRAG. NO:1906) (SEQ. ID NO:1917)

#### Human Major Basic Protein Nucleic Acids and Antisense Oligonucleotide Fragments

5'-GTT TCA TCT TGG CTT TAT CCTCT CCC CTT GTT CCT CCC CTCT CCT GCT CTG GRG TCT CCT C TTC CCT CCC TCC  
CCT GCC GTG TTG TCT GTG GGT GTC GTT TCG CTC TTG TTG CCC TGG GCC CTT CCC TGG TGG GGG GGA GTT TCA TCT  
TGG GTT TCB TCT TGG CTT TBT CCTCT CCC CTT GTT CCT CCC CTCT CCT GCT CTG GRG TCT CCT C TTC CCT CCC TCC  
CCT GCC GTG TTG TCT GTG GGT GTC GTT TCG CTC TTG TTG CCC TGG GCC CTT CCC TGC TGG GGG GGB GTT TCB TCT  
TGG-3' (FRAG. ID:1907) (SEQ. ID NO:1918)

5'-GGG GGA GTT-3' (FRAG. ID:1908) (SEQ. ID NO:1919)

5'-G CCC TGG GCC C-3' (FRAG. ID:1909) (SEQ. ID NO:1920)

5'-GTT TCA TCT TGG CTT TAT CC-3' (FRAG. NO:1508) (SEQ. ID NO:1518)

5'-TCT CCC CTT GTT CCT CCC C-3' (FRAG. NO:1509)(SEQ. ID NO:1519)

5'-TCT CCT GCT CTG GRG TCT CCT C-3' (FRAG. NO:1510)(SEQ. ID NO:1520)

5'-TTC CCT CCC TCC CCT GCC-3' (FRAG. NO:1511)(SEQ. ID NO:1521)

5'-GTG TTG TCT GTG GGT GTC C-3' (FRAG. NO:1512)(SEQ. ID NO:1522)

5'-GTT TCG CTC TTG TTG CCC-3' (FRAG. NO:1513)(SEQ. ID NO:1523)

5'-TGG GCC CTT CCG TGC TGG-3' (FRAG. NO:1514)(SEQ. ID NO:1524)

5'-GGG GGA GTT TCA TCT TGG-3' (FRAG. NO:1515)(SEQ. ID NO:1525)

5'-GTT TCA TCT TGG CTT TAT CCTCT CCC CTT GTT CCT CCC CTCT CCT GCT CTG GRG TCT CCT C TTC CCT CCC TCC  
CCT GCC GTG TTG TCT GTG GGT GTC GTT TCG CTC TTG TTG CCC TGG GCC CTT CCC TGC TGG GGG GGA GTT TCA TCT  
TGG-3' (FRAG. ID:1910) (SEQ. ID NO:1921)

5'-GTT TCB TCT TGG CTT TBT CCTCT CCC CTT GTT CCT CCC CTCT CCT GCT CTG GRG TCT CCT C TTC CCT CCC TCC

CCT GCC GTG TTG TCT GTG GGT GTC GTT TCG CTC TTG TTG CCC TGG GCC CTT CCC TGC TGG GGG GGB GTT TCB TCT TGG-3' (FRAG. ID:1911) (SEQ. ID NO:1922)

**Human Eosinophil Major Basic Protein Nucleic Acids and Antisense Oligonucleotide Fragments**

5'-GGG GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1516)(SEQ. ID NO:1526)

5'-GGG GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1517)(SEQ. ID NO:1527)

5'-GGG GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1518)(SEQ. ID NO:1528)

5'-GGG GGB GTT TCB TCT TGG C-3' (FRAG. NO:1519)(SEQ. ID NO:1529)

5'-GGG GGB GTT TCB TCT TGG-3' (FRAG. NO:1520)(SEQ. ID NO:1530)

5'-GGG GGB GTT TCB TCT TG-3' (FRAG. NO:1521)(SEQ. ID NO:1531)

5'-GGG GGB GTT TCB TCT T-3' (FRAG. NO:1522)(SEQ. ID NO:1532)

5'-GGG GGB GTT TCB TCT-3' (FRAG. NO:1523)(SEQ. ID NO:1533)

5'-GGG GGB GTT TCB TC-3' (FRAG. NO:1524)(SEQ. ID NO:1534)

5'-GGG GGB GTT TCB T-3' (FRAG. NO:1525)(SEQ. ID NO:1535)

5'-GGG GGB GTT TCB-3' (FRAG. NO:1526)(SEQ. ID NO:1536)

5'-GG GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1527)(SEQ. ID NO:1537)

5'-GG GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1528)(SEQ. ID NO:1538)

5'-GG GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1529)(SEQ. ID NO:1539)

5'-GG GGB GTT TCB TCT TGG C-3' (FRAG. NO:1530)(SEQ. ID NO:1540)

5'-GG GGB GTT TCB TCT TGG-3' (FRAG. NO:1531)(SEQ. ID NO:1541)

5'-GG GGB GTT TCB TCT TG-3' (FRAG. NO:1532)(SEQ. ID NO:1542)

5'-GG GGB GTT TCB TCT T-3' (FRAG. NO:1533)(SEQ. ID NO:1543)

5'-GG GGB GTT TCB TCT-3' (FRAG. NO:1534)(SEQ. ID NO:1544)

5'-GG GGB GTT TCB TC-3' (FRAG. NO:1535)(SEQ. ID NO:1545)

5'-GG GGB GTT TCB T-3' (FRAG. NO:1536)(SEQ. ID NO:1546)

5'-G GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1537)(SEQ. ID NO:1547)

5'-G GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1538)(SEQ. ID NO:1548)

5'-G GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1539)(SEQ. ID NO:1549)

5'-G GGB GTT TCB TCT TGG C-3' (FRAG. NO:1540)(SEQ. ID NO:1550)

5'-G GGB GTT TCB TCT TGG-3' (FRAG. NO:1541)(SEQ. ID NO:1551)

5'-G GGB GTT TCB TCT TG-3' (FRAG. NO:1542)(SEQ. ID NO:1552)

5'-G GGB GTT TCB TCT T-3' (FRAG. NO:1543)(SEQ. ID NO:1553)

5'-G GGB GTT TCB TCT-3' (FRAG. NO:1544)(SEQ. ID NO:1554)

5'-G GGB GTT TCB TC-3' (FRAG. NO:1545)(SEQ. ID NO:1555)

5'-GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1546)(SEQ. ID NO:1556)

5'-GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1547)(SEQ. ID NO:1557)

5'-GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1548)(SEQ. ID NO:1558)

5'-GGB GTT TCB TCT TGG C-3' (FRAG. NO:1549)(SEQ. ID NO:1559)

5'-GGB GTT TCB TCT TGG-3' (FRAG. NO:1550)(SEQ. ID NO:1560)

5'-GGB GTT TCB TCT TG-3' (FRAG. NO:1551)(SEQ. ID NO:1561)

5'-GGB GTT TCB TCT T-3' (FRAG. NO:1552)(SEQ. ID NO:1562)

5'-GGB GTT TCB TCT-3' (FRAG. NO:1553)(SEQ. ID NO:1563)

5'-GB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1554)(SEQ. ID NO:1564)

5'-GB GTT TCB TCT TGG CTT-3' (FRAG. NO:1555)(SEQ. ID NO:1565)

5'-GB GTT TCB TCT TGG CT-3' (FRAG. NO:1556)(SEQ. ID NO:1566)

5'-GB GTT TCB TCT TGG C-3' (FRAG. NO:1557)(SEQ. ID NO:1567)

5'-GB GTT TCB TCT TGG-3' (FRAG. NO:1558)(SEQ. ID NO:1568)

5'-GB GTT TCB TCT TG-3' (FRAG. NO:1559)(SEQ. ID NO:1569)

5'-GB GTT TCB TCT T-3' (FRAG. NO:1560)(SEQ. ID NO:1570)

5'-B GTT TCB TCT TGG CTT T-3' (FRAG. NO:1561)(SEQ. ID NO:1571)

5'-B GTT TCB TCT TGG CTT-3' (FRAG. NO:1562)(SEQ. ID NO:1572)

5'-B GTT TCB TCT TGG CT-3' (FRAG. NO:1563)(SEQ. ID NO:1573)

5'-B GTT TCB TCT TGG CT-3' (FRAG. NO:1564)(SEQ. ID NO:1574)

5'-B GTT TCB TCT TGG C-3' (FRAG. NO:1565)(SEQ. ID NO:1575)

5'-B GTT TCB TCT TGG-3' (FRAG. NO:1566)(SEQ. ID NO:1576)

5'-B GTT TCB TCT TG-3' (FRAG. NO:1567)(SEQ. ID NO:1577)

5'-GTT TCB TCT TGG CTT T-3' (FRAG. NO:1568)(SEQ. ID NO:1578)

5'-GTT TCB TCT TGG CTT-3' (FRAG. NO:1569)(SEQ. ID NO:1579)

5'-GTT TCB TCT TGG CT-3' (FRAG. NO:1570)(SEQ. ID NO:1580)

5'-GTT TCB TCT TGG C-3' (FRAG. NO:1571)(SEQ. ID NO:1581)

5'-GTT TCB TCT TGG-3' (FRAG. NO:1572)(SEQ. ID NO:1582)

5'-TT TCB TCT TGG CTT T-3' (FRAG. NO:1573)(SEQ. ID NO:1583)

5'-TT TCB TCT TGG CTT-3' (FRAG. NO:1574)(SEQ. ID NO:1584)

5'-TT TCB TCT TGG CT-3' (FRAG. NO:1575)(SEQ. ID NO:1585)

5'-TT TCB TCT TGG C-3' (FRAG. NO:1576)(SEQ. ID NO:1586)

5'-T TCB TCT TGG CTT T-3' (FRAG. NO:1577)(SEQ. ID NO:1587)

5'-T TCB TCT TGG CTT-3' (FRAG. NO:1578)(SEQ. ID NO:1588)

5'-T TCB TCT TGG CT-3' (FRAG. NO:1579)(SEQ. ID NO:1589)

5'-TCB TCT TGG CTT T-3' (FRAG. NO:1580)(SEQ. ID NO:1590)

5'-TCB TCT TGG CTT-3' (FRAG. NO:1581)(SEQ. ID NO:1591)



5'-GGG GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1582)(SEQ. ID NO:1592)  
5'-GG GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1583)(SEQ. ID NO:1593)  
5'-G GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1584)(SEQ. ID NO:1594)  
5'-GGG GTT TCB TCT TGG CTT T-3' (FRAG. NO:1585)(SEQ. ID NO:1595)  
5'-GB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1586)(SEQ. ID NO:1596)  
5'-B GTT TCB TCT TGG CTT T-3' (FRAG. NO:1587)(SEQ. ID NO:1597)  
5'-GTT TCB TCT TGG CTT T-3' (FRAG. NO:1588)(SEQ. ID NO:1598)  
5'-TT TCB TCT TGG CTT T-3' (FRAG. NO:1589)(SEQ. ID NO:1599)  
5'-T TCB TCT TGG CTT T-3' (FRAG. NO:1590)(SEQ. ID NO:1600)  
5'-TCB TCT TGG CTT T-3' (FRAG. NO:1591)(SEQ. ID NO:1601)  
5'-CB TCT TGG CTT T-3' (FRAG. NO:1592)(SEQ. ID NO:1602)  
5'-GGG GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1593)(SEQ. ID NO:1603)  
5'-GG GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1594)(SEQ. ID NO:1604)  
5'-G GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1595)(SEQ. ID NO:1605)  
5'-GGG GTT TCB TCT TGG CTT-3' (FRAG. NO:1596)(SEQ. ID NO:1606)  
5'-GB GTT TCB TCT TGG CTT-3' (FRAG. NO:1597)(SEQ. ID NO:1607)  
5'-B GTT TCB TCT TGG CTT-3' (FRAG. NO:1598)(SEQ. ID NO:1608)  
5'-GTT TCB TCT TGG CTT-3' (FRAG. NO:1599)(SEQ. ID NO:1609)  
5'-TT TCB TCT TGG CTT-3' (FRAG. NO:1600)(SEQ. ID NO:1610)  
5'-T TCB TCT TGG CTT-3' (FRAG. NO:1601)(SEQ. ID NO:1611)  
5'-TCB TCT TGG CTT-3' (FRAG. NO:1602)(SEQ. ID NO:1612)  
5'-GGG GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1603)(SEQ. ID NO:1613)  
5'-GG GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1604)(SEQ. ID NO:1614)  
5'-G GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1605)(SEQ. ID NO:1615)  
5'-GGG GTT TCB TCT TGG CT-3' (FRAG. NO:1606)(SEQ. ID NO:1616)  
5'-GB GTT TCB TCT TGG CT-3' (FRAG. NO:1607)(SEQ. ID NO:1617)  
5'-B GTT TCB TCT TGG CT-3' (FRAG. NO:1608)(SEQ. ID NO:1618)  
5'-GTT TCB TCT TGG CT-3' (FRAG. NO:1609)(SEQ. ID NO:1619)  
5'-TT TCB TCT TGG CT-3' (FRAG. NO:1610)(SEQ. ID NO:1620)  
5'-T TCB TCT TGG CT-3' (FRAG. NO:1611)(SEQ. ID NO:1621)  
5'-GGG GGB GTT TCB TCT TGG C-3' (FRAG. NO:1612)(SEQ. ID NO:1622)  
5'-GG GGB GTT TCB TCT TGG C-3' (FRAG. NO:1613)(SEQ. ID NO:1623)  
5'-G GGB GTT TCB TCT TGG C-3' (FRAG. NO:1614)(SEQ. ID NO:1624)  
5'-GGG GTT TCB TCT TGG C-3' (FRAG. NO:1615)(SEQ. ID NO:1625)  
5'-GB GTT TCB TCT TGG C-3' (FRAG. NO:1616)(SEQ. ID NO:1626)  
5'-B GTT TCB TCT TGG C-3' (FRAG. NO:1617)(SEQ. ID NO:1627)  
5'-GTT TCB TCT TGG C-3' (FRAG. NO:1618)(SEQ. ID NO:1628)  
5'-TT TCB TCT TGG C-3' (FRAG. NO:1619)(SEQ. ID NO:1629)  
5'-GGG GGB GTT TCB TCT TGG-3' (FRAG. NO:1620)(SEQ. ID NO:1630)  
5'-GG GGB GTT TCB TCT TGG-3' (FRAG. NO:1621)(SEQ. ID NO:1631)  
5'-G GGB GTT TCB TCT TGG-3' (FRAG. NO:1622)(SEQ. ID NO:1632)  
5'-GGG GTT TCB TCT TGG-3' (FRAG. NO:1623)(SEQ. ID NO:1633)  
5'-GB GTT TCB TCT TGG-3' (FRAG. NO:1624)(SEQ. ID NO:1634)  
5'-B GTT TCB TCT TGG-3' (FRAG. NO:1625)(SEQ. ID NO:1635)  
5'-GTT TCB TCT TGG-3' (FRAG. NO:1626)(SEQ. ID NO:1636)  
5'-GGG GGB GTT TCB TCT TG-3' (FRAG. NO:1627)(SEQ. ID NO:1637)  
5'-GG GGB GTT TCB TCT TG-3' (FRAG. NO:1628)(SEQ. ID NO:1638)  
5'-G GGB GTT TCB TCT TG-3' (FRAG. NO:1629)(SEQ. ID NO:1639)  
5'-GGG GTT TCB TCT TG-3' (FRAG. NO:1630)(SEQ. ID NO:1640)  
5'-GB GTT TCB TCT TG-3' (FRAG. NO:1631)(SEQ. ID NO:1641)  
5'-B GTT TCB TCT TG-3' (FRAG. NO:1632)(SEQ. ID NO:1642)  
5'-GGG GGB GTT TCB TCT T-3' (FRAG. NO:1633)(SEQ. ID NO:1643)  
5'-GG GGB GTT TCB TCT T-3' (FRAG. NO:1634)(SEQ. ID NO:1644)  
5'-G GGB GTT TCB TCT T-3' (FRAG. NO:1635)(SEQ. ID NO:1645)  
5'-G GGB GTT TCB TCT T-3' (FRAG. NO:1636)(SEQ. ID NO:1646)  
5'-GGG GTT TCB TCT T-3' (FRAG. NO:1637)(SEQ. ID NO:1647)  
5'-GB GTT TCB TCT T-3' (FRAG. NO:1638)(SEQ. ID NO:1648)  
5'-GGG GGB GTT TCB TCT-3' (FRAG. NO:1639)(SEQ. ID NO:1649)  
5'-GG GGB GTT TCB TCT-3' (FRAG. NO:1640)(SEQ. ID NO:1650)  
5'-G GGB GTT TCB TCT-3' (FRAG. NO:1641)(SEQ. ID NO:1651)  
5'-GGG GTT TCB TCT-3' (FRAG. NO:1642)(SEQ. ID NO:1652)  
5'-GGG GGB GTT TCB TC-3' (FRAG. NO:1643)(SEQ. ID NO:1653)  
5'-GG GGB GTT TCB TC-3' (FRAG. NO:1644)(SEQ. ID NO:1654)  
5'-G GGB GTT TCB TC-3' (FRAG. NO:1645)(SEQ. ID NO:1655)  
5'-GGG GGB GTT TCB T-3' (FRAG. NO:1646)(SEQ. ID NO:1656)  
5'-GG GGB GTT TCB T-3' (FRAG. NO:1647)(SEQ. ID NO:1657)  
5'-GGG GGB GTT TCB-3' (FRAG. NO:1648)(SEQ. ID NO:1658)  
5'-TCT CCC CTT GTT CCT CCC C-3' (FRAG. NO:1649)(SEQ. ID NO:1659)  
5'-TCT CCT GCT CTG GTG TCT CCT C-3' (FRAG. NO:1650)(SEQ. ID NO:1660)

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5'-TTC CCT CCC TCC CCT GCC-3' (FRAG. NO:1651)(SEQ. ID NO:1661)  
5'-GTG TTG TCT GTG GGT GTC C-3' (FRAG. NO:1652)(SEQ. ID NO:1662)  
5'-GTT TCG CTC TTG TTG CCC-3' (FRAG. NO:1653)(SEQ. ID NO:1663)  
5'-TGG GCC CTT CCC TGC TGG-3' (FRAG. NO:1654)(SEQ. ID NO:1664)  
5'-GGG GGB G-3' (FRAG. NO:1912)(SEQ. ID NO:1923)  
5'-GTG GGT GTC C-3' (FRAG. NO:1913) (SEQ. ID NO:1924)

**BP-1 Nucleic Acids and Antisense Oligonucleotide Fragments**

5'-CCGTGTTGTC BGTGGTGCTG CCCGTTTGBG GTBTGGCGCT CCBCCBBTTC CCTTTTCTCC TGTGTTTCCG TTCTCTTGC  
CGTCTGTGGT T-3' (FRAG. NO:1914) (SEQ. ID NO:1925)  
5'-CCCGTTTGBGGTBTGGC-3' (FRAG. NO:1915) (SEQ. ID NO:1926)  
5'-GCTCCBCCBBTTCCTTTTCTCC-3' (FRAG. NO:1916) (SEQ. ID NO:1927)  
5'-TTGTTTTCGTTTCTCTTG-3' (FRAG. NO:1917) (SEQ. ID NO:1928)  
5'-CCGTCTGTGGT-3' (FRAG. NO:1918) (SEQ. ID NO:1929)  
5'-CCCGTTTGAGGTATGGC-3' (FRAG. NO:1919) (SEQ. ID NO:1930)  
5'-GCTCCBCCAATCCCTTTTCTCC-3' (FRAG. NO:1920) (SEQ. ID NO:1931)

**C/EBPNucleic Acids and Antisense Oligonucleotide Antisense Oligonucleotide Fragments**

5'-GGGCCCCBCCCCGCCGCTTTTCTBGCCCC GGCC-3' (FRAG. NO:1921) (SEQ. ID NO:1932)  
5'-GGGCCCCBCCCCGCCGCTTTTCTBGCCCC GGC-3' (FRAG. NO:1922) (SEQ. ID NO:1933)  
5'-GGGCCCCB GCGCCGCCGCTTTTCTBGCCCCGG-3' (FRAG. NO:1923) (SEQ. ID NO:1934)  
5'-GGGCCCCBCCCCGCCGCTTTTCTBGCCCCG-3' (FRAG. NO:1924) (SEQ. ID NO:1935)  
5'-GGGCCCCBCCCCGCCGCTTTTCTBGCCCC-3' (FRAG. NO:1925) (SEQ. ID NO:1936)  
5'-GGGCCCCBCCCCGCCGCTTTTCTBGCCCC-3' (FRAG. NO:1926) (SEQ. ID NO:1937)  
5'-GGGCCCCBCCCCGCCGCTTTTCTBGCC-3' (FRAG. NO:1927) (SEQ. ID NO:1938)  
5'-GGGCCCCBCCCCGCCGCTTTTCTBGC-3' (FRAG. NO:1928) (SEQ. ID NO:1939)  
5'-GGGCCCCBCCCCGCCGCTTTTCTBG-3' (FRAG. NO:1929) (SEQ. ID NO:1940)  
5'-GGGCCCCBCCCCGCCGCTTTTCTB-3' (FRAG. NO:1930) (SEQ. ID NO:1941)  
5'-GGGCCCCBCCCCGCCGCTTTTCT-3' (FRAG. NO:1931) (SEQ. ID NO:1942)  
5'-GGGCCCCBCCCCGCCGCTTTTCT-3' (FRAG. NO:1932) (SEQ. ID NO:1943)  
5'-GGGCCCCBCCCCGCCGCTTTT-3' (FRAG. NO:1933) (SEQ. ID NO:1944)  
5'-GGGCCCCBCCCCGCCGCTTT-3' (FRAG. NO:1934) (SEQ. ID NO:1945)  
5'-GGGCCCCBCCCCGCCGCTT-3' (FRAG. NO:1935) (SEQ. ID NO:1946)  
5'-GGGCCCCBCCCCGCCGCT-3' (FRAG. NO:1936) (SEQ. ID NO:1947)  
5'-GGGCCCCBCCCCGCCGC-3' (FRAG. NO:1937) (SEQ. ID NO:1948)  
5'-GGGCCCCBCCCCGCCG-3' (FRAG. NO:1938) (SEQ. ID NO:1949)  
5'-GGGCCCCBCCCCGCC-3' (FRAG. NO:1939) (SEQ. ID NO:1950)  
5'-GGGCCCCBCCCCGC-3' (FRAG. NO:1940) (SEQ. ID NO:1951)  
5'-GGGCCCCBCCCCG-3' (FRAG. NO:1941) (SEQ. ID NO:1952)  
5'-GGGCCCCBCCCC-3' (FRAG. NO:1942) (SEQ. ID NO:1953)  
5'-GGGCCCCBCCCC-3' (FRAG. NO:1943) (SEQ. ID NO:1954)  
5'-GGGCCCCBCCCC-3' (FRAG. NO:1944) (SEQ. ID NO:1955)  
5'-GGCCCCBCCCCGCCGCTTTTCTBGCCCCGGC-3' (FRAG. NO:1945) (SEQ. ID NO:1956)  
5'-GCCCBGCCCCGCCGCTTTTCTBGCCCCGGC-3' (FRAG. NO:1946) (SEQ. ID NO:1957)  
5'-CCCBGCCCCGCCGCTTTTCTBGCCCCGGC-3' (FRAG. NO:1947) (SEQ. ID NO:1958)  
5'-CCBGCCCCGCCGCTTTTCTBGCCCCGGC-3' (FRAG. NO:1948) (SEQ. ID NO:1959)  
5'-CBGCCCCGCCGCTTTTCTBGCCCCGGC-3' (FRAG. NO:1948) (SEQ. ID NO:1960)  
5'-BGCCCCGCCGCTTTTCTBGCCCCGGC-3' (FRAG. NO:1950) (SEQ. ID NO:1961)  
5'-GCCCCGCCGCTTTTCTBGCCCCGGC-3' (FRAG. NO:1951) (SEQ. ID NO:1962)  
5'-CCCCGCCGCTTTTCTBGCCCCGGC-3' (FRAG. NO:1952) (SEQ. ID NO:1963)  
5'-CCCGCCGCTTTTCTBGCCCCGGC-3' (FRAG. NO:1953) (SEQ. ID NO:1964)  
5'-CCGCCGCTTTTCTBGCCCCGGC-3' (FRAG. NO:1954) (SEQ. ID NO:1965)  
5'-CGCCGCTTTTCTBGCCCCGGC-3' (FRAG. NO:1955) (SEQ. ID NO:1966)  
5'-GCCGCTTTTCTBGCCCCGGC-3' (FRAG. NO:1956) (SEQ. ID NO:1967)  
5'-CCGCTTTTCTBGCCCCGGC-3' (FRAG. NO:1957) (SEQ. ID NO:1968)  
5'-CGCTTTTCTBGCCCCGGC-3' (FRAG. NO:1958) (SEQ. ID NO:1969)  
5'-GCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1959) (SEQ. ID NO:1970)  
5'-CCTTTTCTBGCCCCGGC-3' (FRAG. NO:1960) (SEQ. ID NO:1971)  
5'-CTTTTCTBGCCCCGGC-3' (FRAG. NO:1961) (SEQ. ID NO:1972)  
5'-TTTTCTBGCCCCGGC-3' (FRAG. NO:1962) (SEQ. ID NO:1973)  
5'-TTTCTBGCCCCGGC-3' (FRAG. NO:1963) (SEQ. ID NO:1974)  
5'-TTCTBGCCCCGGC-3' (FRAG. NO:1964) (SEQ. ID NO:1975)  
5'-TCTBGCCCCGGC-3' (FRAG. NO:1965) (SEQ. ID NO:1976)  
5'-CTBGCCCCGGC-3' (FRAG. NO:1966) (SEQ. ID NO:1977)  
5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:1967) (SEQ. ID NO:1978)  
5'-GCGBGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:1968) (SEQ. ID NO:1979)  
5'-GCGBGCTGTBCCTCGCTGGGC-3' (FRAG. NO:1969) (SEQ. ID NO:1980)

5'-GCGBGCTGTCBCCTCGCTGGG-3' (FRAG. NO:1970) (SEQ. ID NO:1981)  
5'-GCGBGCTGTCBCCTCGCTGG-3' (FRAG. NO:1971) (SEQ. ID NO:1982)  
5'-GCGBGCTGTCBCCTCGCTG-3' (FRAG. NO:1972) (SEQ. ID NO:1983)  
5'-GCGBGCTGTCBCCTCGCT-3' (FRAG. NO:1973) (SEQ. ID NO:1984)  
5'-GCGBGCTGTCBCCTCGC-3' (FRAG. NO:1974) (SEQ. ID NO:1985)  
5'-GCGBGCTGTCBCCTCG-3' (FRAG. NO:1975) (SEQ. ID NO:1986)  
5'-GCGBGCTGTCBCCTC-3' (FRAG. NO:1976) (SEQ. ID NO:1987)  
5'-GCGBGCTGTCBCCT-3' (FRAG. NO:1977) (SEQ. ID NO:1988)  
5'-GCGBGCTGTCBCC-3' (FRAG. NO:1978) (SEQ. ID NO:1989)  
5'-GCGBGCTGTCBC-3' (FRAG. NO:1979) (SEQ. ID NO:1990)  
5'-GCGBGCTGTCB-3' (FRAG. NO:1980) (SEQ. ID NO:1991)  
5'-GCGBGCTGTC-3' (FRAG. NO:1981) (SEQ. ID NO:1992)  
5'-GCGBGCTGT-3' (FRAG. NO:1982) (SEQ. ID NO:1993)  
5'-CGBGGCTGTCBCCTCGCTGGGCCC-3' (FRAG. NO:1983) (SEQ. ID NO:1994)  
5'-GBGGCTGTCBCCTCGCTGGGCCC-3' (FRAG. NO:1984) (SEQ. ID NO:1995)  
5'-BGGCTGTCBCCTCGCTGGGCCC-3' (FRAG. NO:1985) (SEQ. ID NO:1996)  
5'-GGCTGTCBCCTCGCTGGGCCC-3' (FRAG. NO:1986) (SEQ. ID NO:1997)  
5'-GCTGTCBCCTCGCTGGGCCC-3' (FRAG. NO:1987) (SEQ. ID NO:1998)  
5'-CTGTGTCBCCTCGCTGGGCCC-3' (FRAG. NO:1988) (SEQ. ID NO:1999)  
5'-TGTCBCCTCGCTGGGCCC-3' (FRAG. NO:1989) (SEQ. ID NO:2000)  
5'-GTCBCCTCGCTGGGCCC-3' (FRAG. NO:1990) (SEQ. ID NO:2001)  
5'-TCBCCTCGCTGGGCCC-3' (FRAG. NO:1991) (SEQ. ID NO:2002)  
5'-CBCCTCGCTGGGCCC-3' (FRAG. NO:1992) (SEQ. ID NO:2003)  
5'-BCCTCGCTGGGCCC-3' (FRAG. NO:1993) (SEQ. ID NO:2004)  
5'-CCTCGCTGGGCCC-3' (FRAG. NO:1994) (SEQ. ID NO:2005)  
5'-CTCGCTGGGCCC-3' (FRAG. NO:1995) (SEQ. ID NO:2006)  
5'-TCGCTGGGCCC-3' (FRAG. NO:1996) (SEQ. ID NO:2007)  
5'-CGCTGGGCCC-3' (FRAG. NO:1997) (SEQ. ID NO:2008)  
5'-GCGCGCCGTCBTGGCGCGTCGGGCCGGC-3' (FRAG. NO:1998) (SEQ. ID NO:2009)  
5'-GCGCGCCGTCBTGGCGCGTCGGGCCGGG-3' (FRAG. NO:1999) (SEQ. ID NO:2010)  
5'-GCGCGCCGTCBTGGCGCGTCGGGCCGG-3' (FRAG. NO:2000) (SEQ. ID NO:2011)  
5'-GCGCGCCGTCBTGGCGCGTCGGGCCG-3' (FRAG. NO:2001) (SEQ. ID NO:2012)  
5'-GCGCGCCGTCBTGGCGCGTCGGGCC-3' (FRAG. NO:2002) (SEQ. ID NO:2013)  
5'-GCGCGCCGTCBTGGCGCGTCGGGC-3' (FRAG. NO:2003) (SEQ. ID NO:2014)  
5'-GCGCGCCGTCBTGGCGCGTCGGG-3' (FRAG. NO:2004) (SEQ. ID NO:2015)  
5'-GCGCGCCGTCBTGGCGCGTCGG-3' (FRAG. NO:2005) (SEQ. ID NO:2016)  
5'-GCGCGCCGTCBTGGCGCGTCG-3' (FRAG. NO:2006) (SEQ. ID NO:2017)  
5'-GCGCGCCGTCBTGGCGCGTC-3' (FRAG. NO:2007) (SEQ. ID NO:2018)  
5'-GCGCGCCGTCBTGGCGCGT-3' (FRAG. NO:2008) (SEQ. ID NO:2019)  
5'-GCGCGCCGTCBTGGCGCG-3' (FRAG. NO:2009) (SEQ. ID NO:2020)  
5'-GCGCGCCGTCBTGGCGG-3' (FRAG. NO:2010) (SEQ. ID NO:2021)  
5'-GCGCGCCGTCBTGGCG-3' (FRAG. NO:2011) (SEQ. ID NO:2022)  
5'-GCGCGCCGTCBTGGC-3' (FRAG. NO:2012) (SEQ. ID NO:2023)  
5'-GCGCGCCGTCBTGG-3' (FRAG. NO:2013) (SEQ. ID NO:2024)  
5'-GCGCGCCGTCBTG-3' (FRAG. NO:2014) (SEQ. ID NO:2025)  
5'-GCGCGCCGTCBT-3' (FRAG. NO:2015) (SEQ. ID NO:2026)  
5'-GCGCGCCGTCB-3' (FRAG. NO:2016) (SEQ. ID NO:2027)  
5'-GCGCGCCGTCB-3' (FRAG. NO:2017) (SEQ. ID NO:2028)  
5'-GCGCGCCGTC-3' (FRAG. NO:2018) (SEQ. ID NO:2029)  
5'-GCGCGCCGT-3' (FRAG. NO:2019) (SEQ. ID NO:2030)  
5'-GCGCGCCGTCBTGGCGCGTCGGGCCGGC-3' (FRAG. NO:2020) (SEQ. ID NO:2031)  
5'-GCGCGCCGTCBTGGCGCGTCGGGCCGGG-3' (FRAG. NO:2021) (SEQ. ID NO:2032)  
5'-GCGCGCCGTCBTGGCGCGTCGGGCCGG-3' (FRAG. NO:2022) (SEQ. ID NO:2033)  
5'-GGCCGTCBTGGCGCGTCGGGCCGGG-3' (FRAG. NO:2023) (SEQ. ID NO:2034)  
5'-GCCGTCBTGGCGCGTCGGGCCGGG-3' (FRAG. NO:2024) (SEQ. ID NO:2035)  
5'-CCGTCBTGGCGCGTCGGGCCGGG-3' (FRAG. NO:2025) (SEQ. ID NO:2036)  
5'-CGTCBTGGCGCGTCGGGCCGGG-3' (FRAG. NO:2026) (SEQ. ID NO:2037)  
5'-GTCBTGGCGCGTCGGGCCGGG-3' (FRAG. NO:2027) (SEQ. ID NO:2038)  
5'-TCBTGGCGCGTCGGGCCGGG-3' (FRAG. NO:2028) (SEQ. ID NO:2039)  
5'-CBTGGCGCGTCGGGCCGGG-3' (FRAG. NO:2029) (SEQ. ID NO:2040)  
5'-BTGGCGCGTCGGGCCGGG-3' (FRAG. NO:2030) (SEQ. ID NO:2041)  
5'-TGGCGCGTCGGGCCGGG-3' (FRAG. NO:2031) (SEQ. ID NO:2042)  
5'-GCGCGCGTCGGGCCGGG-3' (FRAG. NO:2032) (SEQ. ID NO:2043)  
5'-GCGCGCGTCGGGCCGGG-3' (FRAG. NO:2033) (SEQ. ID NO:2044)  
5'-CGCGCGTCGGGCCGGG-3' (FRAG. NO:2034) (SEQ. ID NO:2045)

5'-GGCGTCGGGGCCGGGC-3' (FRAG. NO:2035) (SEQ. ID NO:2046)  
5'-GCGTCGGGGCCGGGC-3' (FRAG. NO:2036) (SEQ. ID NO:2047)  
5'-CGTCGGGGCCGGGC-3' (FRAG. NO:2037) (SEQ. ID NO:2048)  
5'-GTCGGGGCCGGGC-3' (FRAG. NO:2038) (SEQ. ID NO:2049)  
5'-TCGGGGCCGGGC-3' (FRAG. NO:2039) (SEQ. ID NO:2050)  
5'-CGGGCCGGGC-3' (FRAG. NO:2040) (SEQ. ID NO:2051)  
5'-CCGCBGGCCBGGGCGCGCCGCCGGGGCCG-3' (FRAG. NO:2041) (SEQ. ID NO:2052)  
5'-CCGCBGGCCBGGGCGCGCCGCCGGGGCC-3' (FRAG. NO:2042) (SEQ. ID NO:2053)  
5'-CCGCBGGCCBGGGCGCGCCGCCGGGGC-3' (FRAG. NO:2043) (SEQ. ID NO:2054)  
5'-CCGCBGGCCBGGGCGCGCCGCCGGGG-3' (FRAG. NO:2044) (SEQ. ID NO:2055)  
5'-CCGCBGGCCBGGGCGCGCCGCCGGG-3' (FRAG. NO:2045) (SEQ. ID NO:2056)  
5'-CCGCBGGCCBGGGCGCGCCGCCGG-3' (FRAG. NO:2046) (SEQ. ID NO:2057)  
5'-CCGCBGGCCBGGGCGCGCCGCCGG-3' (FRAG. NO:2047) (SEQ. ID NO:2058)  
5'-CCGCBGGCCBGGGCGCGCCGCCGG-3' (FRAG. NO:2048) (SEQ. ID NO:2059)  
5'-CCGCBGGCCBGGGCGCGCCGCCG-3' (FRAG. NO:2049) (SEQ. ID NO:2060)  
5'-CCGCBGGCCBGGGCGCGCCGCC-3' (FRAG. NO:2050) (SEQ. ID NO:2061)  
5'-CCGCBGGCCBGGGCGCGCCGC-3' (FRAG. NO:2051) (SEQ. ID NO:2062)  
5'-CCGCBGGCCBGGGCGCGCG-3' (FRAG. NO:2052) (SEQ. ID NO:2063)  
5'-CCGCBGGCCBGGGCGCG-3' (FRAG. NO:2053) (SEQ. ID NO:2064)  
5'-CCGCBGGCCBGGGCG-3' (FRAG. NO:2054) (SEQ. ID NO:2065)  
5'-CCGCBGGCCBGGGCG-3' (FRAG. NO:2055) (SEQ. ID NO:2066)  
5'-CCGCBGGCCBGGGCG-3' (FRAG. NO:2056) (SEQ. ID NO:2067)  
5'-CCGCBGGCCBGGGCG-3' (FRAG. NO:2057) (SEQ. ID NO:2068)  
5'-CCGCBGGCCBGGGCG-3' (FRAG. NO:2058) (SEQ. ID NO:2069)  
5'-CCGCBGGCCBGGGCG-3' (FRAG. NO:2059) (SEQ. ID NO:2070)  
5'-CCGCBGGCCBGGG-3' (FRAG. NO:2060) (SEQ. ID NO:2071)  
5'-CCGCBGGCCBGG-3' (FRAG. NO:2061) (SEQ. ID NO:2072)  
5'-CCGCBGGCCBG-3' (FRAG. NO:2062) (SEQ. ID NO:2073)  
5'-CCGCBGGCCB-3' (FRAG. NO:2063) (SEQ. ID NO:2074)  
5'-CCGCBGGCC-3' (FRAG. NO:2064) (SEQ. ID NO:2075)  
5'-CGCBGGCCBGGGCGCGCCGCCGGGGCCG-3' (FRAG. NO:2065) (SEQ. ID NO:2076)  
5'-GCBGGCCBGGGCGCGCCGCCGGGGCCG-3' (FRAG. NO:2066) (SEQ. ID NO:2077)  
5'-CBGGCCBGGGCGCGCCGCCGGGGCCG-3' (FRAG. NO:2067) (SEQ. ID NO:2078)  
5'-BGGCCBGGGCGCGCCGCCGGGGCCG-3' (FRAG. NO:2068) (SEQ. ID NO:2079)  
5'-GGCCBGGGCGCGCCGCCGGGGCCG-3' (FRAG. NO:2069) (SEQ. ID NO:2080)  
5'-GCCBGGGCGCGCCGCCGGGGCCG-3' (FRAG. NO:2070) (SEQ. ID NO:2081)  
5'-CCBGGGCGCGCCGCCGGGGCCG-3' (FRAG. NO:2071) (SEQ. ID NO:2082)  
5'-CBGGGCGCGCCGCCGGGGCCG-3' (FRAG. NO:2072) (SEQ. ID NO:2083)  
5'-BGGGCGCGCCGCCGGGGCCG-3' (FRAG. NO:2073) (SEQ. ID NO:2084)  
5'-GGGCGCGCCGCCGGGGCCG-3' (FRAG. NO:2074) (SEQ. ID NO:2085)  
5'-GGCGCGCCGCCGGGGCCG-3' (FRAG. NO:2075) (SEQ. ID NO:2086)  
5'-GCGCGCCGCCGGGGCCG-3' (FRAG. NO:2076) (SEQ. ID NO:2087)  
5'-CGCGCCGCCGGGGCCG-3' (FRAG. NO:2077) (SEQ. ID NO:2088)  
5'-GCGCCGCCGGGGCCG-3' (FRAG. NO:2078) (SEQ. ID NO:2089)  
5'-CGCCGCCGGGGCCG-3' (FRAG. NO:2079) (SEQ. ID NO:2090)  
5'-GCCCGCCGGGGCCG-3' (FRAG. NO:2080) (SEQ. ID NO:2091)  
5'-CCGCCCGGGGGCCG-3' (FRAG. NO:2081) (SEQ. ID NO:2092)  
5'-CGCCGGGGGGCCG-3' (FRAG. NO:2082) (SEQ. ID NO:2093)  
5'-GCCGGGGGGCCG-3' (FRAG. NO:2083) (SEQ. ID NO:2094)  
5'-CCGGGGGGCCG-3' (FRAG. NO:2084) (SEQ. ID NO:2095)  
5'-CGGGGGGGCCG-3' (FRAG. NO:2085) (SEQ. ID NO:2096)  
5'-GGCGGGGGCCG-3' (FRAG. NO:2086) (SEQ. ID NO:2097)  
5'-GGGCGBGGCTCCGCB-3' (FRAG. NO:2087) (SEQ. ID NO:2098)  
5'-GGGCCCCCTGGCTCGGCCCGCGGCCCGCTTGCCCGCCCGGCCG-3' (FRAG. NO:2088) (SEQ. ID NO:2099)  
5'-GGGCCCCCTGGCTCGGCCCGCGGCCCGCTTGCCCGCCCGGCCG-3' (FRAG. NO:2089) (SEQ. ID NO:2100)  
5'-GGGCCCCCTGGCTCGGCCCGCGGCCCGCTTGCCCGCCCGGCC-3' (FRAG. NO:2090) (SEQ. ID NO:2101)  
5'-GGGCCCCCTGGCTCGGCCCGCGGCCCGCTTGCCCGCCCGGC-3' (FRAG. NO:2091) (SEQ. ID NO:2102)  
5'-GGGCCCCCTGGCTCGGCCCGCGGCCCGCTTGCCCGCCCGG-3' (FRAG. NO:2092) (SEQ. ID NO:2103)  
5'-GGGCCCCCTGGCTCGGCCCGCGGCCCGCTTGCCCGCCCG-3' (FRAG. NO:2093) (SEQ. ID NO:2104)  
5'-GGGCCCCCTGGCTCGGCCCGCGGCCCGCTTGCCCGCC-3' (FRAG. NO:2094) (SEQ. ID NO:2105)  
5'-GGGCCCCCTGGCTCGGCCCGCGGCCCGCTTGCCCGC-3' (FRAG. NO:2095) (SEQ. ID NO:2106)  
5'-GGGCCCCCTGGCTCGGCCCGCGGCCCGCTTGCCCG-3' (FRAG. NO:2096) (SEQ. ID NO:2107)  
5'-GGGCCCCCTGGCTCGGCCCGCGGCCCGCTTGCCG-3' (FRAG. NO:2097) (SEQ. ID NO:2108)  
5'-GGGCCCCCTGGCTCGGCCCGCGGCCCGCTTGCC-3' (FRAG. NO:2098) (SEQ. ID NO:2109)  
5'-GGGCCCCCTGGCTCGGCCCGCGGCCCGCTTGCC-3' (FRAG. NO:2099) (SEQ. ID NO:2110)

5'-GGGCCCCTGGCTCGGCCCCCGGGCCCGGCTTGCC-3' (FRAG. NO:2100) (SEQ. ID NO:2111)  
5'-GGGCCCCTGGCTCGGCCCCCGGGCCCGGCTTGCC-3' (FRAG. NO:2101) (SEQ. ID NO:2112)  
5'-GGGCCCCTGGCTCGGCCCCCGGGCCCGGCTTG-3' (FRAG. NO:2102) (SEQ. ID NO:2113)  
5'-GGGCCCCTGGCTCGGCCCCCGGGCCCGGCTT-3' (FRAG. NO:2103) (SEQ. ID NO:2114)  
5'-GGGCCCCTGGCTCGGCCCCCGGGCCCGGCT-3' (FRAG. NO:2104) (SEQ. ID NO:2115)  
5'-GGGCCCCTGGCTCGGCCCCCGGGCCCGGC-3' (FRAG. NO:2105) (SEQ. ID NO:2116)  
5'-GGGCCCCTGGCTCGGCCCCCGGGCCCGG-3' (FRAG. NO:2106) (SEQ. ID NO:2117)  
5'-GGGCCCCTGGCTCGGCCCCCGGGCCCG-3' (FRAG. NO:2107) (SEQ. ID NO:2118)  
5'-GGGCCCCTGGCTCGGCCCCCGGGCC-3' (FRAG. NO:2108) (SEQ. ID NO:2119)  
5'-GGGCCCCTGGCTCGGCCCCCGGGCC-3' (FRAG. NO:2109) (SEQ. ID NO:2120)  
5'-GGGCCCCTGGCTCGGCCCCCGGGC-3' (FRAG. NO:2110) (SEQ. ID NO:2121)  
5'-GGGCCCCTGGCTCGGCCCCCGG-3' (FRAG. NO:2111) (SEQ. ID NO:2122)  
5'-GGGCCCCTGGCTCGGCCCCCG-3' (FRAG. NO:2112) (SEQ. ID NO:2123)  
5'-GGGCCCCTGGCTCGGCCCCG-3' (FRAG. NO:2113) (SEQ. ID NO:2124)  
5'-GGGCCCCTGGCTCGGCCCC-3' (FRAG. NO:2114) (SEQ. ID NO:2125)  
5'-GGGCCCCTGGCTCGGCCC-3' (FRAG. NO:2115) (SEQ. ID NO:2126)  
5'-GGGCCCCTGGCTCGGCC-3' (FRAG. NO:2116) (SEQ. ID NO:2127)  
5'-GGGCCCCTGGCTCGGC-3' (FRAG. NO:2117) (SEQ. ID NO:2128)  
5'-GGGCCCCTGGCTCGG-3' (FRAG. NO:2118) (SEQ. ID NO:2129)  
5'-GGGCCCCTGGCTCG-3' (FRAG. NO:2119) (SEQ. ID NO:2130)  
5'-GGGCCCCTGGCTC-3' (FRAG. NO:2120) (SEQ. ID NO:2131)  
5'-GGGCCCCTGGTC-3' (FRAG. NO:2121) (SEQ. ID NO:2132)  
5'-GGGCCCCTGGT-3' (FRAG. NO:2122) (SEQ. ID NO:2133)  
5'-GGCCCCTGGCTCGGCCCCCGGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2123) (SEQ. ID NO:2134)  
5'-GCCCCTGGCTCGGCCCCCGGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2124) (SEQ. ID NO:2135)  
5'-CCCTGGCTCGGCCCCCGGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2125) (SEQ. ID NO:2136)  
5'-CCCTGGCTCGGCCCCCGGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2126) (SEQ. ID NO:2137)  
5'-CCTGGCTCGGCCCCCGGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2127) (SEQ. ID NO:2138)  
5'-CTGGCTCGGCCCCCGGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2128) (SEQ. ID NO:2139)  
5'-TGGCTCGGCCCCCGGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2129) (SEQ. ID NO:2140)  
5'-GGCTCGGCCCCCGGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2130) (SEQ. ID NO:2141)  
5'-GCTCGGCCCCCGGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2131) (SEQ. ID NO:2142)  
5'-CTCGGCCCCCGGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2132) (SEQ. ID NO:2143)  
5'-TCGGCCCCCGGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2133) (SEQ. ID NO:2144)  
5'-CGGCCCCCGGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2134) (SEQ. ID NO:2145)  
5'-GGCCCCCGGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2135) (SEQ. ID NO:2146)  
5'-GCCCCCGGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2136) (SEQ. ID NO:2147)  
5'-CCCCCGGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2137) (SEQ. ID NO:2148)  
5'-CCCGCGGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2138) (SEQ. ID NO:2149)  
5'-CCGCGGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2139) (SEQ. ID NO:2150)  
5'-CGCGGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2140) (SEQ. ID NO:2151)  
5'-GCGGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2141) (SEQ. ID NO:2152)  
5'-CGGCCCCGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2142) (SEQ. ID NO:2153)  
5'-GGCCCCGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2143) (SEQ. ID NO:2154)  
5'-GCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2144) (SEQ. ID NO:2155)  
5'-CCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2145) (SEQ. ID NO:2156)  
5'-CCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2146) (SEQ. ID NO:2157)  
5'-CGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2147) (SEQ. ID NO:2158)  
5'-GGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2148) (SEQ. ID NO:2159)  
5'-GCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2149) (SEQ. ID NO:2160)  
5'-CTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2150) (SEQ. ID NO:2161)  
5'-TTGCCCGCCCGGCCCGG-3' (FRAG. NO:2151) (SEQ. ID NO:2162)  
5'-TGCCCGCCCGGCCCGG-3' (FRAG. NO:2152) (SEQ. ID NO:2163)

5'-GGCGGGGGCGGCGGCGCCTGGCTCGCCTB-3' (FRAG. NO:2165) (SEQ. ID NO:2176)  
5'-GGCGGGGGCGGCGGCGCCTGGCTCGCCT-3' (FRAG. NO:2166) (SEQ. ID NO:2177)  
5'-GGCGGGGGCGGCGGCGCCTGGCTCGCC-3' (FRAG. NO:2167) (SEQ. ID NO:2178)  
5'-GGCGGGGGCGGCGGCGCCTGGCTCGC-3' (FRAG. NO:2168) (SEQ. ID NO:2179)  
5'-GGCGGGGGCGGCGGCGCCTGGCTCG-3' (FRAG. NO:2169) (SEQ. ID NO:2180)  
5'-GGCGGGGGCGGCGGCGCCTGGCTC-3' (FRAG. NO:2170) (SEQ. ID NO:2181)  
5'-GGCGGGGGCGGCGGCGCCTGGCT-3' (FRAG. NO:2171) (SEQ. ID NO:2182)  
5'-GGCGGGGGCGGCGGCGCCTGGC-3' (FRAG. NO:2172) (SEQ. ID NO:2183)  
5'-GGCGGGGGCGGCGGCGCCTGG-3' (FRAG. NO:2173) (SEQ. ID NO:2184)  
5'-GGCGGGGGCGGCGGCGCCTG-3' (FRAG. NO:2174) (SEQ. ID NO:2185)  
5'-GGCGGGGGCGGCGGCGCCT-3' (FRAG. NO:2175) (SEQ. ID NO:2186)  
5'-GGCGGGGGCGGCGGCGCC-3' (FRAG. NO:2176) (SEQ. ID NO:2187)  
5'-GGCGGGGGCGGCGGCGC-3' (FRAG. NO:2177) (SEQ. ID NO:2188)  
5'-GGCGGGGGCGGCGGCG-3' (FRAG. NO:2178) (SEQ. ID NO:2189)  
5'-GGCGGGGGCGGCGG-3' (FRAG. NO:2179) (SEQ. ID NO:2190)  
5'-GGCGGGGGCGGCG-3' (FRAG. NO:2180) (SEQ. ID NO:2191)  
5'-GGCGGGGGCGGCG-3' (FRAG. NO:2181) (SEQ. ID NO:2192)  
5'-GGCGGGGGCGGCG-3' (FRAG. NO:2182) (SEQ. ID NO:2193)  
5'-GGCGGGGGCGGCG-3' (FRAG. NO:2183) (SEQ. ID NO:2194)  
5'-GCGGGGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2184) (SEQ. ID NO:2195)  
5'-CGGGGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2185) (SEQ. ID NO:2196)  
5'-GGGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2186) (SEQ. ID NO:2197)  
5'-GGGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2187) (SEQ. ID NO:2198)  
5'-GGGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2188) (SEQ. ID NO:2199)  
5'-GGGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2189) (SEQ. ID NO:2200)  
5'-GCGGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2190) (SEQ. ID NO:2201)  
5'-CGGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2191) (SEQ. ID NO:2202)  
5'-GGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2192) (SEQ. ID NO:2203)  
5'-GCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2193) (SEQ. ID NO:2204)  
5'-CGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2194) (SEQ. ID NO:2205)  
5'-GGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2195) (SEQ. ID NO:2206)  
5'-GCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2196) (SEQ. ID NO:2207)  
5'-CGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2197) (SEQ. ID NO:2208)  
5'-GCTTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2198) (SEQ. ID NO:2209)  
5'-CCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2199) (SEQ. ID NO:2210)  
5'-CTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2200) (SEQ. ID NO:2211)  
5'-TGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2201) (SEQ. ID NO:2212)  
5'-GGCTCGCCTBGGGCCCC-3' (FRAG. NO:2202) (SEQ. ID NO:2213)  
5'-GCTCGCCTBGGGCCCC-3' (FRAG. NO:2203) (SEQ. ID NO:2214)  
5'-CTCGCCTBGGGCCCC-3' (FRAG. NO:2204) (SEQ. ID NO:2215)  
5'-TCGCCTBGGGCCCC-3' (FRAG. NO:2205) (SEQ. ID NO:2216)  
5'-CGCCTBGGGCCCC-3' (FRAG. NO:2206) (SEQ. ID NO:2217)  
5'-GCCTBGGGCCCC-3' (FRAG. NO:2207) (SEQ. ID NO:2218)  
5'-CTBGGGCCCC-3' (FRAG. NO:2208) (SEQ. ID NO:2219)  
5'-CTBGGGCCCC-3' (FRAG. NO:2209) (SEQ. ID NO:2220)  
5'-GGGTGGGCBGCGCGGCC-3' (FRAG. NO:2210) (SEQ. ID NO:2221)  
5'-GGTCGGCGBBBGCTCGTCGTGGC-3' (FRAG. NO:2211) (SEQ. ID NO:2222)  
5'-GGTCGGCGBBBGCTCGTCGTGG-3' (FRAG. NO:2212) (SEQ. ID NO:2223)  
5'-GGTCGGCGBBBGCTCGTCGTG-3' (FRAG. NO:2213) (SEQ. ID NO:2224)  
5'-GGTCGGCGBBBGCTCGTCGT-3' (FRAG. NO:2214) (SEQ. ID NO:2225)  
5'-GGTCGGCGBBBGCTCGTCG-3' (FRAG. NO:2215) (SEQ. ID NO:2226)  
5'-GGTCGGCGBBBGCTCGTC-3' (FRAG. NO:2216) (SEQ. ID NO:2227)  
5'-GGTCGGCGBBBGCTCGT-3' (FRAG. NO:2217) (SEQ. ID NO:2228)  
5'-GGTCGGCGBBBGCTCG-3' (FRAG. NO:2218) (SEQ. ID NO:2229)  
5'-GGTCGGCGBBBGCTC-3' (FRAG. NO:2219) (SEQ. ID NO:2230)  
5'-GGTCGGCGBBBGCT-3' (FRAG. NO:2220) (SEQ. ID NO:2231)  
5'-GGTCGGCGBBBG-3' (FRAG. NO:2221) (SEQ. ID NO:2232)  
5'-GGTCGGCGBBBG-3' (FRAG. NO:2222) (SEQ. ID NO:2233)  
5'-GGTCGGCGBBG-3' (FRAG. NO:2223) (SEQ. ID NO:2234)  
5'-GGTCGGCGBB-3' (FRAG. NO:2224) (SEQ. ID NO:2235)  
5'-GTCGGCGBBBGCTCGTCGTGGC-3' (FRAG. NO:2225) (SEQ. ID NO:2236)  
5'-TCGGCGBBBGCTCGTCGTGGC-3' (FRAG. NO:2226) (SEQ. ID NO:2237)  
5'-CGGCGBBBGCTCGTCGTGGC-3' (FRAG. NO:2227) (SEQ. ID NO:2238)  
5'-GGCGBBBGCTCGTCGTGGC-3' (FRAG. NO:2228) (SEQ. ID NO:2239)  
5'-GCGBBBGCTCGTCGTGGC-3' (FRAG. NO:2229) (SEQ. ID NO:2240)



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5'-CGBBGBGCTCGTCGTGGC-3' (FRAG. NO:2230) (SEQ. ID NO:2241)  
5'-GBBGBGCTCGTCGTGGC-3' (FRAG. NO:2231) (SEQ. ID NO:2242)  
5'-BBBGBGCTCGTCGTGGC-3' (FRAG. NO:2232) (SEQ. ID NO:2243)  
5'-BGBGCTCGTCGTGGC-3' (FRAG. NO:2233) (SEQ. ID NO:2244)  
5'-GBGCTCGTCGTGGC-3' (FRAG. NO:2234) (SEQ. ID NO:2245)  
5'-BGCTCGTCGTGGC-3' (FRAG. NO:2235) (SEQ. ID NO:2246)  
5'-GCTCGTCGTGGC-3' (FRAG. NO:2236) (SEQ. ID NO:2247)  
5'-CTCGTCGTGGC-3' (FRAG. NO:2237) (SEQ. ID NO:2248)  
5'-TCGTCGTGGC-3' (FRAG. NO:2238) (SEQ. ID NO:2249)  
5'-GGGGCCCCGCGCCGCC-3' (FRAG. NO:2239) (SEQ. ID NO:2250)  
5'-GGGGCCCCGCGCCGCC-3' (FRAG. NO:2240) (SEQ. ID NO:2251)  
5'-GGGGCCCCGCGCCGCC-3' (FRAG. NO:2241) (SEQ. ID NO:2252)  
5'-GGGGCCCCGCGCCGCC-3' (FRAG. NO:2242) (SEQ. ID NO:2253)  
5'-GGGGCCCCGCGCCGCC-3' (FRAG. NO:2243) (SEQ. ID NO:2254)  
5'-GGGGCCCCGCGCCGCC-3' (FRAG. NO:2244) (SEQ. ID NO:2255)  
5'-GGGGCCCCGCGCCGCC-3' (FRAG. NO:2245) (SEQ. ID NO:2256)  
5'-GGGGCCCCGCGCCGCC-3' (FRAG. NO:2246) (SEQ. ID NO:2257)  
5'-GGGGCCCCGCGCCGCC-3' (FRAG. NO:2247) (SEQ. ID NO:2258)  
5'-GGGGCCCCGCGCCGCCGCC-3' (FRAG. NO:2248) (SEQ. ID NO:2259)  
5'-GGCCCCGCGCCGCCGCCGCC-3' (FRAG. NO:2249) (SEQ. ID NO:2260)  
5'-GCCCGCGCCGCCGCCGCC-3' (FRAG. NO:2250) (SEQ. ID NO:2261)  
5'-CCCCGCGCCGCCGCCGCC-3' (FRAG. NO:2251) (SEQ. ID NO:2262)  
5'-CCCGCGCCGCCGCCGCC-3' (FRAG. NO:2252) (SEQ. ID NO:2263)  
5'-CCGCGCCGCCGCCGCC-3' (FRAG. NO:2253) (SEQ. ID NO:2264)  
5'-CGCGCCGCCGCCGCC-3' (FRAG. NO:2254) (SEQ. ID NO:2265)  
5'-GCGCGCCGCCGCCGCC-3' (FRAG. NO:2255) (SEQ. ID NO:2266)  
5'-CGCCGCCGCCGCCGCC-3' (FRAG. NO:2256) (SEQ. ID NO:2267)  
5'-GCCGCCGCCGCCGCC-3' (FRAG. NO:2257) (SEQ. ID NO:2268)  
5'-GGGGCGCGGGGCGCCGCCGCC-3' (FRAG. NO:2258) (SEQ. ID NO:2269)  
5'-GGCGGGGBGCGGBGGGCGCCGCCGCC-3' (FRAG. NO:2259) (SEQ. ID NO:2270)  
5'-GGCGGTCGCGGTCGCCCCBGTGCGGGCTCGCGC-3' (FRAG. NO:2260) (SEQ. ID NO:2271)  
5'-GCGCGGGBBGBGCGBGGCGGGCGCG-3' (FRAG. NO:2261) (SEQ. ID NO:2272)  
5'-GCGCBGGGCCCCBCTGCGCGGGC-3' (FRAG. NO:2262) (SEQ. ID NO:2273)  
5'-GGGCGGGGTGGGCTGCCCTGCGCGGCC-3' (FRAG. NO:2263) (SEQ. ID NO:2274)  
5'-GGGCTGCTGCGCGGGCTCCGGCGA-3' (FRAG. NO:2264) (SEQ. ID NO:2275)  
5'-CTCCCGGGCGGGCGGGCGGGG-3' (FRAG. NO:2265) (SEQ. ID NO:2276)  
5'-GGGCTGCGCGGTCCGGGCCCTCTTGCGGCG-3' (FRAG. NO:2266) (SEQ. ID NO:2277)  
5'-GCGCTGCGCGGCTGCCGG-3' (FRAG. NO:2267) (SEQ. ID NO:2278)  
5'-GCGCGCTTGCCCTTGTCGCGGC-3' (FRAG. NO:2268) (SEQ. ID NO:2279)  
5'-GCTGCTCCBCGCGTGG-3' (FRAG. NO:2269) (SEQ. ID NO:2280)  
5'-GCCGGBGGCCGCCBGGTCCCGCG-3' (FRAG. NO:2270) (SEQ. ID NO:2281)  
5'-CCCGGCGGGCGCBGGBBGGGCGGGCTGGGC-3' (FRAG. NO:2271) (SEQ. ID NO:2282)  
5'-GTCTCTCCCGCCCCGCGCGCG-3' (FRAG. NO:2272) (SEQ. ID NO:2283)  
5'-GGGCGTCCGCTCCGGGCCGTCGGG-3' (FRAG. NO:2273) (SEQ. ID NO:2284)  
5'-GCGGGCACGCGCGGCTCTGGCGTCGGC-3' (FRAG. NO:2274) (SEQ. ID NO:2285)

**Bradykinin Receptor Nucleic Acids and Antisense Oligonucleotide Fragments**

5'-GGTGBCBTTG BCBTGTCTGG CGCGGTCCCG TTBBBGTGG GCCCGCCAGC CCAGCCACTC CACTTGGGGG CGGGTGGCCA  
GCACGAACG CACCCAGAGG AAGGGGGGCG GCCCAGAAGG GCAGCCCGCA GGCCAGGATC AGGTCTGTG  
CGCCCGGAGA TAATGGCATT CACCACGCGG CGGCCAGCG CAGCCGCGC ATCCGGCCCC GGTCTGACC TGCAGCCCC  
GTCTCCTTGG CATTCTTGGG CCCCAGTCAC TCCTCTCCTT GCCCCCTTG CTGGGGCAGG GACGGGGTG BCBTTGBGCB  
TGTCGGCGCG GTCCCGTTBB GBGTGGGCCC GCCAGCCAG CCACTCCACT TGGGGGCGGG TGGCCAGCAC GAACAGCACC  
CAGAGGAAGG GGGGCGGCCC AGAAGGGCAG CCCGAGGCC AGGATCAGGT CTGCTGCGGC CGGAGATAAT GGCATTACC  
ACGCGCGGCG CCAGCGCAG CCGCGCATCC GGCCCGGGTT CTGACCTGCA GCGCCGCTCT CTTGGCATT CTTGGGCCCC  
AGTCACTCCT CTCCTGCCCC CCCTTGCTGG GGCAGGACG GCGGTGTGT CBGTGGTGT GCGCGTTGB GGTBTGGCGC  
TCCBCCBBTT CCTTTTCTC CTGTTTTCC GTTCTCTTG CCGTCTGTGG TT CAGATTACA AACTGCAGGA CTGGGACGGG  
AGCAGACAGT GAGCAAACGC CAGCAGGGCT GCTGTGAATT TGTGAAGGA TTGAGGGACA GTTGCTTTTC AGCATGGGCC  
CAGGAATGCC AAGGAGACAT CTATGCACGA CTTGGGAAA TGAGTTGATG TCTCCGGTAA AACACCGGAG ACTAATTCCT  
GCCCTGCCCA ATTTGCAGG GAGCATGGCT GTGAGGATGG GGTGAATCA CGCACAGCCA AGGACTCAA AATCACAACA  
GCATTACTGT TCTTATTGCG TGCCACACCT GAGCCAGCTT GCTCCTTCC AGGAGTGGAG GAGGCTGGG GGGAGGAGGA  
GGAGTGACTG AGCTTCCCTC CCGTGTGTTT TCCGTCCCTG CCCCAGCAAG ACAACTTAGA TCTCCAGGAG AACTGGCATC  
CAGCTTTGGT GCAATGGCTG AGTGACAAAG TGAGTTGTTG CCTGGGTTT CTTAATCTA TTCAGCTAGA ACTTTGAAGG  
ACAATTTCTT GCATTAATAA AGGTTAAGCC CTGAGGGGTC CCTGATAACA ACCTGGAGAC CAGGATTTTA TGGTCCCCCT  
CACTGATGGA CAAGGAGGTG TGTGCCAAAG AAGAATCAA TAAGCACATA TTGAGCACTT GCTGTATATG CAGTATTGAG  
CACTGTAGGC AAGACCAAG AAAGAGAAAG AGCCATCTCC ATCTTGAGG AACTCAAAGA CTCAAGTGGG AACGACTGGG  
CACTGCCACC ACCAGAAAGC TGTTGACGA GACGGTCGAG CAGGGTGCTG TGGGTGATAT GGACAGCAGA AGGGGAGAC  
CAAGGTTCCA GCTCAACAA TAACTATTGC ACAACCACT GTCCCTGCCT CAGTTCCTT TTATGTAACA TGAAGTCGT

GTGAGGGTTA AAGGCAGTAA CAGGTATAAA GTACTTAGAA AAGCAAAGGG TGCTACGTAC ATGTGAGGCA TCATTACGCA  
GACGTAACCTG GGATATGTTT ACTATAAGGA AAAGACACTG AGGTCTAGAA ATAGCTCCGT GGAGCAGAAT CAGTATTGGG  
AGCCGGTGGC GGTGTGAAGC ACCAGTGTCT GGCACACAGT AGGTGCTCAT TGGCTCCCTT CCACCTGTCA TCCCACCAC  
CCTGAGGGCC CAACCGCCAC ACACACAGGA GCATTTGGAG AGAAGGCCAT GTCTTCAAAG TCTGATTGTG GATGAGGCAG  
AGGAAGATAT TTCTAATCGG TCTTGCCAG AGGATCACAG TGCTGAGACC CCCCACCACC AGCCGGTACC TGGGAAGGGG  
GAGAGTGCAG GCCTGCTCAG GGAAGTCTCC TGTCTCAGCA ACCAAGGGAT TGTCTCTGT AATCAATGGT TTATTGGAAG  
GTGGCCCAAT ATGAGCCCTA GAAGAGTGTG AAAAGGAATG GCAATGGTGT TCACCATCGG CAGTGCCAGG GCAGCACTCA  
TTCACTTGAT AAATGAATAT TTATTAGCTG GTTGGAGAGC TAGAACCTGG AGAGCTAGAA CCTGGAGAAC TAGAACCTGG  
AGGGCTAGAA CCTGGAGAGG CTAGAACCAA GAAGGGCTAG AACCTGGAGG GGCTAGAACC TAGAGAAGCT AAAACCTGAG  
CTAGAAGCTG GAGGACTAGA ACCTGGAGGG CTGGAATCTG AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA  
ACCTGGAGGG CTAGAACCTG GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTGG AATCTGGAGA GCTAGAACCT  
GGAGGGCTAG AACCTGGAGG GCTAGAACCT AGAAGGGCTA GAACCTGGAG GGCTAGAACC TGGCAGGTAA GAACCTAGAA  
GGGCTAGAAC CTGGAGAGCC AGAAGCTGGA GGGCTAGAAC CTGGAAGGGC TAGAACCTGT AGAGCTAGAA CATGGAGAGC  
TGAACCCCGG CAGGCTAGAA CCTGGCAAGC TAGAACCTGG AGGGAATGAA CCTGGAGGGC TAGAACCTGG AGAATGAGAA  
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TAGTTTCAA TTCCGCACTC AGCAGGCATC TTTCTGATGA TCCGATGGCT TCTCAGAGCC AGGGATGGGC CAGGATCCAT  
CCCTTGGCT ACTGCTTGC TGAGAAATTT ATAAGCAGCA TCTGGTGCTA TACTTGGTC TCTAGTGAGT TAGCTCATGA  
AAGATGATAG ACTCTCCAAG CCAGGGGTAT GCAGGAAATG GGTTTTCTGT AGCTACAGAA ATGGGGTTGA GGGTTGGACC  
AAGGGACTAC CCAGGGGAAG TCTTACCTC AGAGGACTCT GGAAGGAGG GTGCAAGTTT TCATGGGTCA AGAATTCAGA  
GCCAGTAGA GACAGCTTAT CTCTGTTCCA AGATGCTGCG GGCCTGTTGTT GGAAGATTCA AAGCTAGGA AACCAGGAGC  
CACCAAAAGC GTAAGTGGG CCAGAGGATC CACTTTCAAG GTGGCAAGTT GGTTCCTCCC ATGTGGCTGC TTGAGTATCC  
TCACATGGCG GCTCACATCC TTCCAAGTAA GCAATGCAA AGGCCAAGAA AGATGCTGCA AAGATGTTAT GACCTAGCCT  
CAGAAATCAC ACACATCCC TGCCACCATT AGTAAGAAGT CCAGCCCACG TCCAGGAGAA GAGGAAGCAG ATCTCTCTT  
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CTCACTCAAC CTCTTGCTAC TTCCACCTC TCTGTCCAA CATCTAGTGT CACTTTCCAG AACATACCA CAGTCTCCCC  
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CAGGATGCCA CAGACTGTCC AGGAAGACAG AAAGTAGGCA GATGGGCTGG CCATGGTCTC CAAGCCAGAC TGAATCTCC  
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TGCTGCCCTT GAGTGTATC ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG  
GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCTGG TTGTGCTGCT GCTATTATC ATCTGCTGGC TGCCCTTCCA  
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CCCTTCAAAG ATGAGCTGTT CCCGCCGCA CTCCAGTCT GCTTCTGGG CTCCGAGGAG GGTGGGGAC GGTGCTGACG  
GTGGGGACAT CAGGCTGCCC CGCAGTACCA GGGAGCGACT GAAGTGCCCA TGCCGCTTGC TCCGAGAAG GTGGGTGCCG  
GGCAGGGGCT GCTCCAGCCG CCTCACCTCT GCTGGGAGGA CAACTGTCC CAGCACAGAG GGAGGGAGGG AGGGCAGGCA  
GCGGGGAGAA GTTCCCTGT GGTCTGGGG AGTTGGGAAA AGTTCCCTC CTCCGGAGG GAGG -3' (FRAG. NO:2275)  
(SEQ. ID NO:2286)

5'- GAGTCTTCA ATATTTAGT GAAAGCTATA GATGAGGCTC CATAGGGAT AAAGCACAGA CACACCTTT  
CAGAGGGCTT GTGACTCTG GGCAGCCTGT CCATAGACCT CTGTCCCAA CTGGCAAGT AGGAACTCC AGATTAAGGA  
GCCCCAATGT GGTGAACAG CCAGGTGCAG AGTAGTCA ACCACACAGC CAGGCCAGG AGGGCTTCA CTCAAGACC  
TACAGCCAGT TCACAGCCAA GCCAGGGCTA GCGCCAGGCC ACCATAAAC TGATCTGAGA CTCTGTTTCC CTGTCTCCAT  
GATGATGGGA TCAGGCTTGA TTGCTGTTT GTAGGCTTGT TATGAATCAA GTCACAGGGA AGAGGAGCTG ATGGGCTGGG  
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TAAGGCTTCA AAAAAAATG TTTTGAAGT CCCTGCCCTT TCCAGTCTCT ACCGTCTCAG CCCTGGGAGT GTAAAGTGCT  
GCAGATAGTT AGTAAGTCTT TGAGCAAAAC TGAGAAAGCC AGCCTGAGCC TTGACATGGG AGAACTCC GCCATACATC  
TCCGAAGAAA CGGCGCGTG TCTCAGGGGA GCGCAAAAC CCGTACCCAG GAAACAGGAC AGCTTCTGCC ACTGTCGCCC  
TTGGGAGCCG TACGTGGCAT GACAAAGAAA TCCAGGACT CCGCTGCC ACCTGGCCAC CTCTGTTTCA CACCTTCCGC  
GTAAACGCCC ACTGTTTACA TCCAAAATC AGACAAAAA TAACCACCTC AAGAAGATAA ATAATGATAA GAAATAAATG  
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GACTCCAACG GGCAGCCGGG CCTACGAAA CATGGAAATC TTCCAAGAGC CTCCCTGGCC CCCAGGGCTC AGAGGGTGGC  
AGAGCGGAGA GCGAAGGTGG CCGCAGCCT CCCGGCCCCA CAGCCAGCT GGCTCCAGCT GGGCAGGAGT GCAGAGCTCA  
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CTCCAGCTCT GGCTCTGGG CTCCGAGGAG GGTGGGGAC GGTGGTACG GTGGGGACAT CAGGCTGCC CGCAGTACCA  
GGGAGCGACT GAAGTGCCCA TGCCGCTTGC TCCGAGAAG GTGGGTGCCG GGCAGGGGCT GCTCCAGCG CCTCACCTCT  
GCTGGGAGGA CAACTGTCC CAGCACAGAG GGAGGGAGGG AGGGCAGGCA GCGGGGAGAA GTTCCCTGT GGTCTGGGG  
AGTTGGGAAA AGTTCCCTC CTCCGGAGG GAGG -3' (FRAG. NO:2275) (SEQ. ID NO:2461)

5'- GCCCTTCAA GATGAGCTGT TCCCGCCGCC ACTCCAGCTC TGGCTTCTGG GCTCCGAGGA GGGGTGGGGA  
CGGTGGTGAC GGTGGGGACA TCAGGCTGCC CCGCAGTACC AGGGAGCGAC TGAAGTGCC ATGCCGCTTG CTCCGGAGAA  
GGTGGGTGCC GGGCAGGGG TGCTCCAGCC GCCTCACCTC TGCTGGGAGG ACAAAGTGT CCAGCACAGA GGGAGGGAGG  
GAGGGCAGGC AGCGGGGAGA AGTTTCCTG TGGTCTGGG GAGTT -3' (FRAG. NO:2275) (SEQ. ID NO:2460)

5'- GCCCTTCAA GATGAGCTGT TCCCGCCGCC ACTCCAGCTC TGGCTTCTGG GCTCCGAGGA GGGGTGGGGA  
CGGTGGGGAC ATCAGGCTGC CCCGAGTAC CAGGGAGCGA CTGAAGTGCC CATGCCGCTT GCTCCGAGAA AGGTGGGTGC  
CGGGCAGGGG CTGCTCCAGC CGCTCACCT CTGCTGGGAG GACAACTGT CCCAGCACAG AGGGAGGGAG GGAGGGCAGG  
CAGCGGGGAG AAGTTTCCT GTGGTCTGG GGAGTT -3' (FRAG. NO:2275) (SEQ. ID NO:2459)

5'- ATGTTCTCT CCTGGAAGAT ATCAATGTT CTGTCTGTT GTGAGGACTC CTGCCCCACC ACGGCTCTT TCAGCGCCGA  
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GCTGGCTCAA CACCATCCAG CCCCCCTTCT TCTGGGTGCT GTTCGTGCTG GCCACCTAG AGAATCTT TGCTCTCAGC  
GTCTTCTGCC TGCACAAGAG CAGCTGCAG GTGGCAGAGA TCTACCTGGG GAACCTGGCC GCAGCAGACC TGATCTGGC  
CTGCGGCTG CCCTTCTGG CCATCACCAT GTCCAACAAC TCGACTGGC TCTTTGGGA GACGCTCTG CGCGTGGTGA  
ATGCCATTAT CTCCATGAAC CTGTACAGCA GCATCTGTT CTGATGCTG GTGAGCATCG ACCGCTACCT GCGCTGGT  
AAAACCATGT CCATGGGCGG GATGCGCGG GTGCGTGGG CCAAGCTCTA CAGCTTGGT ATCTGGGGT GTACGCTGCT  
CCTGAGCTCA CCCATGCTG TGTCCGGAC CATGAAGGAG TACAGCGAT AGGGCCACAA CGTACCGCT TGTGTCATCA

GCTACCCATC CCTCATCTGG GAAGTGTTC CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCT GAGTGTATC  
ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG GAGATCCAGA CGGAGAGGAG  
GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA  
CGCTGCATCG CCTCGGCATC CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG  
GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA AAGAAGTCTT GGGAGGTGA  
CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC ATTCAGATGG AGAACTCCAT GGGCAGCTG CGGACCTCCA  
TCTCCGTGGA ACGCCAGATT CACAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG  
AATTTGTGTA AGGATTGAGG GACAGTTGCT T -3' (FRAG. NO:2275) (SEQ. ID NO:2458)

5'- ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTT GTGAGGACTC CGTGCCCACC ACGGCTCTT TCAGCGCCGA  
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GCTGGCTCAA CACCATCCAG CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCTCAGC  
GTCTTCTGCC TGCACAAGAG CAGCTGCAG GTGGCAGAGA TCTACCTGGG GAACCTGGCC GCAGCAGACC TGATCTGGC  
CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC TTCGACTGGC TCTTTGGGA GACGCTCTGC CGCGTGTGA  
ATGCCATTAT TCCATGAAC CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG  
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CCTGAGCTCA CCCATGCTGG TGTCCGGAC CATGAAGGAG TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA  
GCTACCCATC CCTCATCTGG GAAGTGTTC CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCT GAGTGTATC  
ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG GAGATCCAGA CGGAGAGGAG  
GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA  
CGCTGCATCG CCTCGGCATC CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG  
GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA AAGAAGTCTT GGGAGGTGA  
CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC ATTCAGATGG AGAACTCCAT GGGCAGCTG CGGACCTCCA  
TCTCCGTGGA ACGCCAGATT CACAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG  
AATTTGTGTA AGGATTGAGG GACAGTTGCT T -3' (FRAG. NO:2275) (SEQ. ID NO:2457)

5'- TGATCCTATC ACAACCTGAG AGTAGTTTTT ACTCCATTTA CAGGTGAGGT CATTGTGTTT CAAGGACGTT AAGTAACCTC  
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CTCGCATCT GTATCTCCA ATCATTTCA GTGCTTGCT GATAGAAGGT ACGGAAATAC GATGCCACAG ACTGTCCAGG  
AAGACAGAAA CTAGGCAGAT GGGCTGGCCA TGGTCTCAA GCCAGACTGG AATCTCCAGG TCTGGAATGA TATCATTTT  
CTCTTTAAT AAATTAATC ACCCACCACA CGGCTTGAG AGGCTCAAAG GTGACCAACT CCCTGGGAG GGCCCGGTT  
GATAAGGAAG GAATGTGAAT CCTCCATCA CGGAAGCTT AAGGAGGTCA AGGTCCAAC ACTTGAGATT GTTAGTGCTG  
TTGGTGGATA CTGAGAATA TCCAGTGGAG CTCAGATGA AGAATGAGT GCGCGTTA GATCCAAGGA TCAGAGGGGG  
CTCTGTAAGA CCCAGGGGAG TCAGGTGCAC TGGAGCGGG GCTGCAGAAA ACAGCCTGAG CTCCACCTCG GCTTCTCCTT  
GCCCTGGCTG GTTGTCTTA ACCCCTGTCT CTTCTGGAC CAGTTTTGT CTTCCCTTG TGACCTGAGG GGTAAACAGCC  
TCTTTTCCAC TTTCTTTCAG CCGGACATG CTCAATGTCA CTTGCAAGG GCGCACTT AACGGGACCT TTGCCAGAG  
CAAATGCCCC CAAGTGGAGT GGCTGGGCTG GCTCAACACC ATCCAGCCCC CTTCTCTCTG GGTGCTGTTT GTGCTGGCA  
CCCTAGAGAA CATCTTTGTC CTCAGCGTCT TCTGCTGCA CAAGAGCAGC TGCACGGTG CAGAGATCTA CCTGGGGAAC  
CTGGCCGAG CAGACCTGAT CCTGGCCTGC GGGCTGCCCT TCTGGGCCAT CACCATCTCC AACAATTCG ACTGGCTCTT  
TGGGAGACG CTCTGCCGCG TGGTGAATGC CATTATCTCC ATGAACCTGT ACAGCAGCAT CTGTTTCTG ATGCTGGTGA  
GCATCGACCG CTACCTGGCC CTGGTGAATA CCATGTCCAT GGGCCGATG CCGGCGTGC GCTGGGCAA GCTTACAGC  
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CCACAACGTC ACCGCTTGTC TCATCAGCTA CCCATCCCTC ATCTGGGAAG TGTTACCAA CATGCTCTG AATGCTGTG  
GCTTCTGCT GCGCTGAGT GTCATCACCT TCTGCAGAT GCAGATCATG CAGGTGCTGC GGAACAACGA GATGCAGAG  
TTCAAGGAGA TCCAGACGGA GAGGAGGGCC ACGGTGCTAG TCCTGGTTGT GCTGCTGTA TTCATCATCT GCTGGCTGCC  
CTCCAGATC AGCACCTTCC TGGATACGCT GCATCGCTC GGCATCTCT CCAGCTGCCA GGACGAGCGC ATCATCGATG  
TAATCACACA GATCGCTCC TTCATGGCCT ACAGCAACAG CTGCCTCAAC CCACTGGTGT ACGTGATCGT GGGCAAGCGC  
TTCCGAAAGA AGTCTTGGGA GGTGTACCAG GGAGTGTGCC AGAAAGGGGG CTGCAGGTCA GAACCCATTC AGATGGAGAA  
CTCCATGGGC AACTGCGGA CTTCATCTC CTGGAACGC CAGATTACA AACTGCAGGA CTGGGCAGGG AGCAGACAGT



CTGCCTCAAC CCACTGGTGT ACGTGATCGT GGGCAAGCGC TTCCGAAAAGA AGTCTTGGGA GGTGTACCAG GGAGTGTGCC  
AGAAAGGGGG CTGCAGGTCA GAACCCATTC AGATGGAGAA CTCCATGGGC AACTGCGGA CCTCCATCTC CGTGGAAACGC  
CAGATTCAAC AACTGCAGGA CTGGGCAGGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT GCTGTGAATT TGTGTAAAGGA  
TTGAGGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC AAGGAGACAT CTATGCACGA CCTTGGGAAA TGAGTTGATG  
TCTCCGGTAA AACACCGGAG ACTAATTCCT GNCCTGCCCA ATTTTGCAGG GAGCATGGCT GTGAGGATGG GGTGAACCTCA  
CGCACAGCCA AGGACTCCAA AATCACAACA GCATTACTGT TCTTATTTGC TGCCACACCT GAGCCAGCCT GCTCCTTCCC  
AGGAGTGGAG GAGGCCTGGG GGCAGGGAGA GGAGTGAAGT AGCTTCCCTC CCGTGTGTTT TCCGTCCTG CCCCAGCAAG  
ACAACCTAGA TCTCCAGGAG AACTGCCATC CAGCTTTGGT GCAATGGCTG AGTGACAAG TGAGTTGTTG CCCTGGGTTT  
CTTTAATCTA TTCAGCTAGA ACTTTGAAGG ACAATTTCTT GCATTAATAA AGGTTAAGCC CTGAGGGGCT CCTGATAACA  
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ATTGAGCACT TGCTGTATAT GCAGTATTGA GCACTGTAGG CAAGAGGGAA GAAAGAGAAG GAGCCATCTC CATCTTGAAG  
GAACTCAAAG ACTCAAGTGG GAACGACTGG CACTGCCACC ACCAGAAAGC TGTTGACGA GACGGTCGAG CAGGGTGTCTG  
TGGGTGATAT GGACAGCAGA AGGGGGAGAC CAAGGTTCCTA GCTCAACCA TAACTATTGC ACAACCACCT GTCCCTGCCT  
CAGTCCCTC TTCTGTAACA TGAAGTCGTT GTGAGGGTTA AAGGCAGTAA CAGGTATAAA GTACTTAGAA AAGCAAAGGG  
TGCTACGTAC ATGTGAGGCA TCATTACGCA GACGTAAGT GGATATGTTT ACTATAAGGA AAAGACACTG AGGTCTAGA -3'  
(FRAG. NO:2275) (SEQ. ID NO:2455)

5'- AAATGATAGA CCGTCAATAA TTTGTTAAAT GCTTTTAAAA ATGAATGCTT TAAGCCGGGT GCAGTGCCTC ACATCTGTAA  
TCCCAGCACT TTGGAGCCGA GCGGGTGGAT TGTGTGAGGT CAGGAGTTCG AGACCAACCT GGCCAACATG GCAAAACCTC  
ACTCTCTACC AAAAATACAA AAATTAGCCA GGCATGGTGG CAGGCACCTG TGATCCAGC TACTCAGGAG GCTGAGACAG  
GAGAATCGCT TGAACCCGGG AGGCAAGGTT GCAGTGAGCC AAGATTACGC CATTGTACTC CAGCTGGGT GACAGAGAGA  
GACTCCGTCT CAAAAAATAA AAAAAAATAA AAAAAATTAC GCTTCAAAACA CATGATCTCT CACCACTGTT GAATTTTCTT  
TCTATGAGCC CAGGAGGGCC TCTCAGAGAG GAAAGCTCCT AGGTCTTCTT TCCCTCTGC AAACCTCCTG CCTTGAAGGT  
TCAGAAGGAC TGTGCGTGCT CGTTGCATCC TTTGCAAGT TCCAAACCT GATCCAGCT GTGCTTAGGG GTTCTGCAAA  
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CTGAACTGAC CGTTGTCTGA TCTCCACCTC CCAACTGAAT TAGGGGAGCT GGGCTTCTGG AAACCCAGGT GCGGGGTGTT  
GCAGAGTGGC TGAAGCTGG GATGTGGCAG ATCCGTGGCT ACATTCATGC ACACACACAC ACCACATAC CCACACATGC  
ACACACACAC ACACACCCGC ACTCACACAC TTGGACATGC ATAGACCACA GCTTCCACA CCCTTCTAG ACAGGGGTCA  
CTTGGTATCC TGGAGAGAGT GTGAAGTCTT GGAATGGAAG GAGGGGGGAT TAAGCCCCAC CTCTAGCCAT GGGACTGAGA  
CAAGTCACCA CCAACCCATC TGCGCCTGT TTAACCTCTC TGTGAGGCAA GCACAGAGCC CATGCCCTGC CCCCTGGATG  
GGAGTGATGT GAAACTGAA GGGCGGTGAG AGCAAGGCT GGGAAATGGA GGGCTTGGG AAAAAAGGCC TTTCAACTA  
GGGGCAGTA GAGGGCCCTG GGCTGAGAAC TTGACAGCAC CTGTGAATTG GTAAGCCAAG CCCGAAGGGA CTGGAATAC  
TCAGATGTGT CTGTCTCCCT TATTAGGTTT AAAGTCCCTC AAGACCTGT CTCCATCACA GTGCTCCAGT CCAGACCCCT  
CCTCTGAGCT CCAGACCCCTG CTGGACCCAA CCAGCCCTAT GGGGTGCGAT CCCCACCTGC CTGGAATTCT CCAAAGAAC  
TCCCCTTAA CAGTTCCAGC CTTTAAACAGT TCCAGTCTAA ACACATGACC TTCTCCTCT AAATCAGCCC CCCATCTCTG  
CCTTTGCAAG AGATGGAAGC CATGACACCT GCCTCGCCCC TGCTCTCACC CCATCCATGT CCAATCAAGC ACTAGGCATG  
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CCAACTGAC TGAGATATCC TCTGCACCA TCATCCCTCC ACCCTGTTTA GTTCTGCTCA CCCTCAGTGT TCTCATCAAT  
AATCCACTCC CCAACAGGC GCGTTTGGGA CCCCATGTTT TATGCTCTCA CAGGACCTTT TGCTTGATT TCACTGTAC  
TTAGGTCACT TTGCAGTTAT TAAGTGAAGT AGCAATGTCT GGCTTCTCCA GTAGACTGTC AGCTCCTAGC CATTGTATAC  
CTAGCACCGC TGTGTGGGAG CACGTGACAA ACGTCCAGTG AGTCAGGGAC TCAGCAGTCT CCATTTCTCC GCCCTGCTGG  
AGAATGCGTG TATTGGCAA TCCCAGCCC CTGTGCCATC TAACCATCTT TTCTTCTCTG TTCAGCCAGG GTGTGGCCCTC  
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AGGGCACATT CCTGGTTGTT ATATGTTTCT ATCTATCCCA GATGAAGTGA GAAGTGAAGG GAAGAGAGTT AAACATTTAA  
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AGAGGATAGG GAGATCTGTT CTGGGGGACA GCATTGCAA GAAACAAGGC TGAGGGGTCC ACTCCAACCT CTCACCCTG  
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ACTGTCTTGC TGAGAAATTT ATAAGCAGCA TCTGGTGCTA TACTTTGCTC TCTAGTGAAT TAGCTCATGA AAGATGATAG  
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GCTCACACT TTCCAAGTAA GCAATGCAA AGGCAAGAA AGATGCTGCA AAGATGTTAT GAGCTAGCTC CAGAAATCAC  
ACACCATCC TCCACCACT AGTAAGAACT CCAGCCACAG TCCAGGAGAA GAGGAAGCAG ATTCTCTCTT TTGAAATGAA  
GAATATCAAG TAATTCGGGG GGCATATGAA AGCCACCACA CACCACAGGG ATCTTTTATAG AGCATACTTC TTATACCATC  
ACTGTAGTTC CTTAAGACTC AGGGGCAAAG CCTCACTTCC TTAGCACCCA GTGAAGACCA CGTTACTCC CTCCTCAAC  
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CAGCTCTAGA GTCACCTCCA ACCCTTACC CACCAGCCCC CTCTCAAGT CTGTGTCCA CAACCCCTCT GCTCCCTCCA  
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CACTCAGGC AGAGCTCAG ACAGAGCAGA CGTCAAAAA ACATTTAAAG GATAGAAGCA TTGATTTGTG GTTCCCCAG  
TCTGGCTCCA GGATGCCAGC CAGTGTCTCC TAGAAGCAAA CGGACTTTTC CTGGGAAATC CCAGAGGTGA TGATCAGTAA  
TCTCTCCCGT GACTCGTAGT TCAGCTCTTC CTCCATGAGC CTGACTATCA GTGGACCTTC CAGAAAGAGC CCCTTTCTCT  
TCTCTACCC ACAGCACAGG GCACTGGGAA AATGCCCAAT GAGTCTGCTC TCTGGGTTGT GCTTTGAGT TTTCACTGTG



TCTCGCATCC ACTCTTCAAC TTGAATGTTG CAACAGCCAT GAAAAAGAA ATGCAAAGCG ATTCAGGATG AGAGCAATAC  
CCTACTCCAA AGAAGGCAAC ATAGAAGCTC AGAGAGATCA AGCAATTTGC CCAAGACCAC ACAGCTAGGA GTGGAACCTCA  
TGGCTGTCCA AGCCCCATGC CTCTGCTGAA GGTAGAGATG AATTACAGCA ACAAGTCTAG AAAGGTGCCT GCCCTATGGT  
CTGTGAGTCT TGCCTAAGAA TGAAAGAGGA GCCAGTGGGT TAAAGATGAG GTCACCAACA ACGGTGGTGT TGGAGTTTAC  
CACTGATAAT AAGGGTGCAA AATGTAAATT ACTAATGTTT ATTGAGCCTA GTGCAGTGC GGGGCATTT TGCACATTGT  
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TAAGTAACCT CCCAGCGTG ACACGGCTTA TAAGTAAGGC AGCCAGGATG TGAACCCAGT AGGACTATCT GGCTGCAAAG  
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CAGACTGTCC AGGAAGACAG AAACCTAGGCA GATGGGCTGG CCATGGTCTC CAAGCCAGAC TGGAACTTCC AGGTCTGGAA  
TGATATCATT TTCTCTTTT AATAAATTAA CTCACCCACC ACACGGCTTT GAGAGGCTCA AAGTTGACCA ACTCCCTTGG  
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TGGCAGAGAT CTACCTGGGG AACCTGGCCG CAGCAGACCT GATCCTGGCC TGCGGGCTGC CCTTCTGGGC CATCACCATC  
TCCAACAAT TCGACTGGCT CTTTGGGGAG ACCTCTGCG GCGTGGTGAA TGCCATTATC TCCATGAACC TGATACAGCAG  
CATCTGTTTC CTGATGCTGG TGAGCATCGA CCGCTACTCG TCCCTGGTGA AAACCATGTC CATGGGCCGG ATGCGCGGCG  
TGGCTGGGC CAAGCTCTAC AGCTTGGTGA TCTGGGGGTG TACGCTGCTC CTGAGCTCAC CCATGCTGGT GTTCCGGACC  
ATGAAGGAGT ACAGCGATGA GGGCCACAAC GTCACCGCTT GTGTCATCAG CTACCCATCC CTCATCTGGG AAGTGTTCAC  
CAACATGCTC CTGAATGTCG TGGGCTTCTC GTCGCCCTG AGTGTATCA CCTTCTGCAC GATGCAGATC ATGCAGGTGC  
TGCGGAACAA CGAGATGCAG AAGTTCAAGG AGATCCAGAC GGAGAGGAGG GCCACGGTGC TAGTCTGGT TGTGCTGCTG  
CTATTCATCA TCTGCTGGCT GCCCTTCCAG ATCAGCACCT TCTGGATAC GCTGCATCGC CTCGGCATCC TCTCCAGCTG  
CCAGGACGAG CGCATCATCG ATGTAATCAC ACAGATCGCC TCCTTCATGG CCTACAGCAA CAGCTGCTC AACCCACTGG  
TGTACGTGAT CGTGGGCAAG CGCTTCCGAA AGAAGTCTTG GGAGGTGTAC CAGGGAGTGT GCCAGAAAGG GGGCTGCAGG  
TCAGAACCCA TTCAGATGGA GAACTCCATG GGCACACTGC GGACCTCCAT CTCCGTGGAA CGCCAGATTC ACAAACCTGCA  
GGACTGGGCA GGGAGCAGAC AGTGAGCAA CGCCAGCAGG CTGCTGTGA ATTTGTGTA GGATGAGGG ACAATGTCTT  
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GAGACTAATT CCTGCCCTGC CCAATTTTGC AGGGAGCATG GCTGTGAGGA TGGGGTGAAC TCACCCACAG CCAAGGACTC  
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AGAATTTGA AGGACAATT CTTCATTAA TAAAGGTTAA GCCCTGAGGG GTCCCTGATA ACAACCTGGA GACCAGGATT  
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GGGAACGACT GGGCACTGCC ACCACCAGAA AGCTGTTTGA TGAGACGGTC GAGCAGGGTG CTGTGGGTGA TATGGACAGC  
AGAAGGGGGA GCCAGGTTCC AGCTACCAA TACTATTGCA CACCACCTGT CTGCTC -3' (FRAG. NO:2275) (SEQ. ID  
NO:2454)

5'- CAGATTCACA AACTGCAGGA CTGGGCAGGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT GCTGTGAATT  
TGTGTAAGGA TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC AAGGAGACAT CTATGCACGA CCTTGGGAAA  
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GGTGAACCTA CGCACAGCCA AGGACTCCAA AATCACAACA GCATTACTGT TCTATTGTC TGCCACACCT GAGCCAGCCT  
GTCCTTCCC AGGAGTGAG GAGGCTGGG GGGAGGGAGA GGAGTACTG AGCTTCCCTC CCGTGTGTTT TCCGTCCCTG  
CCCCAGCAAG ACAACTTAGA TCTCCAGGAG AACTGCCATC CAGCTTGGT GCAATGGCTG AGTGACAAG TGAGTTGTTG  
CCTGGGTTT CTTAATCTA TTCAGCTAGA ACTTTGAAGG ACAATTTCTT GCATTAATAA AGGTAAAGCC CTGAGGGGTC  
CCTGATAACA ACCTGGAGAC CAGGATTTTA TGGTCCCCCT CACTGATGGA CAAGGAGGTC TGTGCCAAG AAGAATCCAA  
TAAGCACATA TTGAGCACTT GCTGTATATG CAGTATTGAG CACTGTAGGC AAGACCCAA AGAAGAGAGG AGCCATCTCC  
ATCTGAAGG AACTCAAAGA CTCAAGTGGG AACGACTGG CACTGCCACC ACCAGAAAGC TGTTCGACGA GACGTCGAG  
CAGGGTGCTG TGGGTGATAT GGACAGCAGA AGGGGGAGAC CAAGGTTCCA GCTCAACCAA TAACATTGC ACAACCACCT  
GTCCCTGCCT CAGTTCCCTT TTATGTAACA TGAAGTCGTT GTGAGGGTTA AAGGCAGTAA CAGGTATAAA GTACTTAGAA  
AAGCAAAGGG TGCTACGTAC ATGTGAGGCA TCATTACGCA GACGTAACCT GGATATGTTT ACTATAAGGA AAAGACACTG  
AGGTCTAGAA ATAGCTCCGT GGACGAGAAT CAGTATTGGG AGCCGGTGGC GGTGTGAAGC ACCAGTGTCT GGCACACAGT  
AGGTGCTCAT TGGTCCCTT CCACCTGTCA TTCCACCAC CCTGAGGCC CAACCGCCAC ACACACAGGA GCATTGGAG  
AGAAGGCCAT GTCTCAAAG TCTGATTTGT GATGAGGCAG AGGAAGATAT TTCTAATCGG TCTTGCCAG AGGATCACAG  
TGCTGAGACC CCCACCACC AGCCGGTACC TGGGAAGGGG GAGAGTGCAG GCCTGCTCAG GGAAGTGTCC TGTCTCAGCA  
ACCAAGGGAT TGTTCTGTC AATCAATGGT TTATTGGAAG GTGGCCAGT ATGAGCCCTA GAAGAGTGTG AAAAGGAATG  
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AGGAATGAA CCTGGAGGGC TAGAACCTGG AGAATGAGAA AAATTTACAT GGCAAGAGC CCATAAATCC TGACCAATCC  
AATCTGAAT TTTAAAGCAA AAGCGTGAAG AAAAAGATT CCTCTTACC CCAACCCAC TCTTTTTC CACCACCCAC  
TCTCTCTG CTAGTAAGT ATCTGGAGGA AGAAACAGG TGAAGAAGA AGTAAACCA ATTAGTATT AGTATTAGAA

CACCAGAGCA CGTGATGGTC TGAGACTCTC TTAGGAGCAG AGCTCTGCCG CAATGGCCAT GTGGGGATCC ACACCTGGTC  
TGAGGGGCAA CTGAGTCTGC GGGAGAAGAG CGGCCCTATG CATGGTGTAG ATGCCCTGAT AAAGAACATC TGCTCTGTGA  
AAGACTCAAT GAGCTGTTAT GTTGTAACA GGAAGCATTT CACATCCAAA CGAGAAAATC ATGTAAACAT GTGTCTTTTC  
TGAGAGCAT AATAAATGGA TGAGGTTTTT GCAAAAAAAA AAAAAAAA -3' (FRAG. NO:2275) (SEQ. ID NO:2453)

5'- GAGCTCTTCA ATATTTTGT GAAAGCTATA GATGAGGCTC CATAGGGGAT AAAGCACAGA CACACCTTTT  
CAGAGGGCTT GTGGACTCTG GGCAGCCTGT CCATAGACCT CTGTCCCAA CTGGCAAGTC AGGAACTCC AGATTAAGGA  
GCCCCAATGT GGTGAACAG CCAGGTGCAC AGATGAGTCA ACCACACAGC CAGGCCAGGG AGGGCCTTCA CTCGAAGAGCC  
TACAGCCAGT TCACAGCCAA GCCAGGGCTA GCGCCAGGCC ACCATAAAC TGATCTGAGA CTCTGTTTCC CTGTCTCCAT  
GATGATGGGA TCAGGCTTGA TTGCTGGTTT GTAGGCTTGT TATGAATCAA GTCACAGGGA AGAGGAGCTG ATGGGCTGGG  
GGGAGCTCT CTGGCCCTCC TGTCTCTTCC CCAGATCCAC TGGGCCCACT CTTATCTGTT CTCTCTGAA GGAAGGGTTT  
TAAGGCTTCA AAAAAAATG TTTTGAAAGT CCCTGCCTT TCCAGTCTT ACCGTCTCAG CCCTGGGAGT GTAAAGTGCT  
GCAGATAGT AGTAAGTCTT TGAGCAAAAC TGAGAAAGCC AGCCTGAGCC TTGACATGGG AGAAACCTCC GCCATACATC  
TCCGAAGAAA CGGCCGCGTG TCTCAGGGGA GCGCAACAC CCGTACCCAG GAAACAGGAG AGCTTCTGCC CCGTCCGCC  
TTGGGAGCCG TACGTGGCAT GACAAAGAAA TCCAGGACT CCGCTGCCC ACCTGGCCAC CTCTGTTTA CACCTTCCGC  
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TTACGCGAGG CAAATTTATT CACATGGGGC TTCCAGGCC ACTTTGTGGT CAGCCGGGAG GGACGTTTTT GCCGTCCAC  
GACTCCAAG GGCAGCCGG CCTACGCAA CATGGAATC TTCAAGAGC CTCCTGGCC CCCAGGGCTC AGAGGGTGGC  
AGAGCGGAGA GCGAAGGTGG CCGCAGCCTT CCCGGCCCCA CAGCCAGCCT GGCTCCAGCT GGGCAGGAGT GCAGAGCTCA  
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CTCCAGCTCT GGCTTCTGGG CTCCGAGGAG GGTGGGGAG GGTGGTACG GTGGGGACG GTGGGGACG CCGTCCGCC CCGATACCA  
GGGAGCGACT GAAGTGCCCA TCCGCTTGC TCCGGAAGAG GTGGGTGCC GGCAGGGGCT GCTCCAGCCG CCTCACCTCT  
GCTGGGAGGA CAACTGTCC CAGCACAGAG GGAGGGAGG AGGGCAGGCA GCGGGGAGAA GTTCCCTGT GGTCGTGGG  
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5'- GCCCTTCAA GATGAGCTGT TCCCGCCGC ACTCAGCTC TGGCTTCTGG GCTCCGAGGA GGGGTGGGA  
CGGTGGTGAC GGTGGGGACA TCAGGCTGCC CCGCAGTACC AGGGAGCGAC TGAAGTGCC ATGCCGCTT CTCCGGAGAA  
GGTGGGTGCC GGCAGGGGC TGCTCCAGC GCCTCACCTC TGCTGGGAGG ACAAAGTGC CCAGCACAGA GGGAGGGAGG  
GAGGGCAGC AGCGGGGAGA AGTTCCCTG TGTCGTGGG GAGTT -3' (FRAG. NO:2275) (SEQ. ID NO:2451)

5'- GCCCTTCAA GATGAGCTGT TCCCGCCGC ACTCAGCTC TGGCTTCTGG GCTCCGAGGA GGGGTGGGA  
CGGTGGGGAC ATCAGGCTGC CCGCAGTACC CAGGGAGCGA CTGAAGTGCC CATGCCGCTT GCTCCGAGA AGGTGGGTGC  
CGGGCAGGG CTGCTCCAGC CGCTCACCT CTGCTGGAG GACAACTGT CCCAGCACAG AGGGAGGGAG GGAGGGCAGG  
CAGCGGGAG AGTTTCCCT GTGGTCTGG GAGTT -3' (FRAG. NO:2275) (SEQ. ID NO:2450)

5'- ATGTTCTCTC CTGGAAGAT ATCAATGTTT CTGTCTGTT GTGAGGACTC CGTGCCACC ACGGCCTCTT TCAGCGCCGA  
CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTTAACGGG ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG  
GCTGGCTCAA CACCATCCAG CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCTAG AGAATCTT TGCTCTCAGC  
GTCTTCTGCC TGACAAGAG CAGCTGCAG GTGGCAGAGA TCTACCTGGG GAACCTGGCC GCAGCAGACC TGATCCTGGC  
CTGCGGGCTG CCCTTCTGG CCATCACCAT CTCGAACAAC TTCGACTGCG TCTTTGGGA GACGCTCTGC CGCGTGGTGA  
ATGCCATTAT CTCCATGAAC CTGTACAGCA GCATCTGTTT CTGATGCTG GTGAGCATCG ACCGCTACCT GGCCTGGTG  
AAAACCATGT CCATGGGCG GATGCGCGG GTGCGTGGG CCAAGCTCTA CAGCTTGGT ATCTGGGGT GTACGCTGCT  
CCTGAGCTCA CCATGCTGG TGTCCGGAC CATGAAGGAG TACAGCGATG AGGGCCACAA CGTACCCTGT TGTGTCATCA  
GCTACCATC CTCTATCTGG GAAGTGTTC CCAACATGCT CTGAATGTC GTGGGCTTCC TGTCGCCCT GAGTGTATC  
ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG GAGATCCAGA CCGAGAGGAG  
GGCCACGGTG CTAGTCTGG TTGTGCTGCT GCTATTCATC ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCTGGATA  
CGCTGCATCG CTCCGCATC CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGAATCA CACAGATCGC CTCCTTCATG  
GCCTACAGCA ACAGCTGCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA AAGAAGTCTT GGGAGGTGTA  
CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA  
TCTCCGTGA ACGCCAGATT CACAACTGC AGGACTGGG AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG  
AATTTGTGA AGGATTGAGG GACAGTTGCT T -3' (FRAG. NO:2449) (SEQ. ID NO:2449)

5'- ATGTTCTCTC CTGGAAGAT ATCAATGTTT CTGTCTGTT GTGAGGACTC CGTGCCACC ACGGCCTCTT TCAGCGCCGA  
CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTTAACGGG ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG  
GCTGGCTCAA CACCATCCAG CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCTAG AGAATCTT TGCTCTCAGC  
GTCTTCTGCC TGACAAGAG CAGCTGCAG GTGGCAGAGA TCTACCTGGG GAACCTGGCC GCAGCAGACC TGATCCTGGC  
CTGCGGGCTG CCCTTCTGG CCATCACCAT CTCGAACAAC TTCGACTGCG TCTTTGGGA GACGCTCTGC CGCGTGGTGA  
ATGCCATTAT CTCCATGAAC CTGTACAGCA GCATCTGTTT CTGATGCTG GTGAGCATCG ACCGCTACCT GGCCTGGTG  
AAAACCATGT CCATGGGCG GATGCGCGG GTGCGTGGG CCAAGCTCTA CAGCTTGGT ATCTGGGGT GTACGCTGCT  
CTGAGCTCA CCATGCTGG TGTCCGGAC CATGAAGGAG TACAGCGATG AGGGCCACAA CGTACCCTGT TGTGTCATC  
GCTACCATC CTCTATCTGG GAAGTGTTC CCAACATGCT CTGAATGTC GTGGGCTTCC TGTCGCCCT GAGTGTATC  
ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG GAGATCCAGA CCGAGAGGAG  
GGCCACGGTG CTAGTCTGG TTGTGCTGCT GCTATTCATC ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCTGGATA  
CGCTGCATCG CTCCGCATC CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGAATCA CACAGATCGC CTCCTTCATG  
GCCTACAGCA ACAGCTGCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA AAGAAGTCTT GGGAGGTGTA  
CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA  
TCTCCGTGA ACGCCAGATT CACAACTGC AGGACTGGG AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG  
AATTTGTGA AGGATTGAGG GACAGTTGCT T -3' (FRAG. NO:2275) (SEQ. ID NO:2448)

5'- TGATCCTATC AACAACCTGAG AGTAGTTTT ACTCCATTTA CAGGTGAGGT CATTGTGGTT CAAGGACGTT AAGTAACTC  
CCCAGCTCAC ACGGCTTATA AGTAAGGCAG CCAGGATGTG AACCAGTAG GACTATCTGG CTGCAAAGTC CCCACCTCC  
CTCGCATCT GTATCTCCA ATCATCTTCA GTGCTTGTCT GATAGAAGGT ACGGAAATAC GATGCCACAG ACTGTCCAGG  
AAGACAGAAA CTAGGCAGAT GGGCTGGCCA TGGTCTCAA GCCAGACTGG AATCTCCAGG TCTGGAATGA TATCATTTTT  
CTCTTTAAT AATTAATC ACCACACCA CGGCTTGTAG AGGCTCAAAG GTGACCAACT CCCTGGGAG GGCCCCGGTT  
GATAAGGAAG GAATGTGAAT CCTCCCATCA CGGAAGCTT AAGGAGGTCA AGGGTCCAAC ACTTGAGATT GTAGTGCTG

TTGGTGGATA CTGCAGAATA TCCAGTGGAG CCTCAGATGA AGAACATGAG GCCCGTTTA GATCCAAGGA TCAGAGGGGG  
CTCTGTAAGA CCCAGGGGAG TCAGGTGCAC TGGAGCGCGG GCTGCAGAAA ACAGCCTGAG CTCACCTCG GCTTCTCCTT  
GCCCTGGCTG GTTGTCTTA ACCCTGTCT CTTCTGGAC CAGTTTTTGT CTTCCCTTG TGACCTGAGG GGTAACAGCC  
TCTTTTCCAC TTTCTTTCAG CGCCGACATG CTCAATGTCA CTTGCAAGG GCCACTCTT AACGGGACCT TTGCCAGAG  
CAAATGCCCC CAAGTGGAGT GGCTGGGCTG GCTCAACACC ATCCAGCCCC CTTCTCTG GGTGCTGTTG GTGCTGGCCA  
CCCTAGAGAA CATCTTTGTC CTCAGCGTCT TCTGCCTGCA CAAGAGCAGC TGCACGGTGG CAGAGATCTA CTGGGGAAC  
CTGGCCGACG CAGACCTGAT CTGGCCCTGC GGGCTGCCCT TCTGGGCCAT CACCATCTCC AACAACTTCG ACTGGCTCTT  
TGGGGAGACG CTCTGCCGCG TGGTGAATGC CATTATCTCC ATGAACCTGT ACAGCAGCAT CTGTTTCTCG ATGCTGGTGA  
GCATCGACCG CTACCTGGCC CTGGTGAATA CCATGTCCAT GGGCCGGATG CGCGGCGTGC GCTGGGCCAA GCTCTACAGC  
TTGGTGTATCT GGGGGTGTAC GCTGCTCTG AGCTCACCA TGCTGGTGT CCGGACCATG AAGGAGTACA GCGATGAGGG  
CCACAACGTC ACCGCTTGTG TCATCAGCTA CCCATCCCTC ATCTGGGAAG TGTTACCAA CATGCTCTG AATGCTGTG  
GCTTCTGCT GCTCCGTGAGT GTCATCACCT TCTGCAGAT GCAGATCATG CAGGTGCTGC GGAACAACGA GATGCAGAAG  
TTCAAGGAGA TCCAGACGGA GAGGAGGGCC ACGGTGCTAG TCTGTTGT GCTGCTGTA TTCATCATCT TCTGGCTGCC  
CTTCCAGATC AGCACTTCC TGGATACGCT GCATCGCTC GGCATCTCT CCAGCTGCCA GGACGAGCGC ATCATCGATG  
TAATCACACA GATCGCTCC TCCATGGCT ACAGCAACAG CTGCCTCAAC CCACTGGTGT ACGTGATCGT GGCAGGCGC  
TTCCGAAAGA AGTCTTGGGA GGTGTACCAG GGAGTGTGCC AGAAAGGGGG CTGCAGGTCA GAACCCATTC AGATGGAGAA  
CTCCATGGG CACTGCGGA CTTCCATCTC CGTGGAACGC CAGATTACA AACTGCAGGA CTGGGACGGG AGCAGACAGT  
GAGCAAACGC CAGCAGGGCT GCTGTGAATT TGTGAAGGA TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC  
AAGGAGACAT CTATGCACGA CCTTGGGAAA TGAGTGTGA TGCTCCGGT AAAACACCGG AGACTAATTC CTGCCCTGCC  
CAATTTTCGA GGGAGCATGG CTGTGAGGAT GGGGTGAAT CACGCACAGC CAAGGACTCC AAAATCACAA CAGCATTACT  
GTTCTTATTT GCTGCCACAC CTGAGCCAGC CTGCTCTTC CCAGGAGTGG AGGAGGCCCTG GGGGAGGGAG AGGAGTGACT  
GAGCTTCCCT CCCGTGTGT CTCCGTCCCT GCCCCAGCA GACAATTAG ATCTCCAGGA GAACTGCCAT CCACGTTTGG  
TGCAATGGCT GAGTGACAA GTGAGTTGT GCCCTGGGT TCTTAATCT ATCAGCTAGA ACTTTGAAGG ACAATTTCTT  
GCATTAATAA AGGTTAAGCC CTGAGGGGTC CTTGATAAC AACCTGGAGA CCAGGATTTT ATGGTCCCC TCACTGATGG  
ACAAGGAGGT CTGTGCCAAA GAAGAATCAA TAAGCACATA TGAGCACTTC TGTATATCAG TATTGAGCAC TGTAGGCA -3'  
(FRAG. NO:2275) (SEQ. ID NO:2447)

5'- CTGCAGAAAA CAGCCTGAGC TCCACCTCGG CTTCTCCTTG CCTGGCTGG TTGTCCTTAA CCCTGTCTC CTTCTGGACC  
AGTTTTTGTC CTTCCCTTGT GACCCTGAGG GGTAACAGCC TCTTTTCCAC TTTCTTTCAG CGCCGACATG CTCAATGTCA  
CCTTGAAGG GCCACTCTT AACGGGACCT TTGCCAGAG CAAATGCCCC CAAGTGGAGT GGCTGGGCTG GCTCAACACC  
ATCCAGCCCC CTTCTCTG GGTGCTGTTG GTGCTGGCCA CCTAGAGAA CATCTTTGTC CTCAGCGTCT TCTGCCTGCA  
CAAGAGCAGC TGCACGGTGG CAGAGATCTA CTGGGGAAC CTGGCCGACG CAGACCTGAT CTGGCCTGC GGGCTGCCCT  
TCTGGCCAT CACCATCTCC AACAACTTCG ACTGGCTCTT TGGGGAGACG CTCTGCCGCG TGGTGAATGC CATTATCTCC  
ATGAACCTGT ACAGCAGCAT CTGTTTCTG ATGCTGGTGA GCATCGACCG CTACCTGGCC CTGGTGAATA CCATGTCCAT  
GGCCCGGATG CGCGGCGTGC GCTGGGCCAA GCTCTACAGC TTGGTGTATCT GGGGGTGTAC GCTGCTCTG AGCTCACCA  
TGCTGGTGT CCGGACCATG AAGGAGTACA GCGATGAGG CCACAACGTC ACCGCTTGTG TCATCAGCTA CCCATCCCTC  
ATCTGGGAAG TGTTACCAA CATGCTCTG AATGCTGGT GCTTCTGCT GCGCTGAGT GTCATCACCT TCTGCAGAT  
GCAGATCATG CAGGTGCTGC GGAACAACGA GATGCAGAAG TTCAAGGAGA TCCAGACGGA GAGGAGGGCC ACGGTGCTAG  
TCTGTTGT GCTGCTGTA TTCATCATCT GCTGGCTGCC CTTCCAGATC AGCACTTCC TGGATACGCT GCATCGCTC  
GGCATCTCT CCAGCTGCCA GGACGAGCGC ATCATCGATG TAATCACACA GATCGCTCC TCCATGGCT ACAGCAACAG  
CTGCCTCAAC CCACTGGTGT ACGTGATCGT GGCAGGCGC TTCCGAAAGA AGTCTTGGGA GGTGTACCAG GGAGTGTGCC  
AGAAAGGGGG CTGCAGGTCA GAACCCATTC AGATGGAGAA CTCCATGGG CACTGCGGA CTTCCATCTC CGTGGAACGC  
CAGATTACA AACTGCAGGA CTGGGACGGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT GCTGTGAATT TGTGAAGGA  
TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC AAGGAGACAT CTATGCACGA CCTTGGGAAA TGAGTTGATG  
TCTCCGGTAA AACACCGGAG ACTAATTCCT GNCCTGCCA ATTTGCAAG GAGCATGGCT GTGAGGATGG GGTGAATCA  
CGCACAGCA AGGACTCAA AATCACAACA GCATTACTGT TCTTATTTG TGCCACACCT GAGCCAGCCT GCTCTTCCC  
AGGAGTGGAG GAGGCTGGG GGCAGGGAGA GGAGTGACTG AGCTTCCCTC CCGTGTGTT TCCGTCCCTG CCCCAGCAAG  
ACAATCTAGA TCTCAGGAG AACTGCCATC CAGCTTTGTT GCAATGGCTG AGTGACAAG TGAGTTGTTG CCCTGGGTTT  
CTTAACTA TTCAGCTAGA ACTTTGAAGG ACAATTTCTT GCATTAATAA AGGTTAAGCC CTGAGGGGCT CTTGATAACA  
ACCTGGAGAC CAGGATTTTA TGGTCCCT CACTGATGGA CAAGGGAGGT CTGTGCCAAA GAAGAATCCA ATAAGACAT  
ATTGAGCACT TGCTGTATAT GCAGTATTGA GCACTGTAGG CAAGAGGGA GAAAGAGAAG GAGCCATCTC CATCTGAAG  
GAACTCAAAG ACTCAAGTGG GAACGACTGG CACTGCCACC ACCAGAAAGC TGTTGACGA GACGGTGCAG CAGGTGCTG  
TGGGTGATAT GGACAGCAGA AGGGGAGAC CAAGTTTCCA GCTCAACCA TAACTATTGC ACAACCACT GTCCCTGCT  
CAGTCCCTC TCTGTAAACA TGAAGTCGT GTGAGGGTTA AAGGCAGTAA CAGGTATAAA GTACTTAGAA AAGCAAAGGG  
TGCTACGTAC ATGTGAGGCA TCATTACGCA GAGGTAATG GGATATGTT ACTATAAGGA AAAGACACTG AGGTCTAGA -3'  
(FRAG. NO:2275) (SEQ. ID NO:2446)

5'- AAATGATAGA CCGTCAATAA TTTGTTAAAT GCTTTTAAA ATGAATGCT TAAGCCGGGT GCAGTGCTC ACATCTGTAA  
TCCCAGCACT TTGGAGCCGA GCGGGTGGAT TGTGTGAGGT CAGGAGTTCG AGACCAACCT GGCCAACATG GAAAAACCTC  
ACTCTTACC AAAAATACAA AAATTAGCCA GGCATGGTGG CAGGCACCTG TGATCCAGC TACTCAGGAG GCTGAGACAG  
GAGAACTCGT TGAACCCGGG AGGCAAGGT GCAGTGAGCC AAGATTACGC CATTGACTC CAGCCTGGGT GACAGAGAGA  
GACTCCGTCT CAAAAA AAAAATAAATAA AAAAAATTAC GCTTCAAACA CATGATCTCT CACCACTGTT GAATTTCTT  
TCTATGAGCC CAGGAGGGCC TCTCAGAGAG AAAAGCTCT AGGTCTTCT TCCCTCTG AAACCTCCCT CTTGAAGGT  
TCAGAAGGAC TGTGCTGCT CGTTGCATCC TTGCAAGTG TCCAAACCT GATCCAGCT GTGCTTAGG GTTCTGCAA  
ACCTTTTCCA GGTGTTAATT ACCTCCCACT TCATTCTG TTTACCAACT CAGCTTTTG TTTAGTGTG TTTGAATTCC  
CTGAAGTAC CGTTGTCTGA TCTCCACCT CCAACTGAAT TAGGGGAGCT GGGCTTCTG AAACCCAGGT GCGGGTGT  
GCAGAGTGGC TGAAAGCTGG GATGTGGCAG ATCCGTGGCT ACATTCATGC ACACACACAC ACCACATAC CCACACATGC  
ACACACACAC ACACACCCGC ACTCACACAC TTGGACATGC ATAGACCACA GCTTTCCACA CCTTCTAG ACAGGGGTCA  
CTGGTATCC TGGAGAGAGT GTGAAGTCTT GGAATGAAA GAGGGGGGAT TAAGCCCCAC CTCTAGCCAT GGGACTGAGA

GGGGCACAGA GGAGGGCCCTG GGCTGAGAAC TTGACAGCAC CTTGTAATTG GTAAGCCAAG CCCGAAGGGA CTGGAAATAC  
TCAGATGTGT CTGTCTCCCT TATTAGGTTT AAAGTCCCTC AAGACCCTGT CTCCATCACA GTGCTCCAGT CCAGACCCCT  
CCTCTGAGCT CCAGACCCTG CTGGACCCAA CCAGCCCTAT GGGGTGCGAT CCCACCTGC CTGGAATTCT CCAAAGAACC  
TCCCTTTAA CAGTTCAGC CTTTAACAGT TCCAGTAC ACACATGACC TTTCTCTCT AAATCAGCCC CCCATCTCTG  
CCTTTGACAG AGATGGAAGC CATGACACCT GCTCGCCCC TGCTCTACC CCATCCATGT CCAATCAAGC ACTAGGCATG  
TCAGGTTTTAC CCTCTAAACT CCTCTGGAAT CCAGTCTCTC AGTCTCCATC ATCCAGGTC GAAGCTAATG GGCTAACTGG  
TCCTTGCTTC CACTCTACCC CCACTGCAGT CCGACTTCC TGAGCAGCAG CCAGGGCCTA ATCGATATTC ACACCAAGCG  
CCAACCTGAC TGAGATATCC TCCTGCACCA TCATCCCTCC ACCCTGTTTA GTTCTGCTCA CCTCAGTGT TCTCATCAAT  
AATCCACTCC CCTCACAGGC GCGTTTGGGA CCCCATGTTT TATGCTCTCA CAGGACCTTT TGCTTGATTT TCACTGTAC  
TTAGGTGACT TTGCAGTTAT TAAGTGACTG AGCAATGTCT GGCTTCTCCA GTAGACTGTC AGTCTCTAGC CATTGTATAC  
CTAGACCCGC TGTGTGGGAG CACGTGACAA ACGTCCAGTG AGTCAGGGAC TCAGCAGTCT CCATTITCCC GCCCTGTGG  
AGAAATGCGTG TATTTGGCAA TCCCAAGCCC CTGTGCCATC TAACCATCTT TCTTCTCTG TTCAGCCGAG GTGTGGCCTC  
ACTCATATCC CACTCTGAGT CCAAATGTTT TCTCCTGGA AGATATCAAT GTTCTGTCT GTTCTGTAGG ACTCCGTGCC  
CACCACGGCC TCTTTCAGGT GAGTCAAAGG GATTCCTCAG TCACTAGTT AGGGGAGGTG GGCAGACACC CTGGAGAACT  
CCTTGAAAG CTCAACTCTC ATGCCCCGGA CAACAGTTGA AGGAACCATG GTGATGTTAA GCCCAAAGAC AAAACCTCTC  
AGGTGTCCAA GTCCCTGTTG GAATCTTGGG AGCAGAGGGA ATGTTCTGTG GTCTAGAGGA AGAGGGGCTC AGGGAGGAGA  
AGGGCACATT CTGGTTGTT ATATGTTTCT ATCTATCCCA GATGAACCTG GAAGTGAAGG GAAGAGAGTT AAACATTTAA  
GTAAATACCC AGTGGATCAG ACAGCAATGT GCCAGATTGC CTGGAAACA AAATATCTCC AACACATGGC TGACATTGG  
TGGGAGATCA GAACACCCTA AAGAGAGAAT TTAAGGGGAG GGGGAGGAG ACCTGAGCCA GAGTAGAAGC  
AGAGGATAGG GAGATCTGTT CTGGGGACA GCATTGCAA GAAACAAGGC TGAGGGGTCC ACTCCAACCT CTCACCCCTG  
CTGCAGGTGC TGCCTATGAT GAAGATGAGC AGATGGCCAT CTCAGCTGGG GCCACAGTGC ACTGGACCTA TAGTTTCCAA  
TTCCGCACTC AGCAGGCATC TTTCTGATGA TCCGATGGCT TCTCAGAGCC AGGGATGGG CAGGATCCAT CCCTTGCT  
ACTGTCTTGC TGAGAAATTT ATAAGCAGCA TCTGGTGCTA TACTTTGGTC TCTAGTGAGT TAGCTCATGA AAGATGATAG  
ACTCTCCAAG CCAGGGGTAT GCAGGAAATG GGTTTTCTGT AGCTACAGAA ATGGGGTTGA GGGTTGGACC AAGGGACTAC  
CCAGGGGAAG TCTTACCTTC AGAGGACTCT GGAAGGAGG CTGCAAGTTT TCATGGGTCA AGAATTCAGA GCCCAGTAGA  
GACAGCTTAT CTCTGTTCCA AGATGTCTGG GGCTTGGTT GGAAGATTCA AAGGCTAGGA AACCAGGAGC CACCAAAGC  
GTAAGTGGG CCAGAGGATC CACTTTCAAG GTGGCAAGTT GGTTCCTCCC ATGTGGCTGC TTGAGTATCC TCATATGGC  
GCTCATATCC TTCCAAGTAA GCAATGCAAA AGGCCAAGAA AGATGCTGCA AAGATGTTAT GACCTAGCCT CAGAAATCAC  
ACACCATCCC TGCCACCATT AGTAAGAAGT CCAGCCACG TCCAGGAGAA GAGGAAGCAG ATTCCTCTT TTGAAATGAA  
GAATATCAAG TAATTCGGGG GGCATATGAA AGCCACCACA CACCACAGGG ATCTTTTATG AGCATACTTC TTATACCATC  
ACTGTAGTTC CTAAAGACTC AGGGGCAAAG CCTCACTTCC TTAGCACCA GTGAAGACCA CGCTTACTCC CTCACCTAAC  
CTCTGTACTC TTCCCACTC TCTGTCCAA CATCTAGTGT CACTTTCCAG CACTTTCCAG AACTATCCAA AGTTCCTGTC  
CTCTGCTCAG GCTGTTCCCC TGCCCTGGTC CACTTGTCT CTTTCTTGT CGGTCAAAAT GCTTCTTATC CTTCAGACC  
CAGCTCTAGA GTCACCTCCA ACCCCTTACC CACCAGCCCC CTCTCCAAGT CTGTGTCCA CAACCCCCCT GTTCCCTCCA  
GGGCAACCCT CACCCTCTGG GCCACAGTTG TCAGGAGTCA GGCAGGGCAG GGGCCGGGTG GTGTCTTCTT TGTGTTCTTG  
CACTCAGGGC AGAGCTCAGC ACAGAGCAGA CGCTCAAAA ACATTTAAAG GATAGAAGCA TTGATTTGTG GGTCCCCCAG  
TCTGGTCCA GGATGCCAGC CAGCTGCTCC TAGAAGCAAA CGGACTTTTC CTGGGAAATC CCAGAGGTGA TGATCAGTAA  
TCTCTCCGT GACTCGTAGT TCAGCTCTTC CTCCATGAGC CTGACTATCA GTGGACCTTC CAGAAAGAGC CCCTTTTCTC  
TCTCTCACCC ACAGCACAGG GCATCTGGGA AATGCCCAAT GAGTCTGCC TCTGGGTTGT CTCTTGAGT TTTCTGTG  
TCTCGCATCC ACTCTTCAAC TTGAATGTTG CAACAGCCAT GAAAAAGAA ATGCAAAGCG ATTCAGGATG AGAGCAATAC  
CCTACTCAA AGAAGGCAAC ATAGAAGCTC AGAGAGATCA AGCAATTTGC CCAAGACCAC ACAGCTAGGA GTGGAATCA  
TGGCTGTCCA AGCCCCATGC CTCTGCTGAA GGTAGAGATG AATTACAGCA ACAAGTCTAG AAAGGTGCTT GCCCTATGGT  
CTGTGAGTCT TGCTAAGAA TGAAAGAGGA GCCAGTGGGT TAAAGATGAG GTCACCAACA ACGGTGGTGT TGGAGTTTAC  
CACTGATAAT AAGGGTGCAA AATGTAATTT ACTAATGTTT ATTGAGCCTA GTGCAGTGCG TGGGGCATT TGCACATTG  
CTGTGATCC TATGACAACC CTGAGAGGTA GTGGTTTAA CTGCCATGT ACAGGTGAGG TCATTGTGT TCAAGGAGT  
TAAGTAACCT CCCACGGTG ACACGGCTTA TAAGTAAAGG ACCAGGATG TGAACCCAGT AGGACTATCT GGTGCAAG  
TCCCCACCC CCTCGCCATC TGTATCTCC AATCACTTCA GTGCTTGTCT GCATAGAAGG TAACGGAAAT CACGATGCCA  
CAGACTGTCC AGGAAGACAG AAATAGGCA GATGGGCTGG CCATGGTCTC CAAGCCAGAC TGAATCTCC AGGTCTGGAA  
TGATATCATT TTTCTTTT AATAAATTA CTACCCACC ACACGGCTT GAGAGGCTCA AAGTTGACCA ACTCCCTTGG  
GAGGGCCCCG GTTGATAAGG AAGGAACGTG AATCCTCCCA TCACGGAAGC TCAAGGAGG TCAAGGGTCC AACACTTGAG  
ATTGTTAGT CTGTTGGTGG ATACTGGCCA AGGAAATAT CCAGTGGAGC CTCGAGATGA AGAATGAGG GCCCCGTTT  
AGAACCAAG ATCAGAGGGG GCTCTGTAAG ACCGAGGGA GTCAGGTGCA CTGGAGCGCG GGCATGCAAA AACAGCCTG  
AGCTCCACT CGGCTTCTC TTGTCTGGC TGGTTGTCT TAACCCCTGT CTCCTTCTG ACCAGTTTTT GTCTTCCCT  
TGTGACCGCT GAGGGGTAAC AGCCTCTTTC CACTTCTTT CAGCGCCGAC ATGCTCAATG TCACCTTGCA AGGGCCACT  
CTTAACGGGA CTTTGGCCA GAGCAAATGC CCCAAGTGG AGTGGCTGG CTGGCTCAAC ACCATCCAGC CCCCTTCT  
CTGGGTGCTG TCTGTGCTGG CCACCTAGA GAACATCTT GTCCTCAGCG TCTTCTGCT GCACAAGAGC AGCTGCACGG  
TGGCAGAGAT CTACCTGGG AACCTGGCCG CAGCAGACT GATCCTGGCC TGCGGGCTGC CTTTCTGGG CATCACCATC  
TCCAACAAT TCGACTGGCT CTTTGGGGAG ACGCTCTGCC GCGTGGTGAA TGCCATTATC TCCATGAAC TGACAGCAG  
CATCTGTTT CTGATGCTGG TGAGCATCGA CCGTACTCT GCCCTGGTGA AAACCATGTC CATGGGCGG ATGCGCGCG  
TGCGCTGGG CAAGCTCTAC AGCTTGGTGA TCTGGGGTG TACGCTGCTC CTGAGCTCAC CCATGCTGGT GTTCCGACC  
ATGAAGGAGT ACAGCGATGA GGGCCACAAC GTCACCGCTT GTGTCATCAG CTACCCATCC CTCATCTGGG AAGTGTTCAC  
CAACATGCTC CTGAATGTCG TGGGCTTCT GCTGCCCTG AGTGTATCA CTTTCTGCAC GATGCAGATC ATGCAGGTGC  
TGCGGAACAA CGAGATGCAG AAGTTCAAGG AGATCCAGAC GGAGAGGAGG GCCACGGTGC TAGTCTGGT TGTGCTGCTG  
CTATTATCA TCTGCTGGCT GCCCTCCAG ATCAGACCT TCTGGATAC GTCGATCGC CTCGGCATCC TCTCAGCTG  
CCAGGACGAG CGCATCATCG ATGTAATCAC ACAGATCGCC TCCTTCATGG CCTACAGCA CAGCTGCCTC AACCACTGG  
TGTAAGTGT CGTGGGCAAG CGCTTCCGAA AGAAGTCTG GGAGGTGTAC CAGGGAGTGT GCCAGAAAGG GGGCTCAGG  
TCAGAACCA TTCAGATGA GAACCTCATG GGCACATGCG GGACCTCCAT CTCGTGGAA GCCAGATTG ACAAACCTGA  
GGACTGGGA GGGAGCAGC AGTGAGCAAA GCCCAGCAGG GCTGCTGTGA ATTTGTGTA GGATTGAGG ACAGTTGCTT  
TTCAGCATGG GCCCAGGAAT GCCAAGGAGA CATCTATGCA CGACCTTGGG AAATGAGTTG ATGTCTCCG TAAACACCG

GAGACTAATT CCTGCCCTGC CCAATTTTGC AGGGAGCATG GCTGTGAGGA TGGGGTGAAC TCACGCACAG CCAAGGACTC  
CAAAATCACA ACAGCATTAC TGTTCTTATT TGCTGCCACA CCTGAGCCAG CCTGCTCCTT CCCAGGAGTG GAGGAGGCCT  
GGGGGCAGGG AGAGGAGTGA CTGAGCTTCC CTCCCGTGTG TTCTCCGTCC CTGCCCCAGC AAGACAACTT AGATCTCCAG  
GAGAACTGCC ATCCAGCTTT GGTGCAATGG CTGAGTGCAC AAGTGAGTTG TTGCCCTGGG TTTCTTTAAT CTATTCAGCT  
AGAAGTTTGA AGGACAATTT CTTCGATTAA TAAAGGTTAA GCCCTGAGGG GTCCCTGATA ACAACCTGGA GACCAGGATT  
TTATGGCTCC CCTACTGAT GGACAAGGAG GTCTGTGCCA AAGAAGAATC CAATAAGCAC ATATTGAGCA CTGTCTGTAT  
ATGCAGTATT GGCAGCTGTA GGCAAGAGGG AAGAAAGAGA AGGAGCCATC TCCATCTTGA AGGAACTCAA AGACTCAAGT  
GGGAACGACT GGGCACTGCC ACCACCAGAA AGCTGTTTGA TGAGACGGTC GAGCAGGGTG CTGTGGGTGA TATGGACAGC  
AGAAGGGGGA GCCAGGTTCC AGCTACCAA TACTATTGCA CACCACCTGT CCTGCCTC -3' (FRAG. NO:2275) (SEQ. ID  
NO:2445)

5'- CAGATTGACA AACTGCAGGA CTGGGCAGGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT GCTGTGAATT  
TGTGTAAGGA TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC AAGGAGACAT CTATGCACGA CCTTGGGAAA  
TGAGTTGATG TCTCCGTAA AACACCGGAG ACTAATTCCT GCCCTGCCCA ATTTGACAGG GAGCATGGCT GTGAGGATGG  
GGTGAACCTA CGCAGACCA AGGACTCCAA AATCACAACA GCATTACTGT TCTTATTGTC TGCCACACCT GAGCCAGCCT  
GCTCCTTCCC AGGAGTGGAG GAGGCCTGGG GGGAGGGAGA GGAGTACTG AGCTTCCCTC CCGTGTGTTT TCCGTCCCT  
CCCCAGCAAG ACAACTTAGA TCTCCAGGAG AACTGCCATC CAGCTTTGGT GCAATGGCTG AGTGACAAAG TGAGTTGTTG  
CCCTGGGTTT CTTTAATCTA TTCAGCTAGA ACTTTGAAGG ACAATTTCTT GCATTAATAA AGGTAAAGCC CTGAGGGGTC  
CCTGATAACA ACCTGGAGAC CAGGATTTTA TGGCTCCCT CACTGATGGA CAAGGAGGTC TGTGCCAAAG AAGAATCCAA  
TAAGCACATA TTGAGCACTT GCTGTATATG CAGTATTGAG CACTGTAGGC AAGACCCAAG AAAGAGAAGG AGCCATCTCC  
ATCTTGAAGG AACTCAAAGA CTCAAGTGGG AACGACTGGG CACTGCCACC ACCAGAAAGC TGTTCCAGCA GACGGTCGAG  
CAGGGTGCTG TGGGTGATAT GGACAGCAGA AGGGGGAGAC CAAGGTTCCA GCTCAACCAA TAACTATTGC ACAACCACCT  
GTCCCTGCCT CAGTCCCTT TTATGTAACA TGAAGTCGTT GTGAGGGTTA AAGGCAGTAA CAGGTATAAA GTACTTAGAA  
AAGCAAAGGG GTCTACGTAC ATGTGAGGCA TCATTACGCA CAGCTAAGTG GGATATGTTT ACTATAAGGA AAAGACACTG  
AGGTCTAGAA ATAGCTCCGT GGACGAGAAT CAGTATTGGG AGCCGGTGGC GGTGTGAAGC ACCAGTGTCT GGCACACAGT  
AGGTGCTCAT TGGCTCCCTT CCACCTGTCA TTCCACCAC CCTGAGGCC CAACCGCCAC ACACACAGGA GCATTTGGAG  
AGAAGGCCAT GTCTTCAAAG TCTGATTTGT GATGAGGCAG AGGAAGATAT TTCTAATCGG TCTTGCCAG AGGATCACAG  
TGCTGAGACC CCCCACCACC AGCCGGTACC TGGGAAGGGG GAGAGTGCAG GCCTGCTCAG GGACTGTTC TGTCTCAGCA  
ACCAAGGGAT TGTTCTGTG AATCAATGGT TTATTGGAAG GTGGCCAGT ATGAGCCCTA GAAGAGTGTG AAAAGGAAATG  
GCAATGGTGT TCACCATCGG CAGTGCCAGG GCAGCACTCA TTCACTTGAT AAATGAATAT TTATTAGCTG GTTGGAGAGC  
TAGAACCTGG AGAGCTAGAA CCTGGAGAAC TAGAACCTGG AGGGCTAGAA CCTGGAGAGG CTAGAACCAA GAAGGGCTAG  
AACCTGGAGG GGCTAGAAC TAGAGAAGCT AAAACCTGAG TAGAAGCTG GAGGACTAGA ACCTGGAGGG CTGGAATCTG  
AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG GAGGGCTAGA ACCTAGAAGG  
GCTAGAACCT GGAGGGCTGG AATCTGGAGA GCTAGAACCT GGAGGGCTAG AACCTGGAGG GCTAGAACCT AGAAGGGCTA  
GAACCTGGAG GGCTAGAAC TGCCAGGTTA GAACCTAGAA GGGCTAGAAC CTGGAGAGCC AGAACCTGGA GGGCTAGAAC  
CTGGAAGGGC TAGAACCTGT AGAGCTAGAA CATGGAGAGC TAGAACCCGG CAGGCTAGAA CCTGGCAAGC TAGAACCTGG  
AGGGAATGAA CCTGGAGGGC TAGAACCTGG AGAATGAGAA AAATTTACAT GGCAAAGAGC CCATAAATCC TGACCAATCC  
AACTCTGAAT TTAAAGCAA AAGCGTGAAG AAAAAGATTG CCTCCTTACC CCAACCCAC TCTTTTTTCC CACCACCAC  
TCTCTCTGC CTAGTAAGT ATCTGGAGGA AGAAAACAGG TGAAGAAGA AGTAAAAACC ATTTAGTATT AGTATTAGAA  
TGAAGTCAA CTGTGCCACA CATGGTGAAT GAAAAAAGG TGTGTTTTGT CACACAGGGC CAGTCTTACG  
CACCAGAGCA CGTGATGGTC TGAGACTCTC TTAGGAGCAG AGCTCTGCCG CAATGGCCAT GTGGGGATCC ACACCTGGTC  
TGAGGGGCAA CTGAGTCTGC GGGAGAAGAG CGGCCCTATG CATGGTGTAG ATGCCCTGAT AAAGAATATC TGTCTGTGA  
AAGACTCAAT GAGCTGTAT GTTGTAACA GGAAGCATT CACATCCAAA CGAGAAAATC ATGTAAACAT GTGTCTTTTC  
TGAGAGCAT AATAAATGGA TGAGGTTTTT GCAAAAAAAA AAAAAAAA -3' (FRAG. NO:2275) (SEQ. ID NO:2444)

5'- GAGCTCTTCA ATATTTTAGT GAAAGCTATA GATGAGGCTC CATAGGGGAT AAAGCACAGA CACACCTTTT  
CAGAGGGCTT GTGACTCTG GGCAGCCTGT CCATAGACCT CTGTCCCCAA CTGGCAAGTC AGGAACTCC AGATTAAGGA  
GCCCCAATGT GTTGAACAG CCAGGTGCAC AGATGAGTCA ACCACACAGC CAGGCCAGGG AGGGCCTTCA CTCAAGAGCC  
TACAGCCAGT TCACAGCCAA GCCAGGGCTA GCGCCAGGCC ACCCAATAAC TGATCTGAGA CTGTGTTTCC CTGTCTCCAT  
GATGATGGGA TCAGGCTTGA TTGCTGGTTT GTAGGCTTGT TATGAATCAA GTCACAGGGA AGAGGAGCTG ATGGGCTGGG  
GGGACGTCCT CTGGCCCTCC TGTCTCTTCC CCAGATCCAC TGGGCCCACT CTATCTGTT CTCTCTGAA GGAAGGGTTT  
TAAGGCTTCA AAAAAAATG TTTGAAAGT CCCTGCCCTT TCCAGCTCCT ACCGTCTCAG CCCTGGGAGT GTAAAGTGCT  
GCAGATAGTT AGTAAGTCTT TGAGCAAAAC TGAGAAAGCC AGCCTGAGCC TTGACATGGG AGAAACCTCC GCCATACATC  
TCCGAAGAAA CGGCCGCGTG TCTCAGGGGA GCGCAAACAC CCGTACCCAG GAAACAGGAC AGCTTCTGCC ACTGTGCCCC  
TTGGGAGCCG TACGTGGCAT GACAAAGAAA TCCAGGACT CCGCTGCCC ACCTGGCCAC CCTCTGTTA CACTTCCCG  
GTAAACGCCC ACTGTTTACA TCCAAACTC AGACACAAA TAACCACCTC AAGAAGATAA ATAATGATAA GAAATAAATG  
TTACGCGAGG CAAATTTATT CACATGGGGC TTCCAGGCC ACTTTGTGT CAGCCGGGAG GGACGTTTTT CCGCTCCAC  
GACTCCAACG GGCAGCCGGG CCTACGCAA CATGGAAATC TTCAAAGAGC CTCCCTGGCC CCCAGGGCTC AGAGGGTGGC  
AGAGCGGAGA GCGAAGGTGG CCGCAGCCTT CCGGCCCA CAGCCAGCCT GGCTCCAGCT GGGCAGGAGT GCAGAGCTCA  
GCTGGAGGCG AGGGGGAAGT GCCAGGAGG CTGATGACAT CACTACCCAG CCCTTCAAAG ATGAGCTGTT CCGCCGCCA  
CTCCAGCTCT GGCTTCTGGG CTCCGAGGAG GGGTGGGGAC GGTGGTGACG GTGGGGACAT CAGGCTGCC CGCAGTACCA  
GGGAGCGACT GAAGTGCCCA TGCCGCTTGC TCCGAGAAG GTGGGTGCCG GGCAGGGGCT GCTCCAGCCG CCTACCTCT  
GCTGGGAGGA CAACTGTCC CAGCACAGAG GGAGGGAGGG AGGGCAGGCA GCGGGGAGAA GTTCCCTGT GGTCTGGGG  
AGTTGGGAAA AGTTCCCTC CTTCGGAGG GAGG -3' (FRAG. NO:2275) (SEQ. ID NO:2443)

5'- GCCCTTCAA GATGAGCTGT TCCCGCCGC ACTCCAGCTC TGGCTTCTGG GCTCCGAGGA GGGGTGGGA  
CGGTGGTGAC GGTGGGGACA TCAGGCTGCC CCGCAGTACC AGGAGCGAC TGAAGTGCC ATGCCGCTTG CTCCGAGAA  
GGTGGGTGCC GGGCAGGGG TGCTCCAGCC GCCTCACCTC TGCTGGGAGG ACAAATGTC CCAGCACAGA GGGAGGGAGG  
GAGGGCAGGC AGCGGGGAGA AGTTCCCTG TGGTCTGGG GAGT -3' (FRAG. NO:2275) (SEQ. ID NO:2442)

5'- AAATGATAGA CCGTCAATAA TTTGTTAAAT GCTTTTAAAT ATGAATGCTT TAAGCCGGGT GCAGTGCCCT ACATCTGTAA  
TCCAGCACT TTGAGCCGA GCGGGTGAT TGTGTGAGGT CAGGAGTTCG AGACCAACT GGCCAACATG GCAAAACCTC  
ACTCTTACC AAAAAATCAA AAATTAGCCA GGCATGGTGG CAGGCACCTG TGATCCAGC TACTCAGGAG GCTGAGACAG



GAGAATCGCT TGAACCCGGG AGGCAAGGTT GCAAGTGAGCC AAGATTACGC CATTGTACTC CAGCCTGGGT GACAGAGAGA  
GACTCCGTCT CAAAAAATAA AAAAAAATTAC GCTTCAAACA CATGATCTCT CACCACTGTT GAATTTTCTT  
TCTATGAGCC TGGAGGGGCC TCTCAGAGAG GAAAGCTCCT AGGTCTTCTT TTCCCTCTGC AAACCTCCCTG CTTTGAAGGT  
TCAGAAGGAC TGTGCGTGCT CGTTGCATCC TTGCAAGCT TCCAAACCTT GATCCAGCT GTGCTTAGGG GTTCTGCAA  
ACCTTTTCCA GGTGTTAATT ACCTCCCACT TCATTTCTGT TTTACCAACT CAGCTTTTGT TTTAGTGTG TTTGAATTCC  
CTGAAGTGAC CGTTGTCTGA TCTCCACCTC CCAACTGAAT TAGGGGAGCT GGGCTTCTGG AAACCCAGGT GCCGGGTGTT  
GCAGAGTGGC TGAAGAGCTGG GATGTGGCAG ATCCGTGGCT ACATTCATGC ACACACACAC ACCACATAC CCACACATGC  
ACACACACAC ACACACCCGC ACTCACACAC TTGGACATGC ATAGACCACA GCTTTCCACA CCTTCCTAG ACAGGGGTCA  
CTTGGTATCC TGGAGAGAGT GTGAAGTCCT GGAATGGAAA GAGGGGGGAT TAAGCCCCAC CTCTAGCCAT GGGACTGAGA  
CAAGTCACCA CCAACCCATC TGCGCCTTGT TTACCTCCTC TGTGAGGCAA GCACAGAGCC CATGCCTGCC CCCCTGGATG  
GGAGTGATGT GAAACTTGAA GGGCGGTGAG AGCAAGGGTC GGGAAATGAA GGGCCTTGGG AAAAAAGGCC CTTTCAACTA  
GGGGCACAGA GGAGGCCCTG GGCTGAGAAC TTGACAGCAC CTTGTAATTG GTAAGCCAAG CCCGAAGGGA GTTGAATAAT  
TCAGATGTGT CTGTCTCCCT TATTAGGTTT AAAGTCCCTC AAGACCCTGT CTCCATCACA GTGCTCCAGT CCAGACCCCT  
CCTCTGAGCT CCAGACCCCTG CTGGACCCAA CCAGCCCTAT GGGGTGCGAT CCCACCTGC CTGGAATTCT CCAAAGAACC  
TCCCCTTTAA CAGTTCCAGC CTTTAACAGT TCCAGTCTAA ACACATGACC TTTCTCTCT AAATCAGCCC CCCATCTCTG  
CCTTTGCAGG AGATGGAAGC CATGACACCT GCCTCGCCCC TGTCTCACC CCATCCATGT CCAATCAAGC ACTAGGCATG  
TCAGGTTTAC CCTCTAACT CCTCTGGAAT CCAGTCTCTC AGTCTCCATC ATCCCAGGTC GAAGCTAATG GGCTAACTGG  
TCCTGTCTC CACTCTACCC CCACTGCAGT CTGACTTCC TGAGCAGCAG CCAGGGCCTA ATCGATATTC ACACCAAGCG  
CCAACCTGAC TGAGATATCC TCCTGCACCA TCATCCCTCC ACCCTGTTTA GTTCTGCTCA CCTCAGTGT TCTCATCAAT  
AATCCACTCC CCTCACAGGC GCGTTTGGGA CCCCATGTTT TATGCTCTCA CAGGACCTTT TGCTTGATT TTTACTGTAC  
TTAGGTGAGT TTGCAGTTAT TAAGTGACTG AGCAATGTCT GGCTTCTCCA GTAGACTGTC AGTCTCTAGC CATTGTATAC  
CTAGCACCGC TGTGTGGGAG CACGTGACAA ACCTCCAGTG AGTCAGGGAC TCAGCAGTCT CCATTTCTCC GCCCTGCTGG  
AGAATGCGTG TATTTGGCAA TCCCAGGCC CTGTGCCATC TAACCATCTT TTCTTCTCTG TTCAGCCCCAG GTGTGGCCTC  
ACTACATCC CACTCTGAGT CCAAAATGTT TCTCCCTGGA AGATATCAAT GTTCTGTCT GTTCTGTAGG ACTCCGTGCC  
CACCACGGCC TCTTTAGGT GAGTCAAAGG GATTCTCTAG TTCACTAGTT AGGGGAGGTG GGCAGACACC CTGGAGAATC  
CCCTGGAAG CTCAACTCTC ATGCCCCGGA CAACAGTTGA AGGAACCATG GTGATGTTAA GCCCAAAGAC AAAACCTCTC  
AGGTGTCCAA GTCCCTGTTG GAATCTTGGG AGCAGAGGGA ATGTTCTGTG GTCTAGAGGA AGAGGGGCTC AGGGAGGAGA  
AGGGCACATT CTGGTTGTT ATATGTTTCT ATCTATCCCA GATGAACCTG GAAGTGAAGG GAAGAGAGTT AAACATTAA  
GTAATACCC AGTGGATCAG ACAGCAATGT GCCAGATTGC CTTGGAAACA AAATATCTCC AACACATGGC TGACATTGG  
TGGGAGATCA GAACACCCTA AAGAGAGAAT TTAAGGGGAG GGGGAGGAGG ACCTGAGCCA GAGTAGAAGC  
AGAGGATAGG GAGATCTGTT CTTGGGGACA GATTGTGCAA GAAACAAGGC TGAGGGGTCC ACTCCAACCT CTCCACCTG  
CTGCAGGTGC TGCCTATGAT GAAGATGAGC AGATGGCCAT CACAGTGGG GCCACAGCT ACTGGACCTA TGATTTCCAA  
TTCCGCACTC AGCAGGCATC TTTCTGATGA TCCGATGGCT TCTCAGAGCC AGGGATGGG CAGGATCCAT CCCCTTGGCT  
ACTGTCTTG TGAGAAATTT ATAAGCAGCA TCTGGTGCTA TACTTTGGTC TCTAGTGAGT TAGCTCATGA AAGATGATAG  
ACTCTCCAAG CCAGGGGTAT GCAGGAAATG GGTTTTCTGT AGCTACAGAA ATGGGGTTGA GGGTTGGACC AAGGGACTAC  
CCAGGGGAAG TCTTACCTC AGAGGACTCT GGAAGGAGG CTGCAAGTT TCATGGGTCA AGAATTCAGA GCCCAGTAGA  
GACAGCTTAT CTCTGTTCCA AGATGTTCTG GGCCTTGGT GGAAGTTCA AAGGCTAGGA AACCAGGAGC CACCAAAAGC  
GTAACCTGGG CCAGAGGATC CACTTCAAG GTGGCAAGTT GGTCTCCCTC ATGTGGCTGC TTGAGTATCC TCAGATGGCG  
GCTCACATCC TTCCAAGTAA GCAATGCAAA AGGCCAAGAA AGATGCTGCA AAGATGTTAT GACCTAGCTC GACAAATCAC  
ACACCATCCC TGCCACCATT AGTAAGAAGT CCAGCCCACG TCCAGGAGAA GAGGAAGCAG ATTCTCTCTT TTGAAATGAA  
GAATATCAAG TAATTCGGGG GGCATATGAA AGCCACCACA CACCACAGG ATCTTTTATG AGCATACTTC TTATACCATC  
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CTCTTGCTAC TTCCACCTC TCCTGTCCAA CATCTAGTGT CACTTTCCAG AACATACCA CAGCTTCCCC AGTTCTGTGC  
CTCTGCTAG GCTGTTCCCC CTGCCTGGTC CACTGTCTCT CCTTCTGTG CGGTCAAAAT GCTTCTTATC CTTCAAGAC  
CAGCTCTAGA GTCACCTCCA ACCCTTACC CACCAGCCCC CTCTCAAGT CTGTGTCCCA CAACCCCTCT GTCCTCCCA  
GGGCACCTC CACCCTCTGG GCCACAGTTG TCAGGAGTCA GGCAGGGCAG GGGCCGGGTG GTGTCTTCTT TGTGTTCTG  
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TCTGGCTCCA GGATGCCAGC CAGCTGCTCC TAGAAGCAAA CGGACTTTTC CTGGGAAATC CCAGAGGTGA TGATCAGTAA  
TCTCTCCCGT GACTCGTAGT TCAGCTCTTC CTCCATGAGC CTGACTATCA GTGGACCTTC CAGAAAGAGC CCCTTTCTCT  
TCTCTACCC ACAGCACAGG GCACTGGGAA AATGCCCAAT GAGTCTGCTC TCTGGGTTGT GCTTTGGACT TTTCAAGTGT  
TCTCGCATC ACTCTTCAAC TTGAATGTTG CAACAGCCAT GAAAAAAGAA ATGCAAAGCC ATTCAGGATG AGAGCAATAC  
CCTACTCAA AGAAGGCAAC ATAGAAGCTC AGAGAGATCA AGCAATTTGC CCAAGACCAC ACAGCTAGGA GTGGAATCA  
TGGCTGTCCA AGCCCCATGC CTCTGCTGAA GGTAGAGATG AATTACAGCA ACAAGTCTAG AAAGGTGCCT GCCCTATGGT  
CTGTGAGTCT TGCCTAAGAA TGAAAGAGGA GCCAGTGGGT TAAAGATGAG GTCACCAACA ACGGTGGTGT TGGAGTTTAC  
CACTGATAAT AAGGGTGCAA AATGTAATTT ACTAATGTTT ATTGAGCCTA GTGCAAGTGC TGGGGCATT TGCACATTGT  
CTCTGATCCC TATGACAACC CTGAGAGGTA GTGGTTTAA CTGCCATGTT ACAGGTGAGG TCATTGTGGT TCAAGGACGT  
TAAGTAACTT CCCAGCGTG ACACGGCTTA TAAGTAAGGC AGCCAGGATG TGAACCCAGT AGGACTATCT GGCTGCAAG  
TCCCCACCC CTCTGCCATC TGTATCTCTC AATCACTTCA GTGCTTTGCT GCATAGAAGG TAACGGAAAT CACGATGCCA  
CAGACTGTCC AGGAAGACAG AAACATAGGCA GATGGGCTGC CCATGGTCTC CAAGCCAGAC TGGAAATCTCC AGGTCTGGAA  
TGATATCAAT TTTCTCTTTT AATAAATTA CTACCCACC ACACGGCTTT GAGAGGCTCA AAGTTGACCA ACTCCCTTGG  
GAGGGCCCCG GTTGATAAGG AAGGAACGTG AATCTCTCCA TCACGGAAGC TTCAAGGAGG TCAAGGGTCC AACACTTGAG  
ATTGTTAGTG CTGTTGGTGG ATACTGGCCA AGGAAATATC CCAAGTGGAGC CTCGAGATGA AGAATATGAG GCCCCGTTT  
AGAACCAAGG ATCAGAGGGG GCTCTGTAAG ACCCAGGGGA GTCAGGTGCA CTGGAGCGCG GGCATGCAGA AAACAGCCTG  
AGCTCCACT CCGCTTCTCC TTGTCTGGC TGGTTGCTT TAACCCCTGT CTCCTTCTGG ACCAGTTTTT GTCCTTCCCT  
TGTGACCGCT GAGGGGTAAC AGCCTCTTTC CACTTCTTCT CAGCGCCGAC ATGCTCAATG TCACCTTGCA AGGGCCACT  
CTTAACGGGA CTTTGGCCCA GAGCAATGAG CCCCCAAGTG AGTGGCTGGG CTGGCTCAAC ACCATCCAGC CCCCCTTCT  
CTGGGTGCTG TTCGTGCTGG CCACCTAGA GAACATCTTT TCTCTAGCG TCTTCTGCTC GCACAAGAGC AGCTCAGCG  
TGGCAGAGAT CTACCTGGGG AACCTGGCCG CAGCAGACCT GATCCTGGCC TGCGGGCTGC CCTTCTGGGC CATCACCATC  
TCCAACAAT TCGACTGGCT CTTGGGGGAG ACGCTCTGCC GCGTGGTGAA TGCCATTATC TCCATGAACC TGTACAGCAG



CATCTGTTTC CTGATGCTGG TGAGCATCGA CCGCTACCTG GCCCTGGTGA AAACCATGTC CATGGGCGCGG ATGCGCGGGC  
TGCGCTGGGC CAAGCTCTAC AGCTTGGTGA TCTGGGGGTG TACGCTGCTC CTGAGCTCAC CCATGCTGGT GTTCCGGACC  
ATGAAGGAGT ACAGCGATGA GGGCCACAAC GTCACCGCTT GTGTCATCAG CTACCCATCC CTCATCTGGG AAGTGTTCAC  
CAACATGCTC CTGAATGTCG TGGGCTTCCT GCTGCCCCTG AGTGTATCA CCTTCTGCAC GATGCAGATC ATGCAGGTGC  
TGCGGAACAA CGAGATGCAG AAGTTCAAGG AGATCCAGAC GGAGAGGAGG GCCACGGTGC TAGTCTGGT TGTGCTGCTG  
CTATTCATCA TCTGCTGGCT GCCCTTCCAG ATCAGCACCT TCCTGGATAC GCTGCATCGC CTCGGCATCC TCTCCAGCTG  
CCAGGACGAG CGCATCATCG ATGTAATCAC ACAGATCGCC TCCTTCATGG CCTACAGCAA CAGCTGCCTC AACCCACTGG  
TGTACGTGAT CGTGGGCAAAG CGCTTCCGAA AGAAGTCTTG GGAGGTGTAC CAGGGAGTGT GCCAGAAAGG GGGCTGCAGG  
TCAGAACCCA TTCAGATGGA GAACTCCATG GGCACACTGC GGACCTCCAT CTCCGTGGAA CGCCAGATTC ACAAACCTGCA  
GGACTGGGCA GGGAGCAGAC AGTGAGCAAA CGCCAGCAGG GCTGCTGTGA ATTTGTGTAA GGATTGAGGG ACAGTTGCTT  
TTCAGCATGG GCCCAGGAAT GCCAAGGAGA CATCTATGCA CGACCTTGGG AAATGAGTTG ATGTCTCCGG TAAACACCCG  
GAGACTAAT CCGTCCCTGC CCAATTTTGC AGGGAGCATG GCTGTGAGGA TGGGGTGAAC TCACGCACAG CCAAGGACTC  
CAAAATCACA ACAGCATTAC TGTCTTATT TGTCTGCCA CCTGAGCCAG CCTGTCTCTT CCCAGGAGTG GAGGAGGCCCT  
GGGGGCAGGG AGAGGAGTGA CTGAGCTTCC CTCCCGTGTG TTCTCCGTCC CTGCCCCAGC AAGACAACCT AGATCTCCAG  
GAGAACTGCC ATCCAGCTTT GGTGCAATGG CTGAGTGCAC AAGTGAGTTG TTGCCCTGGG TTCTTTAAT CTATTCAGCT  
AGAACTTTGA AGGACAATTT CTGCAATTA TAAAGGTAA GCCCTGAGGG GTCCCTGATA ACAACCTGGA GACCAGGATT  
TTATGGCTCC CTCCTACTGAT GGACAAGGAG GTCTGTGCCA AAGAAGAATC CAATAAGCAC ATATTGAGCA CTGTGTGTAT  
ATGCAGTATT GAGCACTGTA GGCAAGAGGG AAGAAAGAGA AGGAGCCATC TCCATCTTGA AGGAACTCAA AGACTCAAGT  
GGGAACGACT GGGCACTGCC ACCACCAGAA AGCTGTTTGA TGAGACGGTC GAGCAGGGTG CTGTGGGTGA TATGGACAGC  
AGAAGGGGGA GCCAGGTTCC AGCTACCAA TACTATTGCA CACCACCTGT CTGCCTC -3' (FRAQ. NO: ) (SEQ. ID NO  
2441)

5'-CAGATTACACA AACTGCAGGA CTGGGCAGGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT GCTGTGAATT  
TGTGTAAGGA TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC AAGGAGACAT CTATGCACGA CCTTGGGAAA  
TGAGTTGATG TCTCCGGTAA AACACCGGAG ACTAATTCCT GCCCTGCCA ATTTGTCAGG GAGCATGGCT GTGAGGATGG  
GGTGAACCTA CGCACAGCCA AGGACTCCAA AATCACAACA GCATTACTGT TCTTATTTGC TGCCACACCT GAGCCAGCCT  
GCTCCTTCCC AGGAGTGGAG GAGGCTGGG GGGAGGGAGA GGAGTACTG AGCTTCCCTC CCGTGTGTTT TCCGTCCCTG  
CCCCAGCAAG ACAACTTAGA TCTCCAGGAG AACTGCCATC CAGCTTGGT GCAATGGCTG AGTGCACAAG TGAGTTGTTG  
CCCTGGGTTT CTTAATCTA TTCAGCTAGA ACTTTGAAGG ACAATTTCTT GCATTAATAA AGGTTAAGCC CTGAGGGGTC  
CCTGATAACA ACCTGGAGAC CAGGATTTTA TGGTCCCT CACTGATGGA CAAGGAGGTC TGTGCCAAAAG AAGAATCCAA  
TAAGCACATA TTGAGCACTT GCTGTATATG CAGTATTGAG CACTGTAGGC AAGACCCAAG AAAGAGAAGG AGCCATCTCC  
ATCTTGAAGG AACTCAAAGA CTCAAGTGGG AAGCACTGG CACTGCCACC ACCAGAAAGC TGTTGACGCA GACGGTGGAG  
CAGGGTGTG TGGGTGATAT GGACAGAGA AGGGGGAGAC CAAGGTTCCTA GCTCAACCAA TAACATTGC ACAACCACT  
GTCCCTGCCT CAGTTCCCTT TTATGTAACA TGAAGTCGTT GTGAGGGTTA AAGGCAGTAA CAGGTATAAA GTACTTAGAA  
AAGCAAAGGG TGCTACGTAC ATGTGAGGCA TCATTACGCA GACGTAACCT GGATATGTTT ACTATAAGGA AAAGACACTG  
AGGTCTAGAA ATAGCTCCGT GGAGCAGAAT CAGTATTGGG AGCCGGTGGC GGTGTGAAGC ACCAGTGTCT GGCACACAGT  
AGGTGCTCAT TGGTCCCTT CCACCTGTCA TTCCACCAC CAGGAGGCC CAACCGCCAC ACACACAGGA GCATTTGGAG  
AGAAGGCCAT GTCTTCAAAG TCTGATTTGT GATGAGGAG AGGAAGATAT TTCTAATCGG TCTTGCCAG AGGATCACAG  
TGCTGAGACC CCCCACCACC AGCCGGTACC TGGGAAGGGG GAGAGTGCAG GCCTGCTCAG GGAAGTGTCC TGCTCAGCA  
ACCAAGGGAT GTTCTCTGTC AATCAATGGT TTATTGGAAG GTGGCCAGT ATGAGCCCTA GAAGAGTGTG AAAAGGAATG  
GCAATGGTGT TCACCATCGG CAGTGCCAGG GCAGCACTCA TTACTTGAT AAATGAATAT TTATTAGCTG GTTGGAGAGC  
TAGAACCTGG AGAGCTAGAA CCTGGAGAAC TAGAACCTGG AGGGCTAGAA CCTGGAGAGG CTAGAACCAA GAAGGGCTAG  
AACTGGAGG GGCTAGAACC TAGAGAAGCT AAAACCTGAG CTAGAAGCTG GAGGACTAGA ACCTGGAGGG CTGGAATCTG  
AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG GAGGGCTAGA ACCTAGAAGG  
GCTAGAACCT GGAGGGCTGG AATCTGGAGA GCTAGAACCT GGAGGGCTAG AACCTGGAGG GCTAGAACCT AGAAGGGCTA  
GAACCTGGAG GGCTAGAACC TGGCAGGTTA GAACCTAGAA GGGCTAGAAC CTGGAGAGCC AGAACCTGGA GGGCTAGAAC  
CTGGAAGGGC TAGAACCTGT AGAGCTAGAA CATGGAGAGC TAGAACCCGG CAGGCTAGAA CCTGGCAAGC TAGAACCTGG  
AGGAATGAA CCTGGAGGGC TAGAACCTGG AGAATGAGAA AAATTTACAT GGCAAAGAGC CCATAAATCC TGACCAATCC  
AACTCTGAAT TTTAAAGCAA AAGCGTGAAG AAAAAGATTC CCTCCTTACC CCAACCCAC TCTTTTTTCC CACCACCCAC  
TCTCTCTGC CTCAGTAAGT ATCTGGAGGA AGAAAACAGG TGAAAAGAAG AGTAAAAACC ATTAGTATT AGTATTAGAA  
TGAAGTCAA CTGTGCCA CATGGTGAAT GAAAAAAGG AAAAAAGGC TGTGTTTGT CACACAGGGC AGTCATTACG  
CACCAGACA CGTGATGGTC TGAGACTCTC TTAGAGCAG AGCTTGCCG CAATGGCCAT GTGGGGATCC ACACCTGGTC  
TGAGGGGCAA CTGAGTCTGC GGGAGAAGAG CGGCCCTATG CATGGTGTAG ATGCCCTGAT AAAGAACATC TGTCTGTGA  
AAGACTCAAT GAGCTGTTAT GTTGTAACA GGAAGCATTT CACATCCAAA CGAGAAAATC ATGTAAACAT GTGCTTTTC  
TGTAAGCAT AATAAATGGA TGAGGTTTTT GCAAAAAAAG AAAAAAAG -3' (FRAQ. NO: ) (SEQ. ID NO 2431)

5'-GGTGBCBTTGBGCBTGTGCGGCC-3' (FRAG. NO:2276) (SEQ. ID NO:2287)

5'-GGTCCCGTTBBGBGTGGGCC-3' (FRAG. NO:2277) (SEQ. ID NO:2288)

5'-GCCAGCCAGCCACTCCACTTGGGGC-3' (FRAG. NO:2278) (SEQ. ID NO:2289)

5'-GGGTGGCCAGCACGAACAGCACCCAGAGGAAGGGGGC-3' (FRAG. NO:2279) (SEQ. ID NO:2290)

5'-GGCCAGAGAGGGCAGCCCGCAGGCCAGGATCAGGTCTGCTGCGGCC-3' (FRAG. NO:2280) (SEQ. ID NO:2291)

5'-GGAGATAATGGCATTACACCGCGGC-3' (FRAG. NO:2281) (SEQ. ID NO:2292)

5'-GGCCAGCGCACGCCGCGCATCCGGCC-3' (FRAG. NO:2282) (SEQ. ID NO:2293)

5'-GGGTCTGACCTGCAGCCCCC-3' (FRAG. NO:2283) (SEQ. ID NO:2294)

5'-GTCTCTTGGCATTCTGCGGCC-3' (FRAG. NO:2284) (SEQ. ID NO:2295)

5'-CAGTCACTCTCTCCCTGCCCC-3' (FRAG. NO:2285) (SEQ. ID NO:2296)

5'-CTTGCTGGGGCAGGGACGG-3' (FRAG. NO:2286) (SEQ. ID NO:2297)

5'-GGTGBCBTTGBGCBTGTGCGGCC-3' (FRAG. NO:2287) (SEQ. ID NO:2298)

5'-GGTCCCGTTBBGBGTGGGCC-3' (FRAG. NO:2288) (SEQ. ID NO:2299)

5'-GGGTGGCCAGCACGAACAGCACCCAGAGGAAGGGGGGC-3' (FRAG. NO:2290) (SEQ. ID NO:2301)  
5'-GGCCAGAAAGGGCAGCCCGCAGGCCAGGATCAGGTCTGCTGCGGCC-3' (FRAG. NO:2291) (SEQ. ID NO:2302)  
5'-GGAGATAATGGCATTACCCACGCGGC-3' (FRAG. NO:2292) (SEQ. ID NO:2303)  
5'-GGCCAGCGCACGCCGCGCATCCGGCCC-3' (FRAG. NO:2293) (SEQ. ID NO:2304)  
5'-GGGTCTGACCTGCAGCCCC-3' (FRAG. NO:2294) (SEQ. ID NO:2305)  
5'-GTCTCCTTGGCATTCTCTGGGCC-3' (FRAG. NO:2295) (SEQ. ID NO:2306)  
5'-CAGTCACTCCTCTCCCTGCCCC-3' (FRAG. NO:2296) (SEQ. ID NO:2307)  
5'-CTTGCTGGGACAGGGACGG-3' (FRAG. NO:2297) (SEQ. ID NO:2308)  
5'-CCGTGTGTCTBGTTGGTGCTG-3' (FRAG. NO:2298) (SEQ. ID NO:2309)  
5'-CCCCTTTBGGTBTGGC-3' (FRAG. NO:2299) (SEQ. ID NO:2310)  
5'-GCTCCBCCBTTCCTTTTCTCC-3' (FRAG. NO:2300) (SEQ. ID NO:2311)  
5'-TTGTTTTCGTTTCTCTTG-3' (FRAG. NO:2301) (SEQ. ID NO:2312)  
5'-CCGTCTGTGGTT-3' (FRAG. NO:2302) (SEQ. ID NO:2313)

## **B2 Adrenergic Receptor Kinase Nucleic Acids and Antisense Oligonucleotide Fragments**

5'- GCCGCCCG CCAAGATGGC GGACCTGGAG GCGGTGCTGG CCGACGTGAG CTACCTGATG GCCATGGAGA  
AGAGCAAGGC CACGCCGGCC GCGCGGCCA GCAAGAAGAT ACTGCTGCC GAGCCAGCA TCCGAGTGT CATGCAGAAG  
TACCTGGAGG ACCGGGGCGA GGTGACCTTT GAGAAGATCT TTTCCAGAA GCTGGGGTAC CTGCTCTCC GAGACTTCTG  
CCTGAACCAC CTGGAGGAGG CCAGGCCCTT GGTGAATTC TATGAGGAGA TCAAGAAGTA CGAGAAGCTG GAGACGGAGG  
AGGAGCGTGT GGGCCGACG CCGGAGATCT TCGACTCATA CATCATGAAG GAGCTGCTGG CCTGCTCGCA TCCCTTCTCG  
AAGAGTGCCA CTGAGCATGT CCAAGGCCAC CTGGGAAGA AGCAGGTGCC TCCGATCTC TTCCAGCCAT ACATCGAAGA  
GATTTGTCAA AACCTCCGAG GGGACGTGTT CCAGAAATTC ATTGAGAGCG ATAAGTTCAC ACGTTTTC CAGTGAAGA  
ATGTGGAGCT CAACATCCAC CTGACCATGA ATGACTTCAG CGTGCATCGC ATCATTGGGC GCGGGGGCTT TGGCGAGGTC  
TATGGGTGCC GGAAGGCTGA CACAGGCAAG ATGATCGCCA TGAAGTGCTT GGACAAAAG CGCATCAAGA TGAAGCAGGG  
GGAGACCTG GGCCTGAACG AGCGCATCAT GCTCTCGCTC GTCAGCACTG GGGACTGCCC ATTCATTGTC TGCATGTCT  
ACGCGTTCCA CACGCCAGAC AAGCTCAGCT TCATCTGGA CCTCATGAAC GGTGGGGACC TGCACTACCA CCTCTCCAG  
CACGGGGTCT TCTCAGAGGC TGACATGCGC TTCTATGCGG CCGAGATCAT CCTGGGCTG GAGCAGATGC ACAACCGCTT  
CGTGGTCTAC CCGGACCTGA AGCCAGCCAA CATCTTCTG GACGAGCATG GCCACGTGCG GATCTCGGAC CTGGGCTGG  
CCTGTGACTT CTCAAGAAG AAGCCCCATG CCAGCGTGGG CACCCACGGG TACATGGCTC CGGAGGTCCT GCAGAAGGGC  
GTGGCCTACG ACAGCAGTGC CCACTGGTTC TCTCTGGGT GCATGCTCT CAAGTTGCTG CCGGGGCACA GCCCTTCCG  
GCAGCACAAG ACCAAAGACA AGCATGAGAT CGACCGCATG ACCTGACGA TGGCCGTGGA GCTGCCCGAC TCCTTCTCC  
CTGAATACG CTCCTGCTG GAGGGGTTGC TGCAGAGGA TGTCACCCG AGATTGGGCT GCCTGGGCGG AGGGGCTCAG  
GAGGTGAAAG AGAGCCCCCT TTTCCGCTCC CTGGACTGC AGATGCTCT CTGCAAGA TACCCTCCC CGCTGATCCC  
CCACAGAGG GAGGTGAACG CGCCGACGC CTCGACATT GGCTCTTCTG ATGAGGAGGA CACAAAGGA ATCAAGTTAC  
TGGACAGTGA TCAGGAGCTC TACCGCAACT TCCCCCTC CATCTCGGAG CGGTGGCAGC AGGAGGTGGC AGAGACTGTC  
TTCGACCA TCAACGCTGA GACAGACCGG CTGGAGGCTC GCAAGAAAGC CAAGAACAAG CAGCTGGGC ATGAGGAAGA  
CTACGCCCTG GGCAAGGACT GCATCATGCA TGGTACATG TCAAGATGG GCAACCCCTT CTGACCCAG TGGCAGCGG  
GGTACTTCTA CTGTTTCCC AACCGCTCG AGTGGCGGG CGAGGGCGAG GCGCCGAGA GCCTGCTGAC CATGGAGGAG  
ATCCAGTCGG TGGAGGAGAC GCAGATCAAG GAGCGCAAGT GCTGCTCT CAAGATCCG GGTGGGAAAC AGTTCATTTT  
GCAGTGCGAT AGCGACCTG AGCTGGTGCA GTGGAAGAAG GAGCTGCGG ACGCTACCG CGAGGCCAG CAGCTGGTGC  
AGCGGTGCC CAAGATGAAG AACAAAGCCG GCTCGCCGT GGTGGAGCTG AGCAAGGTGC CGCTGGTCCA GCGCGGAGT  
GCCAAGCGG TGTACCCG CCACCGCTT CCAGGAAGT ACCTGGAGGA GGTGAGTCTT AGCGGATGAG TAGGAGTTGT  
CCACGAGGA AGGTACACAG AAGGGCTTCC AGGCCAGGA AACAGCAGAG GCACAGAAGT GGAATGGGT GGGTGGTTG  
GTGGGGAAAC TCCAGGTGCA GAGGATGGTA GCGAAACAAA CTGGAGCATT AAGTCCAAG TCCTCAAGA TCTTGACTG  
CAGATTAAG AGTTTGTTC CTAATCTGC TTTGGGAGA GTGTGGTGA TCCTAGAGAC CCTCTAGGT CTCTCTCTC  
AGTAGCCCCA GAAGGCTGG AGAGCTGCTT CTGGTGCCA AGCAGGCACT GACTCCATCA GATCTAGATT TGGGAAAGC  
ATCCTGTGTC AGGGCTGCA TCAGGGCAGT GGCTGCCAT GAGGACCTG AGAAGTAGAC AGATTACGG AGATTCTCAG  
GAGGCCAGAC AGGAGACTAT GTGACAAAT TAGATTAGAG AAGGGGAGAG AATGAAGGAG CAGTTGGGT  
AAAAGAAAC TGAGGCTGAC ATGGGTATAT GGTGGCGAG TGAATCACA CCACTGAGA GGAGAACCCT ACAAGCTCTG  
ACATGCTCTG GTTCCAGGTT CTGTTGGGG TGATCAAGA TGGTAGCTA GAGGTGCACA GAGATGGGG CCTTGCTTTG  
CAAAAGGATG CTGGCTGCTG GCGCACAGCA TGGTAATGAG ATTTGAGCTT TATGTGCCA GGGCTGGGAG GAGGGTCTG  
TCACTTTGAA AGCAAGAGA GGCTCTAGAG AGGGCACTGT TGAGATGAGA ATGCTGCTT GAGACACTG GCTTTCCCA  
CTCTGGGTG CTCTCAGAG GGTGGGTTT CCGTGCCAG GACACTGAA CCTCTGTGC CTTCGGCTG GGAGGTTTT  
TACCGTAAT ACATGTGGA CCATCTGAA GGAACATCTG GATGGGATGG GGTACAGGGA AGGGAGCTGC CAAGAGTGT  
GGCCAGGGAC CTGGTCTAT GAGCTGGTT GGGGGTGGG TTGGGTGCAG GGTACTTGAT CTGAGTGGG CCTTCTGCGG  
CCAGGATTGG TTCTAGAGTA GGAGGGTGG GATCGGGAT GGGGGAAGCC TGTAAGTGC CTGAGTTGT CAGGTCCCAG  
GTCTGGGTG ACCTACTAAG GATTCTGGT CAGTGTGG TCCAGGTTA GACGCTCTAG TCCTGAGTCC GTGTCCACAG  
TTCTGGGTG TGAATCTAG ACAGTATCT GGAGTTGACA GTCCAATCTA GGTCTGAGT CTGACCCAA GTCTAGATT  
CAGGGTCTG GTAGTAGCT AGGGTCAGAA TCAAGGTTG GGTCAAGTAA CAGGATGGGA TCGAGGTCT GGTCCAAAT  
CTGGATCTGG GGACCTGTT GGGGTCTGAG GTGAGTGTG CAGTCTGGT ATGGCGTTG AGACCCAGG CTGTGATCTG  
AGGTCTGTT TAGAGTCTCA GGTGGTGGC CAAGGTTGA GTCTGGGTC CTGTTGGAG TCTGGTGTCA GGTCTGGAC  
TGCGTCAAG GTCAGGAGT CCGGGTTAT AGCCAGGTC TGAGATGAAA GTCCAGATG GTGTTACAG GTCTGAATCT  
GTGCTTGTG GAGGCTCAG GTTCCCTGTG ATCAGTTTGT GTGTCAGGTC TGCGGCCGA TGCGGGAGC TGGATCCAG  
AGATGTGACC CAGGTTGTG GTCAGAGAAT GGTCTCGG TCGTCTCTG GCGGGTCCC TGTCGTGTT CAGGCGGGG  
TCTCCGTCA GCATCAGGG CCGAGGTCAG GGCCAGGTC TGAGCCCGG GTCGAGGTC TGGTTCCGGG TCAGATTCCG  
CGCGGCTCC AGGGGGCGG GTCGCGGCC GGTCTCGGCT CTGCGGGCT CGCTGGGCT GTGCGCGGA GCGGGGGCG

GAGGCGGCGG CGGCTCCGGG GCGCGGGGCC GGGCGGCGGC GGGCGGCGGC CCCCAGTGC AGTCCCGGGG GAGCGGAGC  
GCGAAGCCCG GGGCCGGGCC CGGAGCCGGC GCCATGGGGC GGCGCCGCT GTGAGCGGCG GCGAGCGGAG CCGCGGGCGC  
CGAGCAGGGC CAGGCGGGAG CGTCGGCGCC CGAGGCCGAG CGAGCCGCGG CCGGCGGGG CCGAGCGCCG  
AGCGAGCAGG AGCGGCGGCG GCGGCGGCGG CGGCGGGAGG AGGCAGCGCC GCCGCCAAGA TGGCGGACCT  
GGAGGCGGTG CTGGCCGACG TGAGCTACCT GATGGCCATG GAGAAGAGCA AGGCCACGCC GGCCGCGCGC GCCAGCAAGA  
AGATACTGCT GCCCGAGCCC AGGTGAGGAG AAGCT-3' (FRAG. NO.: ) (SEQ. ID NO:2430)

5'-CCAGGAAGCT ACCTGGAGGA GGTGAGTCTT AGCGGATGAG TAGGAGTTGT CCACGGAGGA AGGTACACAG  
AAGGGCTTCC AGGCCAGGA AACAGCAGAG GCACAGAAGT GAGAATGGGT GGGTGAGTTG GTGGGAAAC TCCAGGTGCA  
GAGGATGGTA GCGAAACAAA CTGGAGCATT AAGGTCCAAG TCCTCCAAGA TCTTGACTTG CAGATTAAGG AGTTTGTTCA  
CCTAATCTGC TTTGGGCAGA GTGTGGTGAG TCCTAGAGAC CCTCTAGGT CTCTCTCTC AGTAGCCCCA GAAGGCCTGG  
AGAGTGCTT CTGGGTGCCA AGCAGGCAGT GACTCCATCA GATCTAGATT TGGGAAAAGC ATCCCTGGTC AGGGCCTGCA  
TCAGGCGAGT GGCTGGCCAT GAGGACCCTG AGAAGTAGAC AGATTACCG AGATTCTCAG GAGGCCAGAC AGGAGACTAT  
GGTGACAAAT TAGATTAGAG AAGGGGAGAG AATGAAGGAG CAGTTGGGGT AAAAGAAAAC TGAGGCTGAC ATGGGTATAT  
GGGTGGCGAG TGACTACCA CCACTGAGA GGAGAACCTC ACAAGCTCTG ACATGCTCTG GTTCCAGGTT CTGTTGGGGC  
TGATCCAAGA TGGTAGCTA GAGGTGCACA GAGATGGGGG CCTTGCTTTG CAAAAGGATG CTGGCTGCTG GCCACAGCA  
TGTAATGAG ATTTGAGCTT TATGTGCCA GGGCTGGGAG GAGGGTCTCTG TCACTTTGAA AGCAAAGAGA GGCTCTAGAG  
AGGGGATGAT TGAGATAGGA ATGCTGCCCT GAGACACCTG GCTTCCCA CTCTGGGTGG CTCTCAGCAG GGTGGGTTTC  
CCCTGCCAGG CAGCACTGAA CCTCTGTGCG CTTCGGCTG GGAGAGTTT TACCGTAACT ACATGTGGAA CCATCCTGAA  
GGAACATCTG GATGGGATGG GTACAGGGA AGGGAGCTGC CAAGAGTGCT GGCCAGGGAC CTGGGTCTAT GAGCTGGTTG  
GGGGTGGGG TTGGGTGCAG GGTACTTGAT CCTGAGTGGG CCTTCTGCGG CCAGGATTGG TTCTAGAGTA GGAGGGGTGG  
GATCGGGGAT GGGGGAAGCC TGTAACGCG CTGCAGTTGT CAGGTCCAG GTTCTGGGTG ACCTACTAAG GATTCTGGGT  
CCAGTGTGGG TCCAGGTTA GACGTCCTAG TCCTGAGTCC GTGTCCACAG TTCTGGGTGT TGAGTCTAGG ACAGTGATCT  
GGAGTTGACA GTCCAATCTA GGTCTGAGTC CTGACCCAA GTCTAGAGTT CAGGGTCATG GTAGTAGCCT AGGGTCAGAA  
TCAAGGTTGG GGTCAAGTAAC CAGGATGGGA TCGAGGTGAT GGTCCAAAT CTGGATCTGG GGACCTGTTG GGGGTCTGAG  
GTGAGTCTG CAGTCTGGGT ATGGCGTTGG AGACCCAGGG CTGTGATCTG AGTCTAGTGT TAGAGTCTCA GGTGGTGGC  
CAAGGTTTGA GTCTGGGGTC CTGTTTGAG TCTGGTGTCA GGTCTGGGAC TGCCTCAAAG GTCAAGGAGT CCGGGGTTAT  
AGCCAGGGTC TGAGATGAAA GTCCAGATG GTGTTACAGAG GTCTGAATCT GTGTCTTGGT GAGCGTCCAG GTTCCCTGTG  
ATCAGTTTG GTGTCAGGGC TGCGGCCGA CTGGGAGGCC TGGGATCCAG AGATGTGACC CGAGGTTGTG GTCAGAGAAT  
GGGTCTCGGG TCGTCTCGT GCCGGGTCCC TGTCGTGTC CAGGCCGGG TCTCCGTCCA GCATCGAGGG CCGAGGTCAC  
GGCCAGGGTC TGAGCCCGCG GTCGCAAGTC TGGTTCGGGG TCAGATTCCG CGCGGCCTCC AGGGGGCGCC GTCGCCGCC  
GGCTCGGCC CTGCGGGGCT CGCTGGCGTT GTGCGCGGCA GCGGGGCGG GAGGCGGCGG CGGCTCCGGG GGCGCGGGCC  
GGGCGGCGG GCGGCGGCG CCCCAGTGC AGTCCCGCG GAGCGGAGC GCGAAGCGG GGGCCGGGCC CCGAGCCGGC  
GCCATGGGG GCGCCGCTG GTGAGCGCG GCGAGCGGAG CCGCGGGCG CGAGCAGGGC CAGGCGGGAG CGTCCGCGCC  
CGAGGCCGAG CGAGCCGCG CCGGGCGCG CCGAGCGCG AGCGAGCAGG AGCGGCGCG GCGGCGGCGG CCGGCGGCGG  
CGGCGGGAGG AGGCAGCGCC GCCGCCAAGA TGGCGGACCT GGAGGCGGTG CTGGCCGACG TGAGTACCT GATGGCCATG  
GAGAAGAGCA AGGCCACGCC GGCCGCGCGC GCCAGCAAGA AGATACTGCT GCCCGAGCCC AGGTGAGGAG AAGCT-3'  
(FRAG. NO.: ) (SEQ. ID NO:2429)

5'-GCCCGCGCG CCAAGATGGC GGACCTGGAG GCGGTGCTGG CCGAGCTGAG CTACCTGATG GCCATGGAGA  
AGAGCAAGGC CACGCCGGCC GCGCGGCCA GCAAGAAGAT ACTGCTGCCC GAGCCAGCA TCCGAGTGT CATGAGAAG  
TACCTGGAGG ACCGGGGCGA GTGACCTTT GAGAAGATCT TTTCCAGAA GCTGGGGTAC CTGCTCTCC GAGACTTCTG  
CCTGAACCAC CTGGAGGAGG CCAGGCCCTT GGTGGAATC TATGAGGAGA TCAAGAACTA CGAAGAGCTG GAGACGGAGG  
AGGAGCGTGT GGCCCGAGC CGGGAGATCT TCGACTATA CATCATAGG GAGCTGCTGG CTGCTCGCA TCCCTTCTCG  
AAGAGTGCCA CTGAGCATGT CCAAGGCCAC CTGGGGAAGA AGCAGGTGCC TCCGATCTC TTCCAGCAT ACATCGAAGA  
GATTTGTCAA AACCTCCGAG GGGACGTGT CCAGAAATTC ATTGAGAGCG ATAAGTTCAC ACGTTTTTGC CAGTGAAGA  
ATGTGGAGCT CAACATCCAC CTGACCATGA ATGACTTCAG CGTGCATCG ATCATTGGGC GCGGGGGCTT TGGCGAGGTC  
TATGGGTGCC GGAAGGCTGA CACAGGCAAG ATGTACGCCA TGAAGTGCT GGACAAAAG CGCATCAAGA TGAAGCAGG  
GGAGACCCTG GCCCTGAACG AGCGCATCAT GCTCTGCTC GTCAGACTG GGGACTGCC ATTCAATTGC TGCATGTCAT  
ACGCGTTCCA CACGCCAGAC AAGCTCAGT TCATCCTGGA CCTCATGAAC GGTGGGGACC TGCACTACCA CCTCTCCAG  
CACGGGGTCT TCTCAGAGG TGACATGCG TCTATGCGG CCGAGATCAT CCTGGGCTG GAGCACATGC ACAACCGCTT  
CGTGGTCTAC GCGACCTGA AGCCAGCAA CATCCTTCT GACGACATG GCCACGTGCG CATCTCGGAG CTGGGCTGG  
CCTGTGACT CTCCAAGAAG AAGCCCATG CCAGCGTGGG CACCCAGGG TACATGGCTC GAGAGTCTCT GCAGAAGGGC  
GTGGCCTACG ACAGCAGTGC CCACTGGTTC TCTCTGGGT GCATGCTCT CAAGTTGCTG CCGGGGCACA GCGCTTCCG  
GCAGCACAAG ACCAAAGACA AGCATGAGAT CGACCGCATG ACGCTGACGA TGGCCGTGGA GCTGCCGAC TCCTTCTCCC  
CTGAACACG CTCCCTGCTG GAGGGGTGCG TGCAGAGGGA TGTAACCGG AGATTGGGT GCCTGGGCGG AGGGGCTCAG  
GAGGTGAAAG AGAGCCCTT TTTCCGCTCC CTGACTGGC AGATGGTCTT CTGCGAGAAG TACCTCCCC CGTGATCCC  
CCCACGAGG GAGGTGAACG CGGCCGACG CTTCGACATT GGCTCCTTG ATGAGGAGGA CACAAAAGGA ATCAAGTTAC  
TGGACAGTGA TCAGGAGCTC TACCGCAAT TCCCCCTCAC CATCTCGGAG CGGTGGCAGC AGGAGGTGGC AGAGACTGTC  
TTCGACACCA TCAACGCTGA GACAGACCG CTGGAGGCTC GCAAGAAAGC CAAGAACAAG CAGTGGGCC ATGAGGAAGA  
CTACGCCCTG GCAAGGACT GCATCATGA TGGTACATG TCCAAGATGG GCAACCCCTT CCTGACCCAG TGGCAGGGC  
GGTACTTCTA CTGTTTCCC AACCGCTCG AGTGGCGAGT CGAGGCGGAG GCCCGCAGA GCTGTGAC CATGGAGGAG  
ATCCAGTCGG TGGAGGAGAC GCAGATCAAG GAGCGCAAGT GCTGTCTCT CAAGATCCG GGTGGGAAAC AGTTATTTT  
GCAGTGGAT AGCGACCTG AGCTGGTGA GTGGAAGAAG GAGTGTGCG ACGCTACCG CGAGGCCAG CAGTGGTGC  
AGCGGTGCC CAAGATGAAG AACAAGCCG GCTCGCCGT GGTGGAGCTG AGCAAGGTGC CGTGGTCCA GCGCGGAGT  
GCCAACGGC TGTACCCG CACCCGCT-3' (FRAG. NO.: ) (SEQ. ID NO:2428)

**CCR-2 CC Chemokine Receptor Nucleic Acids and Antisense Oligonucleotide Fragments**

5'-CTTTGTGAAG AAGGAATTGG CAACACTGAA ACCTCCAGAA CAAAGGCTGT CACTAAGGTC CCGCTGCCTT  
GATGGATTAT AACTTGACC TCAGTGAGC AACAGTGACC GACTACTACT ACCCTGATAT CTCTCAAGC CCCTGTGATG  
CGGAACCTAT TCAGACAAAT GGCAAGTGC TCCTGTCTGT CTTTATTGCT CTCCTGTTG TATTAGTCT TCTGGGAAAC

TGACCTGCTT TTTGTCTTCT CCTTCCCCTT TCAGACCTAC TATCTGCTGG ACCAGTGGGT GTTTGGGACT GTAATGTGCA  
AAGTGGTGTG TGGCTTTTAT TACATTGGCT TCTACAGCAG CATGTTTTTC ATCACCCTCA TGAGTGTGGA CAGGTACCTG  
GCTGTGTGCC ATGCCGTGTA TGCCCTAAAG GTGAGGACGA TCAGGATGGG CACAACGCTG TGCTGGCAG TATGGCTAAC  
CGCCATTATG GCTACCATCC CATTGCTAGT GTTTTACCAA GTGGCCTCTG AAGATGGTGT TCTACAGTGT TATTCAITTT  
ACAATCAACA GACTTTGAAG TGGAAGATCT TCACCAACTT CAAAATGAAC ATTTTAGGCT TGTGTATCCC ATTCACCATC  
TTTATGTTCT GCTACATTAA AATCCTGCAC CAGCTGAAGA GGTGTCAAAA CCACAACAAG ACCAAGGCCA TCAGGTGGT  
GCTCATTGTG GTCATTGCAT CTITACTTTT CTGGGTCCCA TTCAACGTGG TCTTTTCT CACTTCCTG CACAGTATGC  
ACATCTTGA TGGATGTAGC ATAAGCCAAC AGCTGACTTA TGCCACCCAT GTCACAGAAA TCAITTCCTT TACTCACTGC  
TGTGTGAACC CTGTTATCTA TGCTTTTGT GGGGAGAAGT TCAAGAAACA CCTCTCAGAA ATATTTCAGA AAAGTTGCAG  
CCAAATCTTC AACTACCTAG GAAGACAAAT GCCTAGGGAG AGCTGTGAAA AGTCATCATC CTGCCAGCAG CACTCCTCCC  
GTTCTCCAG CGTAGACTAC ATTTTGTGAG GATCAATGAA GACTAAATAT AAAAAACATT TTCTTGAATG GCATGCTAGT  
AGCAGTGAGC AAAGGTGTGG GTGTGAAAGG TTTCCAAAAA AAGTTCAGCA TGAAGGATGC CGTGTGTGTT GTTGCCAACA  
CTTGGAACAC AATGACTGGA GACATAGTTG TGCATGCCG GCACAACATC AAGCCTGTGA TTGTGTTTAT TGATGATGT  
GAACAAGTGG TGGCTTTGAG GGATTCTGTA TGCCAAGTGG AAAAAAAGA TGCTCCGGA ATTCGACAGG TTATCA-3'  
(FRAG. NO.:) (SEQ. ID NO:2462)

**CCR-4 CC Chemokine Receptor Nucleic Acids and Antisense Oligonucleotide Fragments**

5'-TTTCATCTCT CCGGGCTTAT TGCTGGTTT CTCCGAATGC GGGCCTTGTC TGGTTCACGC TGGATCCCCA ACGCCTAGAA  
CAGTGCCTGG CACGCAGTTC GTCTTCTAT AAATATCGGA CTAATGCAT CTCTGTGATG GTAATACCCA CACGGTGTG  
TGAGAATGAA TGAGTGATTC TGTGCAAGTT CCTAGTGATC TGTACAAAA AGTACTGGTC GCTAAATTAC TCTTATAATA  
AAGCATACTT TTAGGATAAT AAAGCACTAT TCGCAATTG GTTACCGCTA TTATGAAAT ACTGAGCAAT ACATATCTAC  
ATCTGATCAG TCTCCAGAT TATGCCAAT CTCACTTCT TCTGAAAGTA TCTCTAAT ATCTGCACCT GACCCATAGT  
ATGCTGTGAA TGTGCAAGTA TAGCTACATC CTCCGAAGGA AGGATCTTTA CTCCTTTTAC CTCCTGAATG GGCTCGCTCT  
GCTGAAAGCG CGGGGGAATG GGCGGTTGGA AGCTTGGCCC TACTTCCAGC ATTGCCGCT ACTGGTTGGG TTAATCCAGC  
AAGTCACTCC CTTCCCTGG GCCTCAGTGT CTCTACTGTA GCATTCCAG GTCTGGAAT CCATCCACTT TAGCAAGGAT  
GGACGCGCCA CAGAGAGACG CGTTCCTAGC CCGCGCTTCC CACCTGTCTT CAGGCGCATC CCGTTCCTT CAACTTAGG  
AAATGCCTCT GGGAGTCTT GTCCGGCTCC GGACTCACTA CCGACCACCC GAAACAGCA GGGTCCCTG GGCTTCCCAA  
GCCGCGCAC TCTCGCCCC GCGCTGCGC CTCTTCTCT CCGCTCTGCC CCTCTCCCC ACCCGCTT CTCCCTCCCC  
GCCCGAGCG CGCATGCGCC GCGCTCGGAG CGTGTTTTA TAAAGTCCG CCGCGGCCA GAACTTCCG TTTGTGGCT  
GCGGCAGCAG GTAGCAAAGT GACGCGGAG CCGTAGTGC TCCAGTAGCC ACCGCATCTG GAGAACCAG GGTTACCATG  
GAGGGGATCA GTGTAAGTCC AGTTTCAACC TGCTTTGTCA TAAATGTACA AACGTTTGA CTTAGAGCGC AGCCCTCTC  
CGAGCGGGCA GAAGCGGCCA GGACATTGGA GGTACCCGTA CTCAAAAAA GGGTACCAG AAGGAGTTT CTGACCATG  
CCTATATAGT GCGGTGGGT GGGGGGGGAG CAGGATTGGA ATCTTTTCT CTGTGAGTC AGGAGAAACG ACTGGAAAGA  
GCGTTCAGT GGCTGCATGT GTCTCCCCCT TGAGTCCCGC CGCGCGCGGC GGCTTGACG CTGTTTGCAA ACCTAAGAAC  
ATCTGTGCA CAAGTGACA GAAGGCGTGC GCGCTGCTC GGGACTCAGA CCACCGGTCT CTCTCTGGG GAAGCGGGGA  
TGTCTTGGAG CGAGTTACAT TGCTGAATT TAGAGCGGA GGGCGCGCTG CTTGGGCTGA CTCCCAAGG GAGATTGCG  
CCCGCTTAA CTTCGGGTT AAGCGCTGG TGAAGTCTT TGACACTGGG TCGTGTGTT TAAACTCTG TGCGGCGGAC  
GGAGCTGTGC CAGTCTCCA GCACAGTAGG CAGAGGGCGG GAGAGGCGGG TGGACCCACC GCGCCGATCC TCTGAGGGGA  
TCGAGTGGT GCAGAGCTA GGAGTTGATC CGCCCGCGC CTTTGGGTT GAGGGGAAA CTTCCCGCC GTCCGAAGCG  
CGCTCTTCC CCACGGCCG GAGTGGTCC TGCAATTGGA GAGTTTGGG TCGTGACAG GTCAGCGGAG TGGTTGACC  
TCCCTTTGA CACCGCGCAG CTGCCAGCC TGAGATTGCT GCTCCGGGA TAGGAGCGG TACGGGTGA GGGGCGGGG  
CGGTAAGAC CGCAGCTGG CTGCCAGGTC GCGCGCGCA AGACTGGCAG GTGCAAGTGG GGAACCGTT TGGCTCTC  
CGAGTCCAGT TGTGATGTTT AACCGTCGGT GGTTCAGCA AACCTTTGA AACCTCTG CTAGGGAGT TTTGTTTCC  
TGCAGCGCG CGCAATTCAA AGACGCTCG GCGGAGCGG CCCAGTCTCT CCCAGCACC CTGTGGGACA GAGCTGGCG  
TGTCGCCCAG CGGAGCCCT GCAGCGTGC TTGCGGGCG TTGGCGTGG TGTAGTGGG AGCCGCGCG GCGCGGGCT  
GGACGACCG GCGCCCGCG TGCCACCGC CTGGAGGCTT CCAGCTGCC ACCTCCGCC GGGTAACTG GATCAGTGG  
GGGTAATGG GAAGCCACCC GGGAGAGTGA GGAATGAAA CTGGGGCGA GGACCAGGG TGACAGCCCC GTTACCTTCT  
CCACCCAGGA AAATGCCCC CTCCCTAACG TCCCAACCG GCAAGTGAT AAACAGAGG ATGGCAAGAG ACCCACAC  
CGGAGGCG CCGCTTGGG GGAGGAGTG CGGTTGTTT ATTTCTGAC ACTCCGCCC AATATACCC AAGCAGGAA  
GGGCTTCTG TTTAAGACCG CATTCTTTT ACCCACTA AGTTGCTTGA AGCCAGAAT GGTGTGTATT TAGGAGGCG  
TGGGAAAATT AAGTTTTTGC GCTTTAGGAG AATGAGTCTT TGCAACGCC CCGCCCTCC CCGTGATCC TCCCTTCTC  
CTCTTCCCT CCTGGGCGA AAACTTCTT AAAAAAGT AATCACTGCC CTCTAGCA GCACCCACCC CACCCCCAC  
GCCGCTGGG AGTGGCTCT TGTGTGTAT TTTTCTTCT CTCCTAAGGA AGGTTTTTT TCTTCCCTCT AGTGGGCGG  
GCAGAGGAGT TAGCCAAGAT GTGACTTTGA AACCTCAGC GTCTCAGTGC CTTTGTGTT TAAACAAAGA ATTTGTAAT  
TGGTTCTACC AAAGAAGGAT ATAATGAAGT CACTATGGA AAAGATGGG AGGAGAGTT TAGGATTCTA CATTAACTT  
CTGTGCTCC TACCCCACTA CTTAGAATT TCTGAAGAA AGCAAGCTG AATTGGTTT TAAATTTGT TAAATTAAT  
TTTTAACTG GGTAAATGCT TGCTGAATTG GAAGTGAATG TCCATTCCTT TGCTCTTT GCAGATATAC ACTACAGATA  
ACTACACCGA GGAATGGG TCAGGGGACT ATGACTCCAT GAAGGAACCC TGTTCCTG AAGAAAATGC TAATTTCAAT  
AAAATCTTCC TGCCACCAT CACTCCATC ATCTTCTTAA CTGGCATTGT GGGCAATGGA TTGGTCATCC TGGTCATGG  
TTACCAGAAG AAATGAGAA GCATGACGGA CAAGTACAGG CTGCACCTGT CAGTGGCGA CCTCTCTT GTCATCACG  
TTCCCTCTG GGCAGTTGAT GCGTGGCAA ACTGTACTT TGGGAACCT CTATGCAAG CAGTCCATGT CATCTACACA  
GTCAACCTCT ACAGCAGTGT CCTATCCTG GCCTTCATCA GTCTGGACCG CTACCTGGCC ATCGTCCAG CCACCAACAG  
TCAGAGGCCA AGGAAGCTGT TGGCTGAAA GGTGGTCTAT GTTGGCGTCT GGATCCCTGC CCTCTGCTG ACTATTCCC  
ACTTATCTT TGCCAACGTC AGTAGGCGAG ATGACAGATA TATCTGTGAC CGCTTCTACC CCAATGACTT GTGGGTGGT  
GTGTTCCAGT TTCAGCACAT CATGGTTGGC CTATCTCTG CTGGTATGT CATCTGTCC TGCTATTGCA TTATCATCTC  
CAAGCTGTCA CACTCCAAGG GCCACAGAA GCGCAAGGCC CTCAAGACCA CAGTCATCT CATCTGGCT TTCTTCCCT  
GTTGGCTGCC TTAATACATT GGGATCAGCA TCGACTCTT CATCTCTCT GAAATCATCA AGCAAGGGTG TGAGTTTGA  
AACACTGTG ACAAGTGGAT TTCCATCACC GAGGCCCTAG CTTTCTTCCA CTGTGTCTG AACCCATCC TCTATGCTT  
CCTGGAGCC AAATTTAAA CCTTGGCCA GCACGCACT ACCTCTGTGA GCAGAGGGT CAGCCTAAG ATCTCTCCA  
AAGGAAAGCG AGGTGGACAT TCATCTGTTT CCACTGAGTC TGAGTCTTCA AGTTTCACT CCAGTAACA CAGATGAAA

AGACTTTTT TTATACGATA AATAACTTTT TTTTAAGTTA CACATTTTC AGATATAAAA GACTGACCAA TATTGTACAG  
TTTTTATTGC TTGTTGGATT TTGTCTTGT GTTCTTTAG TTTTGTGAA GTTTAATTGA CTTATTATA TAAATTTTT  
TTGTTTCATA TTGATGTGTG TCTAGGCAGG ACCTGTGGCC AAGTTCTTAG TTGCTGTATG TCTCGTGGTA GGACTGTAGA  
AAAGGGAAC GAACATTCCA GAGCGTGTAG TGAATCACGT AAAGCTAGAA ATGATCCCCA GCTGTTTATG CATAGATAAT  
CTCTCCATTC CCGTGGAAACG TTTTCTGT TCTTAAGACG TGATTTTGTG GTAGAAGATG GCACTTATAA CCAAAGCCCA  
AAGTGGTATA GAAATGCTGG TTTTTCAGTT TTCAGGAGTG GGTGATTTT AGCACCTACA GTGTACAGTC TTGTATTAAG  
TTGTTAATAA AAGTACATGT TAAACTTACT TAGTGTATG TTCTGATTC GTTGTACATT CTTTGGCTA GTAGAAGACA  
AAAGTAATAC ATTTATGGTA TGCAAAGCAC TATCCTAGGT ATTTCAATGT AATATTTTAC TTACCCTTA TCACAACTCT  
GATAGATTCT GCTTCTGTTA CTAATTACAT TTTATAGAAG AGGAAACGGA GGCACAGAAA GCCTAAGTAA CTGGTTAA  
GGCATGTAGT AAGTATCAAA TCCTGTATTT TAAACCAGGT AACATGACTT AACGAATCTG AAGCCTTCAC CACTTTAAAT  
TCAATGGAA GTTTAGAAAT GGCCAGCCAG CACCTATTTG TATGAAAGGT CATCTTCAG AGGATAAGCA TGTATAAGA  
AGAAAAGGTA TGCAGTCGTG TTTGGATTTT ACTCCACCAT C-3' (FRAG. NO: ) (SEQ. ID NO: 2463)

**CD-34 Nucleic Acids and Antisense Oligonucleotide Fragments**

5'-AGGATGATGG TGATGGGGA CTAATGGGG AAATATGGAA GGTCACAGGA AAAGTTAACA CAAGTTAGCA  
AAAGTTAAC ATAACACAAA AAGGTCTTGC AGGAAAAA AAAGAAAGA AAAGAAAGAA AAAGTCTCCA AGAATGGTTT  
GGACAGCCAA AATGAATACT TATAGTCAG TATACCTGCT CACTCCTGAC GTTCACTCA CACACAGCAC AGGATCTGGT  
GAGGCTATCA TAAATGTGC CACATTGTGG TTAAGTTTA CTGATTAAC GAAATGCTCA CACTTCTAAA CTGAGGTCTT  
TACAGTAGAT TCCTTTTGCA AGATTGTAC TGCTTACAA CTAAAAATA AAGGAAATC ACAAGGAAAG AAAAGTGGGG  
AAAAATCGG AGGAACTTG CCCTGCCCT GGCCACCGGC AAGGCTGCCA CAAAGGGGT AAAAGTTAAG TGAAGTGGG  
GCTGAAGAA GTGGGATGGG GCCTCTCCAG GAAAGCTGAA CGAGGCATCT GGAGCCCGAA CAAACCTCCA CTTTTTTGG  
CCTCGACGGC GGCAACCCAG CCTCCCTCCT AACGCCCTCC GCCTTTGGGA CCAACCAGGG GAGCTCAAGT TAGTAGCAGC  
CAAGGAGAGG CGCTGCCTTG CCAAGACTAA AAAGGGAGGG GAGAAGAGAG GAAAAAGCA AGAATCCCCC ACCCTCTCC  
CGGGCGGAGG GGGCGGGAAG AGCGCTCCT GGCCAAGCCG AGTAGTGTCT TCCACTCGGT GCGTCTCTCT AGGAGCCGCG  
CGGGAAGGAT GCTGGTCCGC AGGGGCGCGC GCGCAGGGCC CAGGATGCCG CGGGGCTGGA CCGCGCTTTG CTGCTGAGT  
TTGCTGC CTTTTTTGG CCTCGACGGC GGCAACCCAG CCTCCCTCCT AACGCCCTCC GCCTTTGGGA CCAACCAGGG  
GAGCTCAAGT TAGTAGCAGC CAAGGAGAGG CGCTGCCTTG CCAAGACTAA AAAGGGAGGG GAGAAGAGAG  
GAAAAAGCA AGAATCCCCC ACCCTCTCC CGGGCGGAGG GGGCGGGAAG AGCGCTCCT GGCCAAGCCG AGTAGTGTCT  
TCCACTCGGT GCGTCTCTCT AGGAGCCGCG CGGGAAGGAT GCTGGTCCG AGGGGCGCGC GCGAGGGCCC AGGATGCCG  
GGGGCTGGAC CGCGCTTTGC TTGCTGAGTT TGCTGCCTTC TGGGTTTATG AGTCTTGACA ACAACGGTAC TGCTACCCCA  
GAGTTACCTA CCCAGGGAAC ATTTTCAAAT GTTCTACAA ATGTATCTA CCAAGAACT ACAACACCTA GTACCTTGG  
AAGTACCAGC CTGACCCCTG TGTCTCAACA TGGCAATGAG GCCACAACA ACATCAGAGA AACGACAGTC AAATTCACAT  
CTACCTCTGT GATAACCTCA GTTTATGGAA ACACAACTC TTCTGTCCAG TCACAGACCT CTGTAATCAG CACAGTGTTC  
ACCACCCAG CCAACGTTT AACTCCAGAG ACAACCTTGA AGCCTAGCCT GTCACCTGGA AATGTTTCAG ACCTTTCAAC  
CACTAGCACT AGCCTTGCA CATCTCCAC TAAACCTAT ACATCATCT CTCCTATCCT AAGTGACATC AAGGCAGAAA  
TCAATGTTT AGGCTCAGA GAAGTGAAT TGACTCAGGG CATCTGCCTG GAGCAAAATA AGACCTCCAG CTGTGCGGAG  
TTTAAGAAGG ACAGGGGAGA GGGCCTGGCC CGAGTGCTGT GTGGGGAGGA GCAGGCTGAT GCTGATGCTG GGGCCAGGT  
ATGCTCCCTG CTCCTTGCCC AGTCTGAGGT GAGGCCTCAG TGTCTACTGC TGGTCTTGGC CAACAGAACA GAAATTTCCA  
GCAAACTCCA ACTTATGAAA AAGCACCAAT CTGACCTGAA AAAGCTGGGG ATCTAGATT TCACTGAGCA AGATGTTGCA  
AGCCACCAGA GCTATTCCCA AAAGACCCTG ATTGCACTGG TCACCTCGGG AGCCTGCTG GCTGTCTTGG GCATCACTGG  
CTATTTCTG ATGAATCGCC GCAGCTGGAG CCCACAGGA GAAAGGCTGG GCGAAGACCC TTATTACAG GAAAACGGTG  
GAGGCCAGGG CTATAGCTCA GGACCTGGGA CCTCCCTGA GGCTCAGGGA AAGGCCAGTG TGAACCGAGG GGCTCAGAAA  
AACGGGACCG GCCAGGCCAC CTCCAGAAAC GGCCATTCAG CAAGACAACA CGTGGTGGCT GATACCGAAT TGTGACTCGG  
CTAGGTGGGG CAAGGCTGGG CAGTGTCGA GAGAGCACCC CTCTCTGCAT CTGACCAGT GCTACCCCA TGCTGGAGGT  
GACATCTCT ACGCCCAACC CTTCCTCACT GCACACACT CAGAGGCTGT TCTTGGGGCC CTACACCTTG AGGAGGGGGC  
AGGTAACTC CTGTCTTTA CACATTGGC TCCCTGGAG CAGACTCTGG TCTTCTTGG GTAAACGTGT GACGGGGGAA  
AGCCAAGTC TGGAGAAGCT CCCAGGAACA ATCGATGGCC TTGCAAGCACT CACACAGGAC CCCCTCCCC TACCCCTCC  
TCTCTGCCG AATACAGGAA CCCCAGGGG AAAGATGAGC TTTTCTAGG TACAATTTT TCCAGGAAG CTTTGATTT  
TACCGTTCT TCCCTGATT TTTTCTCT ACTTTGAGGA AACCAAAGTA ACCTTTTGCA CTGTCTCT TGTAATGATA  
TAGCCAGAAA AACGTGTTG CTTGAACCAC TTCCCTCATC TCTCTCAA GACACTGTGG ACTTGGTCAC CAGCTCCTCC  
CTTGTCTCT AAGTTCCACT GAGCTCCATG TGCCCCCTT ACCATTGCA GAGTCTGCA CAGTTTTCTG GCTGGAGCCT  
AGAACAGGCC TCCCAAGTTT TAGGACAAAC AGCTCAGTT TAGTCTCT GGGGCCACAC AGAACTCTT TTTGGGTCC  
TTTTCTCC TCTGGATCAA AGTAGGACG ACCATGGGAC CAGGTCTTGG AGCTGAGCCT CTCACCTGTA CTCTCCGAA  
AAATCTCTT CCTCTGAGC TGGATCCTAG CTTATCTC TGATCTCCAT GGCTTCTCC TCCCTCTGC GACTCCTGG  
GTTGAGCTGT TGCTCAGTC CCCAACAGA TGCTTTCTG TCTCTGCC CCAACCTG AGCCCTTCC TTGCTCTGCA  
CCCCCATATG GTCATAGCCC AGATCAGCT CTAACCTTA TCACCAGCTG CCTTCTCTG GGTGACCCA GGTCTTGT  
TGCTGTTGAT TTTTTCAG AGGGGTTGAG CAGGATCCT GGTTCATG ACGGTTGGAA ATAGAAATTT CCAGAGAAGA  
GAGTATTGG TAGATATTT TCTGAATAC AAAGTGATGT GTTAAATAC TGCAATTAAG GTGATACTGA AACAC-3'  
(FRAG. NO: ) (SEQ. ID NO: 2466)



GCGTCTCTCT AGGAGCCGCG CGGGAAGGAT GCTGGTCCGC AGGGGCGCGC GCGAGGGCCC AGGATGCCGC GGGGCTGGAC  
CGCGCTTTGC TTGCTGAGTT TGCTGCCTTC TGGGTTTCATG AGTCTTGACA ACAACGGTAC TGCTACCCCA GAGTTACCTA  
CCCAGGGAAC ATTTTCAAAT GTTTCTACAA ATGTATCCTA CCAAGAACT ACAACACCTA GTACCCTTGG AAGTACCAGC  
CTGCACCTGT TGCTCAACA TGGCAATGAG GCCACAACA ACATCACAGA AACGACAGTC AAATTCACAT CTACCTCTGT  
GATAACCTCA GTTTATGGAA ACACAACTC TTCTGTCCAG TCACAGACCT CTGTAATCAG CACAGTGTTC ACCACCCCAAG  
CCAACGTTTC AACTCCAGAG ACAACCTTGA AGCCTAGCCT GTCACCTGGA AATGTTTCAG ACCTTTCAAC CACTAGCACT  
AGCCTTGCAA CATCTCCAC TAAACCTAT ACATCATCTT CTCCTATCCT AAGTGACATC AAGGCAGAAA TCAAATGTTC  
AGGCATCAGA GAAGTGAAT TGAATCAGG CATCTGCCTG GAGCAAAATA AGACCTCCAG CTGTGCGGAG TTTAAGAAGG  
ACAGGGGAGA GGGCCTGGCC CGAGTGCTGT GTGGGGAGGA GCAGGCTGAT GCTGATGCTG GGGCCAGGT ATGCTCCCTG  
CTCCTTGCCC AGTCTGAGGT GAGGCCTCAG TGTCTACTGC TGGTCTTGGC CAACAGAACA GAAATTTCCA GCAAACCTCA  
ACTTATGAAA AAGCACCAT CTGACCTGAA AAAGCTGGGG ATCCTAGATT TCACTGAGCA AGATGTTGCA AGCCACCAGA  
GCTATTCCCA AAAGACCTG ATTGCACTGG TCACCTCGGG AGCCTGCTG GCTGTCTTGG GCATCACTGG CTATTTCTCTG  
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GCCAGGCCAC CTCAGAAAAC GGCCATTGAG CAAGACAACA CGTGGTGGCT GATACCGAAT TGTGACTCGG CTAGGTGGGG  
CAAGGCTGGG CAGTGCCGA GAGAGCACCC CTCTGTGCAT CTGACCAGT GCTACCCCA TGCTGGAGGT GACATCTCTT  
ACGCCCAACC CTTCCTCACT GCACACACCT CAGAGGCTGT TCTTGGGGCC CTACACCTTG AGGAGGGGGC AGGTAACTC  
CTGTCTTTA CACATTCGGC TCCCTGGAGC CAGACTCTGG TCTTCTTGG GTAAACGTGT GACGGGGGAA AGCCAAGGTC  
TGGAGAAGCT CCCAGGAACA ATCGATGGCC TTGCAGCACT CACACAGGAC CCCCTTCCC TACCCCTCC TCTGTCCGC  
AATACAGGAA CCCCAGGGG AAAGATGAGC TTTTCTAGGC TACAATTTTC TCCAGGAAG CTTTGATT TACCCTTTCT  
TCCCTGTATT TTCTTCTCT ACTTTGAGGA AACCAAAGTA ACCTTTTGCA CCTGCTCTCT TGTAATGATA TAGCCAGAAA  
AACGTGTTGC CTGAACCAC TTCCCTCATC TCTCTCAA GACACTGTGG ACTTGGTCAC CAGCTCCTCC CTGTCTCT  
AAGTCCACT GAGCTCCATG TGCCCCCTCT ACCATTGCA GAGTCTGCA CAGTTTCTG GCTGGAGCCT AGAACAGGCC  
TCCCAAGTTT TAGGACAAAC AGCTCAGTTC TAGTCTCTCT GGGGCCACAC AGAACTCTT TTTGGGCTCC TTTTCTCCC  
TCTGGATCAA AGTAGGCAGG ACCATGGGAG CAGGTCTTGG AGCTGAGCCT CTCACCTGTA CTCTCCGAA AAATCCTCTT  
CCTCTGAGGC TGGATCCTAG CCTTATCCTC TGATCTCAT GGCTCTCTCC TCCCTCTGC CGACTCTGG GTTGAGCTGT  
TGCCTCAGTC CCCCACAGA TGCTTTCTG TCTGTGCTC CCTCACCTG AGCCCTTCC TGCTCTGCA CCCCATATG  
GTCATAGCCC AGATCAGCTC TAAACCTTA TCACCAGCTG CCTCTCTGT GGGTGACCA GGTCTTGTG TGCTGTGAT  
TTCTTTCCAG AGGGGTTGAG CAGGGATCCT GGTTCATG ACGGTTGGAA ATAGAAATTT CCAGAGAAGA GAGTATTGGG  
TAGATATTTT TTCTGAATAC AAAGTGATGT GTTAAATAC TGCAATTAAG GTGATACTGA AACAC-3' (FRAG. No.) (SEQ. ID  
NO:2465)

#### Eotaxin Antisense Nucleic Acids and Oligonucleotide Fragments

5'-GCATTTTTC AAGTTTATG ATTTATTTAA CTGTGGAAC AAAATAAAC CAGAAACCAC CACCTCTCAC GCCAAAGCTC  
ACACCTTCAG CCTCCAACAT GAAGGTCTCC GCAGCACTTC TGTTGGTCTG GTCATAGCA GCTGCCTTCA GCCCCAGGG  
GCTCGCTGGG CCAGCTTCTG TCCCAACCAC CTGCTGCTTT AACCTAGGCA ATAGGAAGAT ACCCTTCAG CGACTAGGA  
GCTACAGGAG AATCACCAGT GGCAATGTC CCCAGAAAGC TGTGATCTC AAGACCAAAC TGGCCAAAGGA TATCTGTGCA  
GACCCCAAGA AGAAGTGGT GCAGGATTCC ATGAAGTATC TGGACCAAAA ATCTCCAAC CCAAAGCCAT AAATAATCAC  
CATTTTGAAC ACCAAACCAG AGCCTGAGTG TTGCCTAAT TGTTTTCCCT TCTTACAATG CATTCTGAGG TAACCTCATT  
ATCAGTCAA AGGGCATGGG TTTTATTATA TATATATATA TTTTTTTTT AAAAAAAAC GTATTGCATT TAATTATTG  
AGGCTTTAAA ACTTATCCTC CATGAATATC AGTTATTTT AAACCTGAAA GCTTTGTGCA GATTCTTAC CCCCTGGGAG  
CCCCAATTCG ATCCCTGTG ACGTGTGGGC AATGTTCCCT CTCCTCTC TTCTCCCTG GAATCTGTA AAGGTCCTGG  
CAAAGATGAT CAGTATGAAA ATGTCATTGT TCTTGTGAAC CCAAAGTGTG ACTCATTAAA TGAAGTAAA TGTGTTTAA  
GGAATAC ATGAAGGTCT CCGCAGCACT TCTGTGGCTG CTGCTCATAG CAGCTGCCTT CAGCCCCAG GGGCTCGCTG  
GGCCAGCTTC TGTCCTCAAC ACCTGCTGCT TTAACCTGGC CAATAGGAAG ATACCCCTT AGCGACTAGA GAGCTACAGG  
AGAATCACA GTGGCAAATG TCCCAGAAA GCTGTGATCT TCAAGACCA ACTGGCCAAG GATATCTGTG CCGACCCAA  
GAAGAAGTGG GTGCAGGATT CCATGAAGTA TCTGGACCA AAATCTCAA CTCCTCAAGCC ATAA CCACATATTC  
CCCTCTTTT CCAAGGCAAG ATCCAGATGG ATTAATAAAT GTACCAAGTC CCTCTACTA GCTTGCCTCT CTCTGTCTT  
GCTTGACTTC CTAGGATCTG GAATCTGGTC AGCAATCAGG AACTCCTTCA TCGTGACCC CGCATGGGA AAGGCTTCCC  
TGGAATCTCC CACACTGTCT GCTCCCTATA AAAGGCAGGC AGATGGGCCA GAGGAGCAGA GAGGCTGAGA CCAACCCAGA  
AACCACCACC TCTACGCCA AAGCTCACAC CTTCAGCCTC CAACATGAAG GTCTCCGAG CACTCTGTG GCTGCTGCTC  
ATAGCAGCTG CTTTCAGCCC CCAGGGGCTC GCTGGGCCAG GTAAGCCCC CACTCCTTA CAGGAAAGGT AAGGTAACCA  
CCTCCAGGCT ACTAGGTCAG CAAGAATCTT TACAGACTCA CTGCAAATTC TCCATTGAA AAATAGGGAA ACAGGTTTTG  
TGGGTGGA CAAGAATGCCT CAACGTCAC ATCCAGTCAT TGAAGAGCC AGAAGTAGAA AGCTCCGAG TCTTTTCCCC  
ACATTCAAGA GGGCCGCTGG GTGCATCCTT ACCAGCTAT CCTTCACTG TTTGGGAATG GGAATGGCT CTGTCTTACT  
GTGGGCATGG TGGGCATTTT TGGCAGTGGG AGAAGAGGA AATCTGTTGA TTAGAAGCTC AGTATGTTAA TTAGCTCCA  
GGACAGCTT CAGAGACAGT GGCTAAGAGA AGAACGAGGT CCCAGGGGAT CTCTGAGGT GACTTATTT GACACTCTT  
GGGAAAGTTA TCTAGGAGAT TTGTTCCATA ACTCATTTT CCATACTCTG GTGACAAAT TACTGAGTGT ATCGTCCCA  
CTGAGCCAGT GCATAGCATG GTAACAAACA GTTCTAAAT ATCAATGACT TAACAGAAT AACTAAATTA ACAAAGTTA  
CTTTCTCACT TGTACTAAAT ATCTATAATG TATGGGCTCA GGCTCTGCA TTTTATACTC AGGATTCTAG ACTGATGGAG  
AAGTTGCCAT GTGGGGGAAC ATTGATGGAT ACTGTGATA AGCAGAAGAA AGCTCTCAGG AGTCTGCAAT AGGCAATGCA  
CTGTGGCTCA AAAATGACAC CCATCACTTT GTCTCTTCT TTATTGATCA AAATAATTA ATGCTCCAA CCAAACAAAA  
GTGGCCAAAGA AATGCAAGTC TACCTGTGT CTCAAAACAG AGGATGGAGA ATATTGGTG AAAATTACCA TGACCATCAC  
ATGGCCACGT AGGTCTTTAT AATGACAGAG CTAGCATTTG TCACATTGAC CAAGCTTTGT CCATACACTC TACAGTAATG  
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ATTCTCCCTC CACCTCTCGC AATCCTTGC TTTCTCTAA CTTCCTTAC AAAGTCATGC TTGGAAATGT CTATGTATCA  
TCATGTGGCT CATTTTTTTC TCTGTTTATT TTTTCCCC AAAATTCAGC TTCTGTCCCA ACCACTGCT GCTTAACTC  
GGCCAATAGG AAGATACCCC TTCAGCGACT AGAGAGCTAC AGGAGAATCA CCAGTGCAA ATGTCCCCAG AAAGCTGTGA  
TGTAAGTAAA TAAAGTTCAC CCTCCCCTAG AAAAAAAT AATGTCTAGG GCACAGAGTC AAGAACTGTG GGAGTCATAG  
ACTCTGATAG TTTGACCTCT ATGGTCCAAT TCATTAATTT TCACAAGTGA GTGTTCACTC CCAGCTCCCT GCCTGGGAGA



TTGCTGTAGT CATATCAATT TCTTCAAGTC AAGAGCAAAG ATGGTTTAC TGGGCCTTTA AGAGCAGCAA CTAACCCAAG  
AGTCTCATCC TTCCTCTCT CCGTAGCAAC CCTTTGTCCA GGGGCAGATG GTCCTTAAAT ATTTAGGGTC AAATGGGCAG  
AATTTTCAAA AACAATCCTT CCAATTGCAT CCGATTCTC CCCACAGCTT CAAGACCAAA CTGGCCAAGG ATATCTGTGC  
CGACCCCAAG AAGAAGTGGG TGCAGGATTC CATGAAGTAT CTGGACCAAA AATCTCCAAC TCCAAAGCCA TAAATAATCA  
CCATTTTGA AACCAACCA GAGCCTGAGT GTTGCCTAAT TTGTTTTCCC TTCTTACAAT GCATTCTGAG GTAACCTCAT  
TATCAGTCCA AAGGGCATGG GTTTTATTAT ATATATATAT ATATATTTT TTTTAAAAA AAACGTATTG CATTTAATTT  
ATTGAGGCTT TAAAACTTAT CCTCCATGAA TATCAGTTAT TTTTAAACTG TAAAGCTTTG TGCAGATTCT TTACCCCTG  
GGAGCCCCAA TCGATCCCC TGTCACGTGT GGGCAATGTT CCCCCTCTCC TCTCTCTC CTGGAATCT TGTAAGGTC  
CTGGCAAAGA TGATCAGTAT GAAAATGTCA TTGTTCTTGT GAACCCAAAG TGTGACTCAT TAAATGGAAG TAATGTTGTT  
TTAGGAATAC ATAAAGTATG TGCATATTTT ATTATAGTCA CTAGTTGTAA TTTTTTGTG GGAAATCCAC ACTGAGCTGA  
GGGG-3- (FRAG. NO: ) (SEQ. ID NO:2494)

5'-GCATTTTTC AAGTTTATG ATTTATTTAA CTGTGGAAC AAAAATAAAC CAGAAACCAC CACCTCTCAC GCCAAAGCTC  
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GCTCGCTGGG CCAGCTTCTG TCCCAACCAC CTGCTGCTT AACCTGGCCA ATAGGAAGAT ACCCTTCAG CGACTAGAGA  
GCTACAGGAG AATCACCAGT GGCAATGTG CCCAGAAAGC TGTGATCTC AAGACCAAA TGGCCAAGGA TATCTGTGCC  
GACCCCAAGA AGAAGTGGGT GCAGGATTCC ATGAAGTATC TGGACCAAAA ATCTCCAAC CCAAGCCAT AAATAATCAC  
CATTTTGAAC ACCAAACCAG AGCCTGAGTG TTGCCTAAT TGTTCCTT TCTTACAATG CATTCTGAGG TAACCTCATT  
ATCAGTCCAA AGGGCATGGG TTTTATTATA TATATATATA TTTTTTTTT AAAAAAAAC GTATTGCATT TAATTTATTG  
AGGCTTTAAA ACTTATCTC CATGAATATC AGTTATTTT AAAGTGTAAA GCTTTGTGCA GATTCTTTAC CCCCTGGGAG  
CCCCAATTG ATCCCTGTC ACGTGTGGG AATGTTCCCT CTCTCTCTC TTCTCCCTG GAATCTGTG AAGGTCTGTG  
CAAAGATGAT CAGTATGAAA ATGTCATTGT TCTGTGAAC CCAAAGTGTG ACTCATTTAA TGGAAGTAAA TGTGTTTTA  
GGAATAC-3' (FRAG.NO: ) (SEQ. ID NO:2491)

5'-ATGAAGTCT CCGCAGCACT TCTGTGGCTG CTGCTCATAG CAGTGCCTT CAGCCCCAG GGGCTCGCTG GGCCAGCTTC  
TGTCCCAACC ACCTGCTGCT TTAACCTGGC CAATAGGAAG ATACCCCTTC AGCGACTAGA GAGCTACAGG AGAATCACCA  
GTGGCAAATG TCCCAGAAA GCTGTGATCT TCAAGACCA ACTGGCCAAG GATATCTGTG CCGACCCCA GAAGAAGTGG  
GTGCAAGATT CCATGAAGTA TCTGGACCA AAATCTCCA CTCCAAGCC ATAA-3' (FRAG. NO: ) (SEQ. ID NO:2492)

5'-CCACATATTC CCCTCTTTT CCAAGGCAAG ATCCAGATGG ATTAATAAAT GTACCAAGTC CCTCTACTA GCTTGCCTCT  
CTTCTGTTCT GCTTGAATTC CTAGGATCTG GAATCTGGT AGCAATCAGG AATCCCTTCA TCGTGACCCC CGCATGGGCA  
AAGGCTTCCC TGGAAATCTC CACACTGTCT GCTCCCTATA AAAGGCAGGC AGATGGGCA GAGGAGCAGA GAGGCTGAGA  
CCAACCCAGA AACCAACCAC TCTCAGCCA AAGTCCACAC CTTCAGCTC CAACATGAAG GTCTCCGAG CACTTCTGTG  
GCTGCTGCTC ATAGCAGCTC CTTTCAGCCC CCAGGGGCTC GCTGGGCCAG GTAAGCCCC CAATCCTTA CAGGAAAGGT  
AAGGTAACCA CCTCCAGCT ACTAGGTCAG CAAGAATCTT TACAGTCA CTGCAATTC TCCATTGAA AAATAGGGAA  
ACAGGTTTTG TGGGTGGACA AGAAATGCCT CAACGTCAC ATCCAGTCA TGAAGAGCC TGAAGAGCC AGCTCCGAG  
TCTTTTCCC ACATTCAAGA GGGCCGCTGG GTGCATCCT ACCCAGCTAT CCTTACAGTG TTTGGGAATG GGAATGGCT  
CTGTCTTACT GTGGGCATGG TGGGCATTTT TGGCAGTGGG AGAGAAGGAA AATCTGTTGA TTAGAAGCTC AGTATGTTAA  
TTCGACTCCA GGACAGCTT CAGAGACAGT GGCTAAGAGA AGAAGGAGT CCCAGGGGAT CTCTTGAGGT GACTTATTT  
GACACTCTT GGGAAAGTTA TCTAGGAGAT TTGTTCCATA ACTCATTTT CCATACTCTG GTGACAAAT TACTGAGTGT  
ATCGGTCCA CTGAGCCAGT GCATAGCATG GTAACAAACA GTTCTAAAT ATCAATGACT TAACAGAAAT AACTAAATTA  
ACAAAAGTTA CTTTCTACT TGTACTAAAT ATCTATAATG TATGGGCTCA GGCTTCTGCA TTTTATACTC AGGATTCTAG  
ACTGATGGAG AAGTTGCCAT GTGGGGGAAC ATTGATGGAT ACTGTGATAA AGCAGAAGAA AGCTCTCAGG AGTCTTGCA  
AGGCAATGCA CTGTGGCTCA AAAATGACAC CCATCACTT GTCTCCTTCT TTATTGATCA AAATAATTA ATGCTCCAA  
CCAAACAAA GTGGCCAAGA AATGCAAGTC TACCTGTGT CTCAAACAG AGGATGGAGA ATATTTGGTG AAAATTACCA  
TGACCATCAC ATGGCCAGT AGGTCTTAT AATGACAGT CTAGCATTTG TCACATTGAC CAAGCTTGT CCATACACTC  
TACAGTAATG ATGAGTCTC AGTGCACAGG GGAGGATGCT GAAGACACAG GACAGCATCC TCCAGACACA TAAGACTTCA  
GAGCAGAGGG ATTCTCCCTC CACCTCTCGC AATTCCTTGC TTTCTCTAA CTTCCTTAC AAAGTCATGC TTGGAATGT  
CTATGTATCA TCATGTGGCT CATTTTTTT TCTGTTTATT TTTTTTCCC AAAATTCAGC TTCTGTCCA ACCACCTGCT  
GCTTTAACTT GGCCAATAGG AAGATACCCC TTCAGCGACT AGAGAGCTAC AGGAGAATCA CCAGTGCCA ATGTCCCCAG  
AAAGCTGTGA TGTAAAGTAA TAAAGTTCAC CCTCCCTAG AAAAAAAT AATGTCTAGG GCACAGAGTC AAGAAGTGTG  
GGAGTCATAG ACTCTGATAG TTTGACCTCT ATGTTCCAAT TCATTAATTT TCACAAGTGA GTGTTCACTC CCAGCTCCCT  
GCCTGGGAGA TTGCTGTAGT CATATCAATT TCTTCAAGTC AAGAGCAAAG ATGGTTTAC TGGGCCTTTA AGAGCAGCAA  
CTAACCCAAG AGTCTCATCC TTCCTCTCT CCGTAGCAAC CCTTTGTCCA GGGGCAGATG GTCCTTAAAT ATTTAGGGTC  
AAATGGGCAG AATTTTCAAA AACAATCCTT CCAATTGCAT CCGATTCTC CCCACAGCTT CAAGACCAAA CTGGCCAAGG  
ATATCTGTGC CGACCCCAAG AAGAAGTGGG TGCAGGATTC CATGAAGTAT CTGGACCAAA AATCTCCAAC TCCAAAGCCA  
TAAATAATCA CCATTTTGA AACCAACCA GAGCCTGAGT GTTGCTAAT ATATATTTT TTTTAAAAA AAACGTATTG  
GTAACCTCAT TATCAGTCCA AAGGGCATGG GTTTTATTAT ATATATATAT ATATATTTT TTTTAAAAA AAACGTATTG  
CATTAAATTT ATTGAGGCTT TAAAACTTAT CCTCCATGAA TATCAGTTAT TTTTAAACTG TAAAGCTTTG TGCAGATTCT  
TTACCCCTG GGAGCCCAA TCGATCCCC TGTCACGTGT GGGCAATGTT CCCCCTCTCC TCTCTCTC CTGGAATCT  
TGTAAGGTC CTGGCAAAGA TGATCAGTAT GAAAATGTCA TTGTTCTTGT GAACCCAAAG TGTGACTCAT TAAATGGAAG  
TAATGTTGTT TTAGGAATAC ATAAAGTATG TGCATATTTT ATTATAGTCA CTAGTTGTAA TTTTTTGTG GGAAATCCAC  
ACTGAGCTGA GGGGG-3' (FRAG. NO: ) (SEQ. ID NO:2493)

#### **FK-506 Binding Protein Nucleic Acids and Oligonucleotide Fragments**

5'-GCCAGTGC TGTGTTCCA CGCCGCCGT CGCGCCGCC GCGGCTCAG CGTCCGCCG CGCCATGGGA  
GGCCGGAGCC GAGCCGGGT CGGGCAGCAG CAGGGACCC CCAGAGGCGG GGCCTGTGG ACCGCTATGG GCGTGGAGAT  
CGAGACCATC TCCCCGGAG ACGGAAGGAC ATTCCCAAG AAGGGCCAA CGTGTGTTG GCACTACACA GGAATGCTCC  
AAAATGGGAA GAAGTTTGT TCATCCAGAG ACAGAAACA ACCTTCAAG TTCAGAATTG GCAAACAGGA AGTCATCAA  
GGTTTGAAG AGGGTGCAGC CCAGATGAGC TTGGGGCAGA GGGCGAAGCT GACCTGCACC CCGATGTGG CATATGGAGC  
CAGGGGCCA CCGGTGTCA TCCCTCCAA TGCCACCCCT ATCTTTGACG TGGAGCTGCT CAACTTAGAG TGAAGGCAGG  
ACCAACTCA AGCTGCTCC GCGGCTCC GCGGCTCC

AGTGTTTCATG CGAATTCTTG CTTGAGGAAA CTTGCGTTGC AGATTGAAGC ATTTGAGGTT GTGCATTTTG TGTGATGCAT  
GTAGTAGCCT TTCTGATGA CAGAACACAG ATCTCTGTT CGCACAATCT AACTGCTT ACCTTCACTT AAACCACACA  
CACAAGGTGC TCAGACATGA AATGTACATG GCGTACCGTA CACAGAGGGA CTTGAGCCAG TTACCTTTGC TGTCACTTTC  
TCTCTTATAA ATTCTGTTAG CTGCTCACTT AAACAATGTC CTCTTTGAGA AAATGTAATAA TAAAGGCTCT GTGCTTGACA  
GAATTCGGGC CGCCGCCAGG TCGCTGTTGG TCCACGCCGC CCGTCGCCGC GCCCGCCCGC TCAGCGTCCG CCGCCGCCAT  
GGGAGTGCAG GTGGAAACCA TCTCCCCAGG AGACGGGGCG ACCTTCCCCA AGCGCGGCCA GACCTGCGTG GTGCACTACA  
CCGGGATGCT TGAAGATGGA AAGAAATTTG ATTCCTCCCG GGACAGAAAC AAGCCCTTTA AGTTTATGCT AGGCAAGCAG  
GAGGTGATCC GAGGCTGGGA AGAAGGGGTT GCCCAGATGA GTGTGGGTCA GAGAGCCAAA CTGACTATAT CTCCAGATTA  
TGCTATGTT GCCACTGGGC ACCCAGGCAT CATCCACCA CATGCCACTC TCGTCTTGA TGTGGAGCTT CTAAGCTGG  
AATGACAGGA ATGGCCTCT CCCTAGCTC CCGTCTTCTG GATCTGCCAT GGAGGGATCT GGTGCTCCA GACATGTGCA  
CATGAGTCCA TATGGAGCTT TTCTGATGT TCCACTCCAC TTGTATAGA CATCTGCCCT GACTGAATGT GTTCTGTCAC  
TCAGCTTTC TCCGACACC TCTGTTTCTT CTCTCCCTT CTCTCGTAT GTGTGTTTAC CTAAGCTATA TGCCATAAAC  
CTCAAGTTAT TCATTTTATT TTGTTTCTT TTTGGGGTGA AGATTGAGTT TCAGTCTTTT GGATATAGGT TTCCAATTAA  
GTACATGGTC AAGTATTAAC AGCACAAGTG GTAGGTTAAC ATTAGAATAG GAATTGGTGT TGGGGGGGGG GTTTGCAAGA  
ATATTTTATT TTAATTTTTT GGATGAAATT TTTATCTATT ATATATTAAG CATTCTTGCT GCTGCGCTGC AAAGCCATAG  
CAGATTGAG GCGCTGTTGA GGAAGTGAAT ACTCTCCAAG TTGAGAGATG TCTTTGGGTT AAATTAAG CCCTACCTAA  
AACTGAGGTG GGGATGGGGA GAGCCTTTC CTCCACCATT CCCACCCACC CTCCCTTAA ACCCTCTGCC TTTGAAAGTA  
GATCATGTT ACTGCAATGC TGGACACTAC AGGTATCTGT CCTGGGGCCA GCAGGGACCT CTGAAGCCTT CTTTGTGGCC  
TTTTTTTTT TTCATCTGT GGTTTTTCTA ATGGACTTTC AGGAATTTT TAATCTCATA ACTTTCCAAG CTCCACCATT  
TCCTAAATCT TAAGAACTTT AATTGACAGT TTCAATTGAA GGTGCTGTTT GTAGACTTAA CACCCAGTGA AAGCCAGCC  
ATCATGACAA ATCCTTGAAT GTTCTCTTAA GAAAATGATG CTGGTCATCG CAGCTTCAGC ATCTCTGTT TTTGATGCT  
TGGCTCCCTC TGCTGATCTC AGTTTCTGG CTTTCTCTC CTCAGCCCT TCTCACCCT TTGCTGCTT GTGTAGTGAT  
TTGGTGAGAA ATCGTTGCTG CACCCTTCCC CCAGCACCATT TTATGAGTCT CAAGTTTTAT TATTGCAATA AAAGTGCTTT  
ATGCCGAAT TC GCCCGGCCA TGGGAGTGCA GGTGGAAC ACCCTCCAG GAGACGGGCG CACCTTCCCC  
AAGCGCGGC AGACCTGCGT GGTGCACTAC ACCGGGATGC TTGAAGATGG AAAGAAATTT GATTCTCCC GGGACAGAAA  
CAAGCCCTTT AAGTTTATGC TAGGCAAGCA GGAGGTGATC CGAGGCTGGG AAGAAGGGGT TGCCAGATG AGTGTGGGTC  
AGAGAGCCAA ACTGACTATA TCTCCAGATT ATGCTATGG TGCCACTGGG CACCCAGGCA TCATCCACC ACATGCCACT  
CTCGTCTTCG ATGTGGAGCT TCTAAACTG GAATGACAGG AATGGCCTCC TCCCTTAGCT CCCTGTTCTT GGATCTGCCR  
TGGAGGGATC TGGTGCCTCC AGACATGTGC ACATGARTCC ATATGGAGCT TTTCTGATG TTCCACTCCA CTTGTATAG  
ACATCTGCCC TGACTGAATG TGTCTGTCA CTCAGCTTTG CTTCCGACAC CTCTGTTTC TCTTCCCTT TCTCTCGTA  
TGTGTGTTA CTAAACTAT ATGCCATAAA CCTCAAGTTA TTCA-3' (FRAG. NO.: ) (SEQ. ID NO:2499)

5'-GCCAGGTCG TGTGTGTC CCGCGCCCGT CGCGCCGCC GCGCGTCCAG CGTCCGCCG CGCCATGGGA-3' (FRAG.  
No.: ) (SEQ. ID NO: 2495)

5'-GGCCGGAGCC GAGCCGGGGT CGGGCAGCAG CAGGGACCCC CCAGAGGCGG GGCTGTGGG ACCGCTATGG  
GCGTGAGAT CGAGACCATC TCCCCGGAG ACGGAAGGAC ATTCCCCAAG AAGGGCCAAA CGTGTGTGGT GCACTACACA  
GGAATGCTCC AAAATGGGAA GAAGTTTAT TCATCCAGAG ACAGAAACAA ACCTTTCAAG TTCAGAATTG GCAACAGGA  
AGTCATCAAA GGTTTTGAAG AGGGTGCAGC CCAGATGAGC TTGGGGCAGA GGGCGAAGCT GACCTGCACC CCTGATGTGG  
CATATGGAGC CACGGGCCAC CCGGTGTCA TCCCTCCAA TGCCACCCTC ATCTTTGACG TGGAGCTGCT CACTTAGAG  
TGAAGCAGG AAGGAATCA AGGTGGCTGG AGATGGCTGC TGCTCACCCT CTAGCCTGC TGTGCCACTG GGACGGCTCC  
TGCTTTGGG GCTCTTGATC AGTGTGCTAA CCTCACTGCC CTATGCCATC ATCCATTCTC TGTGCCAAG TTGCTCTGTA  
TGTGTTGCTC AGTGTTCATG CGAATTCTTG CTTGAGGAAA CTTGCGTTGC AGATTGAAGC ATTTGAGGT GTGATTTTG  
TGTGATGCAT GTAGTAGCTT TTCTGATGA CAGAACACAG ATCTCTGTT CGCACAATCT AACTGCTT ACCTTCACTT  
AAACCACACA CACAAGGTGC TCAGACATGA AATGTACATG GCGTACCGTA CACAGAGGGA CTTGAGCCAG TTACCTTTGC  
TGTCATTTT TCTCTTATAA ATTCTGTTAG CTGCTCACTT AAACAATGTC CTCTTTGAGA AAATGTAATAA TAAAGGCTCT  
GTGCTTGACA-3' (FRAG. NO.: ) (SEQ. ID NO:2496)

5'-GAATTCGGGC CGCCGCCAGG TCGCTGTTGG TCCACGCCGC CCGTCGCCGC GCCCGCCCGC TCAGCGTCCG CCGCCGCCAT  
GGGAGTGCAG GTGGAAACCA TCTCCCCAGG AGACGGGGCG ACCTTCCCCA AGCGCGGCCA GACCTGCGTG GTGCACTACA  
CCGGGATGCT TGAAGATGGA AAGAAATTTG ATTCCTCCG GGACAGAAAC AAGCCCTTTA AGTTTATGCT AGGCAAGCAG  
GAGGTGATCC GAGGCTGGGA AGAAGGGGTT GCCCAGATGA GTGTGGGTCA GAGAGCCAAA CTGACTATAT CTCCAGATTA  
TGCTATGTT GCCACTGGG ACCCAGGCAT CATCCACCA CATGCCACTC TCGTCTTGA TGTGGAGCTT CTAAGCTGG  
AATGACAGGA ATGGCCTCT CCCTAGCTC CCGTCTTCTG GATCTGCCAT GGAGGGATCT GGTGCTCCA GACATGTGCA  
CATGAGTCCA TATGGAGCTT TTCTGATGT TCCACTCCAC TTGTATAGA CATCTGCCCT GACTGAATGT GTTCTGTCAC  
TCAGCTTTC TCCGACACC TCTGTTTCTT CTCTCCCTT CTCTCGTAT GTGTGTTTAC CTAAGCTATA TGCCATAAAC  
CTCAAGTTAT TCATTTTATT TTGTTTCTT TTTGGGGTGA AGATTGAGTT TCAGTCTTTT GGATATAGGT TTCCAATTAA  
GTACATGGTC AAGTATTAAC AGCACAAGTG GTAGGTTAAC ATTAGAATAG GAATTGGTGT TGGGGGGGGG GTTTGCAAGA  
ATATTTTATT TTAATTTTTT GGATGAAATT TTTATCTATT ATATATTAAG CATTCTTGCT GCTGCGTGC AAAGCCATAG  
CAGATTGAG GCGCTGTTGA GGAAGTGAAT ACTCTCCAAG TTGAGAGATG TCTTTGGGTT AAATTAAG CCCTACCTAA  
AACTGAGGTG GGGATGGGGA GAGCCTTTC CTCCACCATT CCCACCCACC CTCCCTTAA ACCCTCTGCC TTTGAAAGTA  
GATCATGTT ACTGCAATGC TGGACACTAC AGGTATCTGT CCTGGGGCCA GCAGGGACCT CTGAAGCCTT CTTTGTGGCC  
TTTTTTTTT TTCATCTGT GGTTTTTCTA ATGGACTTTC AGGAATTTT TAATCTCATA ACTTTCCAAG CTCCACCATT  
TCCTAAATCT TAAGAACTTT AATTGACAGT TTCAATTGAA GGTGCTGTTT GTAGACTTAA CACCCAGTGA AAGCCAGCC  
ATCATGACAA ATCCTTGAAT GTTCTCTTAA GAAAATGATG CTGGTCATCG CAGCTTCAGC ATCTCTGTT TTTGATGCT  
TGGCTCCCTC TGCTGATCTC AGTTTCTGG CTTTCTCTC CTCAGCCCT TCTCACCCT TTGCTGCTT GTGTAGTGAT  
TTGGTGAGAA ATCGTTGCTG CACCCTTCCC CCAGCACCATT TTATGAGTCT CAAGTTTTAT TATTGCAATA AAAGTGCTTT  
ATGCCGAAT TC-3' (FRAG. NO.: ) (SEQ. ID NO:2497)

5' GCCCGGCCA TGGGAGTGCA GGTGGAAC ACCCTCCAG GAGACGGGCG CACCTTCCCC AAGCGCGGCC  
AGACCTGCGT GGTGCACTAC ACCGGGATGC TTGAAGATGG AAAGAAATTT GATTCTCCC GGGACAGAAA CAAGCCCTTT  
AAGTTTATGC TAGGCAAGCA GGAGGTGATC CGAGGCTGGG AAGAAGGGGT TGCCAGATG AGTGTGGGTC AGAGAGCCAA  
ACTGACTATA TCTCCAGATT ATGCTATGG TGCCACTGGG CACCCAGGCA TCATCCACC ACATGCCACT CTCGTCTTCG

ATGTGGAGCT TCTAAACTG GAATGACAGG AATGGCCTCC TCCCTAGCT CCCTGTTCTT GGATCTGCCR TGGAGGGATC  
 TGGTGCCTCC AGACATGTGC ACATGARTCC ATATGGAGCT TTTCCTGATG TTCCACTCCA CTTTGTATAG ACATCTGCCC  
 TGACTGAATG TGTTCGTCA CTCAGCTTTG CTTCCGACAC CTCTGTTCC TCTCCCCTT TCTCCTCGTA TGTGTGTTA  
 CCTAACTAT ATGCCATAAA CCTCAAGTTA TTCA-3' (FRAG. NO. )(SEQ. ID NO:2498)

The present agents are also provided as a pharmaceutical composition comprising an anti-sense oligonucleotide as given above in an amount effective to reduce expression of a target mRNA, by passing through a cell membrane and binding specifically with target mRNA in the cell so as to prevent its translation are another aspect of the present invention. Such compositions are provided in a suitable pharmaceutically acceptable carrier, e.g. sterile pyrogen-free saline solution. The agent of the invention may be formulated with a hydrophobic carrier capable of passing through a cell membrane, e.g. in a liposome, with the liposomes carried in a pharmaceutically acceptable aqueous carrier. The oligonucleotides may be coupled to an agent which inactivates mRNA, such as a ribozyme. Such oligonucleotides may be administered to a subject in need of such treatment to inhibit the activation of A<sub>1</sub>, A<sub>2b</sub> and/or A<sub>3</sub> adenosine receptors. The pharmaceutical formulation may also comprise chimeric molecules comprising anti-sense oligonucleotides attached to molecules which are known to be internalized by cells. These oligonucleotide conjugates utilize cellular up-take pathways to increase intracellular concentrations of the oligonucleotide. Examples of molecules used in this manner are macromolecules including transferrin, asialoglycoprotein (bound to oligonucleotides via polylysine) and streptavidin, among others.

The anti-sense compound may be contained in the pharmaceutical formulation within a lipid particle or vesicle, such as a liposome or microcrystal. The particles may be of any suitable structure, such as unilamellar or plurilamellar. The one preferred embodiment, the anti-sense oligonucleotide is comprised within the liposome. Positively charged lipids such as N-[1-(2, 3 -dioleoyloxi) propyl] -N, N, N-trimethylammoniummethylsulfate, or "DOTAP", are particularly preferred for such particles and vesicles. However, others are also suitable. The preparation of such lipid particles is well known. See, e.g., US Patent Nos. 4,880,635 to Janoff et al., 4,906,477 to Kurono et al., 4,911,928 to Wallach, 4,917,951 to Wallach, 4,920,016 to Allen et al., 4,921,757 to Wheatley et al., the relevant sections of all of which are herein incorporated in their entireties by reference. The composition of the invention may be administered by any means which transports the agent to the lung(s). The present agent(s) may be administered to the lungs of a patient by any suitable means, but are preferably administered through the respiratory system as a respirable formulation, more preferably in the form of an aerosol comprising respirable particles which, in turn, comprise the agent for respiration or inhalation by the subject. The respirable particles may be in gaseous, liquid or solid form, and they may, optionally, contain other therapeutic ingredients and formulation components. The particles of the present invention are preferably particles of respirable size, preferably of a size sufficiently small to pass, upon inhalation, through the mouth and larynx and into the bronchi and alveoli of the lungs. In general, particles ranging from about 0.5 to 10 microns in diameter are respirable. However, other sizes may also be suitable. Particles of non-respirable size, of considerably larger diameter, which are included in the respirable formulation tend to deposit in the throat and may be swallowed. Accordingly, it is desirable to minimize the quantity of non-respirable particles in the aerosol. For nasal administration, a particle size in the range of 10-500 μm is preferred to ensure their retention in the nasal cavity. Liquid pharmaceutical compositions of the agent of the invention for producing a respirable formulation, e.g. an aerosol may be prepared by combining the anti-sense oligo with a suitable vehicle or carrier, such as sterile pyrogen-free water and/or other known pharmaceutically or veterinarily acceptable carrier. Other therapeutic compounds may be included as well as other formulation

100, and still more preferably about 50 mg/Kg are typically employed. Higher and lower doses may also be administered as an artisan will see suitable for specific application. These amounts are preferably administered every 24 hrs, although other regimens are also suitable. Depending on the solubility of the particular formulation of active compound administered, a daily dose may be divided among one or several unit dose administrations. Administration of the anti-sense compounds may be carried out therapeutically, i.e. as a rescue treatment, prophylactically, or as a chronic maintenance regimen.

Aerosols of liquid particles comprising the agent may be produced by any suitable means, such as with an insufflator or nebulizer. See, e.g., US Patent No. 4,501,729. Nebulizers are commercially available devices which transform solutions or suspensions of an agent into a therapeutic aerosol mist either by means of acceleration of a compressed gas, typically air or oxygen, e.g. through a narrow venturi orifice or by means of ultrasonic agitation. Suitable formulations for use in insufflators and nebulizers comprise the present agent, the agent of this invention, in an amount of about 0.01 to about 40%, preferably less than 20% w/w in a liquid carrier which is typically water or a dilute aqueous alcoholic solution, preferably made isotonic with body fluids by the addition of, for example, sodium chloride. Other carriers are also suitable. Optional additives include preservatives if the formulation is not prepared sterile, for example, methyl hydroxybenzoate, antioxidants, flavoring agents, volatile oils, buffering agents and surfactants, among others.

The pharmaceutical compositions provided herein comprise nucleic acid(s) comprising the anti-sense oligonucleotide(s) described above and one or more surfactants. Suitable surfactants or surfactant components for enhancing the uptake of the anti-sense oligonucleotides of the invention include synthetic and natural as well as full and truncated forms of surfactant protein A, surfactant protein B, surfactant protein C, surfactant protein D and surfactant Protein E, di-saturated phosphatidylcholine (other than dipalmitoyl), dipalmitoylphosphatidylcholine, phosphatidylcholine, phosphatidylglycerol, phosphatidylinositol, phosphatidylethanolamine, phosphatidylserine, phosphatidic acid, ubiquinones, lysophosphatidylethanolamine, lysophosphatidylcholine, palmitoyl-lysophosphatidylcholine, dehydroepiandrosterone, dolichols, sulfatidic acid, glycerol-3-phosphate, dihydroxyacetone phosphate, glycerol, glycerol-3-phosphocholine, dihydroxyacetone, palmitate, cytidine diphosphate (CDP) diacylglycerol, CDP choline, choline, choline phosphate; as well as natural and artificial lamellar bodies which are the natural carrier vehicles for the components of surfactant, omega-3 fatty acids, polyenic acid, polyenoic acid, lecithin, palmitic acid, non-ionic block copolymers of ethylene or propylene oxides, polyoxypropylene, monomeric and polymeric, polyoxyethylene, monomeric and polymeric, poly (vinyl amine) with dextran and/or alkanoyl side chains, Brij 35, Triton X-100 and synthetic surfactants ALEC, Exosurf, Survan and Atovaquone, among others. These surfactants may be used either as single or part of a multiple component surfactant in a formulation, or as covalently bound additions to the 5' and/or 3' ends of the anti-sense oligonucleotides (oligos).

The composition of the invention may be administered by any means which transports the anti-sense nucleotide and the surfactant composition to the lung. The antisense compounds disclosed herein may be administered to the lungs of a patient by any suitable means, but are preferably administered by inhalation of an aerosol comprised of respirable particles which comprise the anti-sense compound. The respirable particles may be liquid or solid, and they may optionally contain other therapeutic or diagnostic ingredients as well as other typical ingredients for a particular formulation. Examples of other agents are analgesics such as acetaminophen, anilerdine, aspirin, buprenorphine, butabital, butorphanol, Choline Salicylate, Codeine, Dezocine, Diclofenac, Diflunisal, Dihydrocodeine, Elcatonin, Etodolac, Fenoprofen, Hydrocodone, Hydromorphone, Ibuprofen, Ketoprofen, Ketorolac, Levorphanol, Magnesium Salicylate, Meclofenamate, Mefenamic Acid, Meperidine, Methadone, Methotrimeprazine, Morphine, Nalbuphine, Naproxen, Opium, Oxycodone, Oxymorphone, Pentazocine, Phenobarbital, Propoxyphene, Salsalate, Sodium Salicylate, Tramadol and Narcotic analgesics in addition to those listed above. See, Mosby's Physician's GenRx. Anti-anxiety agents are also useful including Alprazolam, Bromazepam, Buspirone, Chlordiazepoxide, Chlormezanone, Clorazepate, Diazepam, Halazepam, Hydroxyzine, Ketasolam, Lorazepam, Meprobamate, Oxazepam and Prazepam, among others. Anti-anxiety agents associated with mental depression, such as Chlordiazepoxide, Amitriptyline, Loxapine, Maprotiline and Perphenazine, among others. Anti-inflammatory agents such as non-rheumatic Aspirin, Choline Salicylate, Diclofenac, Diflunisal, Etodolac, Fenoprofen, Fluctafenine, Flurbiprofen, Ibuprofen, Indomethacin, Ketoprofen, Magnesium Salicylate, Meclofenamate, Mefenamic Acid, Nabumetone, Naproxen, Oxaprozin, Phenylbutazone, Piroxicam, Salsalate, Sodium Salicylate, Sulindac, Tenoxicam, Tiaprofenic Acid, Tolmetin, anti-inflammatories for

ocular treatment such as Diclofenac, Flurbiprofen, Indomethacin, Ketorolac, Rimexolone (generally for post-operative treatment), anti-inflammatories for, non-infectious nasal applications such as Beclomethaxone, Budesonide, Dexamethasone, Flunisolide, Triamcinolone, and the like. Soporifics (anti-insomnia/sleep inducing agents) such as those utilized for treatment of insomnia, including Alprazolam, Bromazepam, Diazepam, Diphenhydramine, Doxylamine, Estazolam, Flurazepam, Halazepam, Ketazolam, Lorazepam, Nitrazepam, Prazepam, Quazepam, Temazepam, Triazolam, Zolpidem and Sopiclone, among others. Sedatives including Diphenhydramine, Hydroxyzine, Methotrimeprazine, Promethazine, Propofol, Melatonin, Trimeprazine, and the like. Sedatives and agents used for treatment of petit mal and tremors, among other conditions, such as Amitriptyline HCl; Chlordiazepoxide, Amobarbital; Secobarbital, Aprobital, Butabarbital, Ethchlorvynol, Glutethimide, L-Tryptophan, Mephobarbital, Methohexital Na, Midazolam HCl, Oxazepam, Pentobarbital Na, Phenobarbital, Secobarbital Na, Thiamylal Na, and many others. Agents used in the treatment of head trauma (Brain Injury/Ischemia), such as Enadoline HCl (e.g. for treatment of severe head injury; orphan status, Warner Lambert), cytoprotective agents, and agents for the treatment of menopause, menopausal symptoms (treatment), e.g. Ergotamine, Belladonna Alkaloids and Phenobarbital, for the treatment of menopausal vasomotor symptoms, e.g. Clonidine, Conjugated Estrogens and Medroxyprogesterone, Estradiol, Estradiol Cypionate, Estradiol Valerate, Estrogens, conjugated Estrogens, esterified Estrone, Estropipate, and Ethinyl Estradiol. Examples of agents for treatment of pre menstrual syndrome (PMS) are Progesterone, Progestin, Gonadotrophic Releasing Hormone, Oral contraceptives, Danazol, Luprolide Acetate, Vitamin B6. Examples of agents for treatment of emotional/psychiatric treatments such as Tricyclic Antidepressants, including Amitriptyline HCl (Elavil), Amitriptyline HCl, Perphenazine (Triavil) and Doxepin HCl (Sinequan). Examples of tranquilizers, antidepressants and anti-anxiety agents are Diazepam (Valium), Lorazepam (Ativan), Alprazolam (Xanax), SSRIs (selective Serotonin reuptake inhibitors), Fluoxetine HCl (Prozac), Sertaline HCl (Zoloft), Paroxetine HCl (Paxil), Fluvoxamine Maleate (Luvox), Venlafaxine HCl (Effexor), Serotonin, Serotonin Agonists (Fenfluramine), and other over the counter (OTC) medications.

The composition of the present invention may be administered into the respiratory system as a formulation including particles of respirable size, e.g. particles of a size sufficiently small to pass through the nose, mouth and larynx upon inhalation and through the bronchi and alveoli of the lungs. In general, respirable particles range from about .5 to 10 microns in size. Particles of non-respirable size which are included in the aerosol tend to deposit in the throat and be swallowed, and the quantity of non-respirable particles in the aerosol is thus minimized. For nasal administration, a particle size in the range of 10-500  $\mu$ m is preferred to ensure retention in the nasal cavity. Aerosols or mists of solid particles comprising the agent of the invention may likewise be produced with any device that generates solid particulate medicament aerosols or mists. Aerosol and mist generators are suitable for administering solid particulate medicaments. These devices produce respirable particles, as explained above, and generate a volume of aerosol or mist containing a predetermined metered dose of a medicament at a rate suitable for human or animal administration. One illustrative type of solid particulate aerosol generator is an insufflator. Suitable formulations for administration by insufflation include finely comminuted powders which may be delivered by means of an insufflator or taken into the nasal cavity in the manner of a snuff. In the insufflator, the powder, e.g. a metered dose of the agent effective to carry out the treatments described herein, is contained in a capsule or a cartridge. These capsules or cartridges are typically made of gelatin or plastic, and may be pierced or opened in situ, and the powder delivered by air drawn through the device upon inhalation or by means of a manually-operated pump. The powder employed in the insufflator may consist either solely of the agent or of a powder blend comprising the agent, a suitable powder diluent, such as lactose, and an optional surfactant as well as other agents. The agent typically comprises from 0.01 to 100 w/w of the formulation. A second type of illustrative aerosol generator comprises a metered dose inhaler. Metered dose inhalers are pressurized aerosol dispensers, typically comprising a suspension or solution formulation of the active ingredient in a liquified propellant. During use these devices discharge the formulation through a valve adapted to deliver a metered volume, typically about 10 to 150  $\mu$ l, although other volumes are also suitable, to produce a fine particle spray containing the active ingredient. Suitable propellants include solvents such as certain chlorofluorocarbon compounds, for example, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, and/or mixtures thereof. The formulation may additionally

30 to 150 liters per minute, and most preferably about 60 liters per minute. Aerosols containing greater amounts of medicament may be administered more rapidly.

The following examples are provided to illustrate the present invention, and should not be construed as limiting thereon. In these examples,  $\mu$ M means micromolar, ml means milliliters,  $\mu$ M means micrometers, mm means millimeters, cm means centimeters, EC means degrees Celsius,  $\mu$ g means micrograms, mg means milligrams, g means grams, kg means kilograms, M means molar, and h means hours.

### EXAMPLES

#### Example 1: Design and Synthesis of Anti-sense Oligonucleotides

The design of anti-sense oligonucleotides against the  $A_1$  and  $A_2$  adenosine receptors may require the solution of the complex secondary structure of the target  $A_1$  receptor mRNA and the target  $A_2$  receptor mRNA. After generating this structure, anti-sense nucleotides are designed which target regions of mRNA which might be construed to confer functional activity or stability to the mRNA and which optimally may overlap the initiation codon. Other target sites are readily usable. As a demonstration of specificity of the anti-sense effect, other oligonucleotides not totally complementary to the target mRNA, but containing identical nucleotide compositions on a w/w basis, are included as controls in anti-sense experiments. The mRNA secondary structure of the adenosine  $A_1$  receptor was analyzed and used as described above to design a phosphorothioate anti-sense oligonucleotide. The anti-sense oligonucleotide which was synthesized was designated HAdA<sub>1</sub>AS and had the following sequence: 5'-GAT GGA GGG CGG CAT GGC GGG-3' (SEQ ID NO:1). As a control, a mismatched phosphorothioate anti-sense nucleotide designated HAdA<sub>1</sub>MM1 was synthesized with the following sequence: 5'-GTA GCA GGC GGG GAT GGG GGC-3' (SEQ ID NO:2). Each oligonucleotide had identical base content and general sequence structure. Homology searches in GENBANK (release 85.0) and EMBL (release 40.0) indicated that the anti-sense oligonucleotide was specific for the human and rabbit adenosine  $A_1$  receptor genes, and that the mismatched control was not a candidate for hybridization with any known gene sequence.

The secondary structure of the adenosine  $A_1$  receptor mRNA was similarly analyzed and used as described above to design two phosphorothioate anti-sense oligonucleotides. The first anti-sense oligonucleotide (HAdA<sub>3</sub>AS1) synthesized had the following sequence: 5'-GTT GTT GGG CAT CTT GCC-3' (SEQ ID NO:3). As a control, a mismatched phosphorothioate anti-sense oligonucleotide (HAdA<sub>3</sub>MM1) was synthesized, having the following sequence: 5'-GTA CTT GCG GAT CTA GGC-3' (SEQ ID NO:4). A second phosphorothioate anti-sense oligonucleotide (HAdA<sub>3</sub>AS2) was also designed and synthesized, having the following sequence: 5'-GTG GGC CTA GCT CTC GCC-3' (SEQ ID NO:5). Its control oligonucleotide (HAdA<sub>3</sub>MM2) had the sequence: 5'-GTC GGG GTA CCT GTC GGC-3' (SEQ ID NO:6). Phosphorothioate oligonucleotides were synthesized on an Applied Biosystems Model 396 Oligonucleotide Synthesizer, and purified using NENSORB chromatography (DuPont, MD).

#### Example 2: In Vivo Testing of Adenosine $A_1$ Receptor Anti-sense Oligos

The anti-sense oligonucleotide against the human  $A_1$  receptor (SEQ ID NO:1) described above, was tested for efficacy in an in vitro model utilizing lung adenocarcinoma cells HTB-54. HTB-54 lung adenocarcinoma cells were demonstrated to express the  $A_1$  adenosine receptor using standard northern blotting procedures and receptor probes designed and synthesized in the laboratory. HTB-54 human lung adenocarcinoma cells (106/100 mm tissue culture dish) were exposed to 5.0  $\mu$ M HAdA<sub>1</sub>AS or HAdA<sub>1</sub>MM1 for 24 hours, with a fresh change of media and oligonucleotides after 12 hours of incubation. Following 24 hour exposure to the oligonucleotides, cells were harvested and their RNA extracted by standard procedures. A 21-mer probe corresponding to the region of mRNA targeted by the anti-sense (and therefore having the same sequence as the anti-sense, but not phosphorothioated) was synthesized and used to probe northern blots of RNA prepared from HAdA<sub>1</sub>AS-treated, HAdA<sub>1</sub>MM1-treated and non-treated HTB-54 cells. These blots showed clearly that HAdA<sub>1</sub>AS but not HAdA<sub>1</sub>MM1 effectively reduced human adenosine receptor mRNA by >50%. This result showed that HAdA<sub>1</sub>AS is a good candidate for an anti-asthma drug since it depletes intracellular mRNA for the adenosine  $A_1$  receptor, which is involved in asthma.

#### Example 3: In Vivo Efficacy of Adenosine $A_1$ Receptor Anti-sense Oligos

A fortuitous homology between the rabbit and human DNA sequences within the adenosine  $A_1$  gene overlapping the initiation codon permitted the use of the phosphorothioate anti-sense oligonucleotides initially designed for use against the human adenosine  $A_1$  receptor in a rabbit model. Neonatal New Zealand white Pasteurella-free rabbits were immunized intraperitoneally within 24 hours of birth with 312 antigen units/ml house dustmite (*D. farinae*) extract (Berkeley Biologicals, Berkeley, CA), mixed with 10% kaolin. Immunizations were



repeated weekly for the first month and then biweekly for the next 2 months. At 3-4 months of age, eight sensitized rabbits were anesthetized and relaxed with a mixture of ketamine hydrochloride (44 mg/kg) and acepromazine maleate (0.4 mg/kg) administered intramuscularly. The rabbits were then laid supine in a comfortable position on a small molded, padded animal board and intubated with a 4.0-mm intratracheal tube (Mallinkrodt, Inc., Glens Falls, NY). A polyethylene catheter of external diameter 2.4 mm with an attached latex balloon was passed into the esophagus and maintained at the same distance (approximately 16 cm) from the mouth throughout the experiments. The intratracheal tube was attached to a heated Fleisch pneumotachograph (size 00; DOM Medical, Richmond, VA), and flow was measured using a Validyne differential pressure transducer (Model DP-45161927; Validyne Engineering Corp., Northridge, CA) driven by a Gould carrier amplifier (Model 11-4113; Gould Electronic, Cleveland, OH). The esophageal balloon was attached to one side of the differential pressure transducer, and the outflow of the intratracheal tube was connected to the opposite side of the pressure transducer to allow recording of transpulmonary pressure. Flow was integrated to give a continuous tidal volume, and measurements of total lung resistance (RL) and dynamic compliance (C<sub>dyn</sub>) were calculated at isovolumetric and flow zero points, respectively, using an automated respiratory analyzer (Model 6; Buxco, Sharon, CT). Animals were randomized and on Day 1 pretreatment values for PC<sub>50</sub> were obtained for aerosolized adenosine. Anti-sense (HAdA1AS) and mismatched control (HAdA1MM) oligonucleotides were dissolved in sterile physiological saline at a concentration of 5000 µg (5 mg) per 1.0 ml. Animals were subsequently administered the aerosolized anti-sense or mismatch oligonucleotide via the intratracheal tube (approximately 5000 µg in a volume of 1.0 ml), twice daily for two days. Aerosols of either saline, adenosine, or anti-sense or mismatch oligonucleotides were generated by an ultrasonic nebulizer (DeVilbiss, Somerset, PA), producing aerosol droplets 80% of which were smaller than 5 µm in diameter. In the first arm of the experiment, four randomly selected allergic rabbits were administered anti-sense oligonucleotide and four the mismatched control oligonucleotide. On the morning of the third day, PC<sub>50</sub> values (the concentration of aerosolized adenosine in mg/ml required to reduce the dynamic compliance of the bronchial airway 50% from the baseline value) were obtained and compared to PC<sub>50</sub> values obtained for these animals prior to exposure to oligonucleotide. Following a 1 week interval, animals were crossed over, with those previously administered mismatch control oligonucleotide now administered anti-sense oligonucleotide, and those previously treated with anti-sense oligonucleotide now administered mismatch control oligonucleotide. Treatment methods and measurements were identical to those employed in the first arm of the experiment. It should be noted that in six of the eight animals treated with anti-sense oligonucleotide, adenosine-mediated bronchoconstriction could not be obtained up to the limit of solubility of adenosine, 20 mg/ml. For the purpose of calculation, PC<sub>50</sub> values for these animals were set at 20 mg/ml. The values given therefore represent a minimum figure for anti-sense effectiveness. Actual effectiveness was higher. The results of this experiment are illustrated in Table 3 below.

**Table 3:** Effect of Adenosine A<sub>1</sub> Receptor Anti-sense Oligo upon PC<sub>50</sub> Values in Asthmatic Rabbits

Mismatch Control		A <sub>1</sub> Receptor Anti-sense Oligo	
Pre Oligonucleotide	Post Oligonucleotide	Pre Oligonucleotide	Post Oligonucleotide
3.56 ± 1.02	5.16 ± 1.03	2.36 ± 0.68	>19.5 ± 0.34**

The results are presented as the mean (n=8) ± SEM.

The significance was determined by repeated-measures analysis of variance (ANOVA), and Tukey's protected test.

\*\*Significantly different from all other groups, p<0.01.

In both arms of the experiment, animals receiving the anti-sense oligonucleotide showed an order of magnitude increase in the dose of aerosolized adenosine required to reduce dynamic compliance of the lung by 50%. No effect of the mismatched control oligonucleotide upon PC<sub>50</sub> values was observed. No toxicity was observed in any animal receiving either anti-sense or control inhaled oligonucleotide. These results show clearly that the lung has exceptional potential as a target for anti-sense oligonucleotide-based therapeutic intervention in lung disease. They further show, in a model system which closely resembles human asthma, that downregulation of the adenosine A<sub>1</sub> receptor largely eliminates adenosine-mediated bronchoconstriction in asthmatic airways. Bronchial hyperresponsiveness in the allergic rabbit model of human asthma is an excellent endpoint for anti-sense intervention since the tissues involved in this response lie near to the point of contact with aerosolized oligonucleotides, and the model closely simulates an important human disease.

At the conclusion of the cross-over experiment of Example 3 above, airway smooth muscle from all rabbits was quantitatively analyzed for adenosine  $A_1$  receptor number. As a control for the specificity of the anti-sense oligonucleotide, adenosine  $A_2$  receptors, which should not have been affected, were also quantified. Airway smooth muscle tissue was dissected from each rabbit and a membrane fraction prepared according to the method of Kleinstein et al. (Kleinstein, J. and Glossmann, H., Naunyn-Schmiedeberg's Arch. Pharmacol. 305: 191-200 (1978)), the relevant portion of which is hereby incorporated in its entirety by reference, with slight modifications. Crude plasma membrane preparations were stored at 70EC until the time of assay. Protein content was determined by the method of Bradford (M. Bradford, Anal. Biochem. 72, 240-254 (1976), the relevant portion of which is hereby incorporated in its entirety by reference). Frozen plasma membranes were thawed at room temperature and were incubated with 0.2 U/ml adenosine deaminase for 30 minutes at 37EC to remove endogenous adenosine. The binding of [ $^3$ H] DPCPX ( $A_1$  receptor-specific) or [ $^3$ H] CGS-21680 ( $A_2$  receptor-specific) was measured as previously described by Ali et al. (Ali, S. et al., J. Pharmacol. Exp. Ther. 268, Am. J. Physiol. 266, L271-277 (1994), the relevant portion of which is hereby incorporated in its entirety by reference). The animals treated with adenosine  $A_1$  anti-sense oligonucleotide in the cross-over experiment had a nearly 75% decrease in  $A_1$  receptor number compared to controls, as assayed by specific binding of the  $A_1$ -specific antagonist DPCPX. There was no change in adenosine  $A_2$  receptor number, as assayed by specific binding of the  $A_2$  receptor-specific agonist 2-[p-(2-carboxyethyl)-phenethylamino]-5'- (N-ethylcarboxamido) adenosine (CGS-21680). This is illustrated in Table 4 below.

**Table 4: Specificity of Action of Adenosine  $A_1$  Receptor Anti-sense Oligonucleotide**

	Mismatch Control Oligonucleotide	$A_1$ Anti-sense Oligonucleotide
$A_1$ -Specific Binding	1105 $\pm$ 48**	293 $\pm$ 18
$A_2$ -Specific Binding	302 $\pm$ 22	442 $\pm$ 171

The results are presented as the mean (n = 8)  $\pm$  SEM.

The significance was determined by repeated-measures analysis of variance (ANOVA), and Tukey's protected test.

\*\*Significantly different from mismatch control, p<0.01.

The above results illustrate the effectiveness of anti-sense oligonucleotides in treating airway disease. Since the anti-sense oligos described above eliminate the receptor systems responsible for adenosine-mediated bronchoconstriction, it may be less imperative to eliminate adenosine from them. However, it would be preferable to eliminate adenosine from even these oligonucleotides to reduce the dose needed to attain a similar effect. Described above are other anti-sense oligonucleotides targeting mRNA of proteins involved in inflammation. Adenosine has been eliminated from their nucleotide content to prevent its liberation during degradation.

#### **Example 5: Anti-sense Oligos directed to other Target Nucleic Acids**

This work was conducted to demonstrate that the present invention is broadly applicable to anti-sense oligonucleotides ("oligos") specific to nucleic acid targets broadly. The following experimental studies were conducted to show that the method of the invention is broadly suitable for use with anti-sense oligos designed as taught by this application and targeted to any and all adenosine receptor mRNAs. For this purpose, various anti-sense oligos were prepared to adenosine receptor mRNAs exemplified by the adenosine  $A_1$ ,  $A_{2b}$  and  $A_3$  receptor mRNAs. Anti-sense Oligo I was disclosed above (SEQ. ID NO:1). Five additional anti-sense phosphorothioate oligos were designed and synthesized as indicated above.

- 1- Oligo II (SEQ. ID NO: 7) also targeted to the adenosine  $A_1$  receptor, but to a different region than Oligo I.
- 2- Oligo V (SEQ. ID NO: 10) targeted to the adenosine  $A_{2b}$  receptor.
- 3- Oligos III (SEQ. ID NO: 8) and IV (SEQ. ID NO: 9) targeted to different regions of the adenosine  $A_3$  receptor.
- 4- Oligo I-PD (SEQ. ID NO: 1681) (a phosphodiester oligo of the same sequence as Oligo I).

These anti-sense oligos were designed for therapy on a selected species as described above and are generally specific for that species, unless the segment of the target mRNA of other species happens to contain a similar sequence. All anti-sense oligos were prepared as described below, and tested in vivo in a rabbit model for bronchoconstriction, inflammation and allergy, which have breathing difficulties and impeded lung airways, as is the case in ailments such as asthma, as described in the above-identified application.

#### **Example 6: Design & Sequences of other Anti-sense Oligos**

Six oligos and their effects in a rabbit model were studied and the results of these studies are reported and discussed below. Five of these oligos were selected for this study to complement the data on Oligo I (SEQ ID NO: 1) provided in Examples 1 to 4 above. This oligo is anti-sense to one region of the adenosine A<sub>1</sub> receptor mRNA. The oligos tested are identified as anti-sense Oligos I (SEQ ID NO: 1) and II (SEQ. ID No: 7) targeted to a different region of the adenosine A<sub>1</sub> receptor mRNA, Oligo V (SEQ. ID No:8) targeted to the adenosine A<sub>2b</sub> receptor mRNA, and anti-sense Oligos III and IV (SEQ. ID NOS: 9 and 10) targeted to two different regions of the adenosine A<sub>1</sub> receptor mRNA. The sixth oligo (Oligo I-PD) is a phosphodiester version of Oligo I (SEQ. ID NO:1). The design and synthesis of these anti-sense oligos was performed in accordance with Example 1 above.

(I) **Anti-sense Oligo I:** The anti-sense oligonucleotide I referred to in Examples 1 to 4 above is targeted to the human A<sub>1</sub> adenosine receptor mRNA (EPI 2010). Anti-sense oligo I is 21 nucleotide long, overlaps the initiation codon, and has the following sequence: 5'-GAT GGA GGG CGG CAT GGC GGG-3' (SEQ. ID No 1). The oligo I was previously shown to abrogate the adenosine-induced bronchoconstriction in allergic rabbits, and to reduce allergen-induced airway obstruction and bronchial hyperresponsiveness (BHR), as discussed above and shown by Nyce, J. W. & Metzger, W. J., *Nature*, 385:721 (1977), the relevant portions of which reference are incorporated in their entirety herein by reference.

(II) **Anti-sense Oligo II:** A phosphorothioate anti-sense oligo (SEQ. ID NO:7) was designed in accordance with the invention to target the rabbit adenosine A<sub>1</sub> receptor mRNA region +936 to +956 relative to the initiation codon (start site). The anti-sense oligo II is 21 nucleotide long, and has the following sequence: 5'-CTC GTC GCC GTC GCC GGC GGG-3' (SEQ. ID NO:7).

(III) **Anti-sense Oligo III:** A phosphorothioate anti-sense oligo other than that provided in Example 1 above (SEQ. ID NO:8) was designed in accordance with the invention to target the anti-sense A<sub>1</sub> receptor mRNA region +3 to +22 relative to the initiation codon start site. The anti-sense oligo III is 20 nucleotide long, and has the following sequence: 5'-GGG TGG TGC TAT TGT CGG GC-3' (SEQ. ID NO:8).

(IV) **Anti-sense Oligo IV:** Yet another phosphorothioate anti-sense oligo (SEQ. ID NO:9) was designed in accordance with the invention to target the adenosine A<sub>1</sub> receptor mRNA region +386 to +401 relative to the initiation codon (start site). The anti-sense oligo IV is 15 nucleotide long, and has the following sequence: 5'-GGC CCA GGG CCA GCC-3' (SEQ. ID NO:9).

(V) **Anti-sense Oligo V:** A phosphorothioate anti-sense oligo (SEQ. ID NO:10) was designed in accordance with the invention to target the adenosine A<sub>2b</sub> receptor mRNA region -21 to -1 relative to the initiation codon (start site). The anti-sense oligonucleotide V is 21 nucleotide long, and has the following sequence: 5'-GGC CGG GCC AGC CGG GCC CGG-3' (SEQ. ID NO:10).

(VI) **A<sub>1</sub> Mismatch Oligos:** Two different mismatched oligonucleotides having the following sequences were used as controls for anti-sense oligo I (SEQ. ID NO: 1) described in Example 5 above.

A<sub>1</sub>MM2 5'-GTA GGT GGC GGG CAA GGC GGG-3' (SEQ. ID NO:1682)

A<sub>1</sub>MM3 5'-GAT GGA GGC GGG CAT GGC GGG-3' (SEQ. ID NO:1683)

Anti-sense oligo I and the two mismatch anti-sense oligos had identical base content and general sequence structure. Homology searches in GENBANK (release 85.0) and EMBL (release 40.0) indicated that the anti-sense oligo I was specific, not only for the human, but also for the rabbit, adenosine A<sub>1</sub> receptor genes, and that the mismatched controls were not candidates for hybridization with any known human or animal gene sequence.

(VII) **Anti-sense Oligo A<sub>1</sub>-PD (Oligo VI):** A phosphodiester anti-sense oligo (Oligo VI; SEQ. ID NO:1681) having the same nucleotide sequence as Oligo I was designed as disclosed in the above-identified application. Anti-sense oligo I-PD is 21 nucleotide long, overlaps the initiation codon, and has the following sequence:

5'-GAT GGA GGG CGG CAT GGC GGG-3' (SEQ. ID NO:1681)

(VIII) **Controls:** Each rabbit was administered 5.0 ml aerosolized sterile saline following the same schedule as for the anti-sense oligos in (II), (III), and (IV) above.

#### **Example 7: Synthesis of Anti-sense Oligos**

Phosphorothioate anti-sense oligos having the sequences described in (a) above, were synthesized on an Applied Biosystems Model 396 Oligonucleotide Synthesizer, and purified using NENSORB chromatography (DuPont, DE). TETD (tetraethylthiuram disulfide) was used as the sulfurizing agent during the synthesis. Anti-sense oligonucleotide II (SEQ. ID NO:7), anti-sense oligonucleotide III (SEQ. ID NO: 8) and anti-sense oligonucleotide IV (SEQ. ID NO: 9) were each synthesized and purified in this manner.

**Example 8: Preparation of Allergic Rabbits**

Neonatal New Zealand white Pasturella-free rabbits were immunized intraperitoneally within 24 hours of birth with 0.5 ml of 312 antigen units/ml house dust mite (*D. farinae*) extract (Berkeley Biologicals, Berkeley, CA) mixed with 10% kaolin as previously described (Metzger, W. J., in Late Phase Allergic Reactions, Dorsch, W., Ed., CRC Handbook, pp. 347-362, CRC Press, Boca Raton (1990); Ali, S., Metzger, W. J. and Mustafa, S. J., Am. J. Resp. Crit. Care Med. 149: 908 (1994)), the relevant portions of which are incorporated in their entirety here by reference. Immunizations were repeated weekly for the first month and then biweekly until the age of 4 months. These rabbits preferentially produce allergen-specific IgE antibody, typically respond to aeroallergen challenge with both an early and late-phase asthmatic response, and show bronchial hyperresponsiveness (BHR). Monthly intraperitoneal administration of allergen (312 units dust mite allergen, as above) continues to stimulate and maintain allergen-specific IgE antibody and BHR. At 4 months of age, sensitized rabbits were prepared for aerosol administration as described by Ali et al. (Ali, S., Metzger, W. J. and Mustafa, S. J., Am. J. Resp. Crit. Care Med. 149 (1994)), the relevant section being incorporated in its entirety here by reference.

### **DOSE-RESPONSE STUDIES**

#### **Example 9: Experimental Setup**

Aerosols of either adenosine (0-20 mg/ml), or anti-sense or one of two mismatch oligonucleotides (5 mg/ml) were separately prepared with an ultrasonic nebulizer (Model 646, DeVilbiss, Somerset, PA), which produced aerosol droplets, 80% of which were smaller than 5 µm in diameter. Equal volumes of the aerosols were administered directly to the lungs via an intratracheal tube. The animals were randomized, and administered aerosolized adenosine. Day 1 pre-treatment values for sensitivity to adenosine were calculated as the dose of adenosine causing a 50% loss of compliance (PC<sub>50</sub>, Adenosine). The animals were then administered either the aerosolized anti-sense or one of the mismatch anti-sense oligos via the intratracheal tube (5 mg/1.0 ml), for 2 minutes, twice daily for 2 days (total dose, 20 mg). Post-treatment PC<sub>50</sub> values were recorded (post-treatment challenge) on the morning of the third day. The results of these studies are provided in Example 21 below.

#### **Example 10: Crossover Experiments**

For some experiments utilizing anti-sense oligo I (SEQ ID NO: 1) and a corresponding mismatch control oligonucleotide A1MM2, following a 2 week interval, the animals were crossed over, with those previously administered the mismatch control A1MM2, now receiving the anti-sense oligo I, and those previously treated with the anti-sense oligo I, now receiving the mismatch control A1MM2 oligo. The number of animals per group was as follows. For mismatch A1MM2 (Control 1), n=7, since one animal was lost in the second control arm of the experiment due to technical difficulties, for mismatch A1MM3 n=4 (Control 2) and for A1AS anti-sense oligo I, n=8. The A1MM3 oligo-treated animals were analyzed separately and were not part of the cross-over experiment. The treatment methods and measurements employed following the cross-over were identical to those employed in the first arm of the experiment. In 6 of the 8 animals treated with the anti-sense oligo I (SEQ. ID NO: 1), no PC<sub>50</sub> value could be obtained for adenosine doses of up to 20 mg/ml, which is the limit of solubility of adenosine. Accordingly, the PC<sub>50</sub> values for these animals were assumed to be 20 mg/ml for calculation purposes. The values given, therefore, represent a minimum figure for the effectiveness of the anti-sense oligonucleotides of the invention. Other groups of allergic rabbits (n=4 for each group) were administered 0.5 or 0.05 mg doses of the anti-sense oligo I (SEQ ID NO: 1), or the A1MM2 oligo in the manner and according to the schedule described above (the total doses being 2.0 or 0.2 mg). The results of these studies are provided in Example 22 below.

#### **Example 11: Anti-sense Oligo Formulation**

Each one of anti-sense oligos were separately solubilized in an aqueous solution and administered as described for anti-sense oligo I (SEQ. ID No:1) in (e) above, in four 5 mg aliquots (20 mg total dose) by means of a nebulizer via endotracheal tube, as described above. The results obtained for anti-sense oligo I and its mismatch controls confirmed that the mismatch controls are equivalent to saline, as described in Example 19 below and in Table 1 of Nyce & Metzger, Nature 385, 721-725 (1997). Because of this finding, saline was used as a control for pulmonary function studies employing anti-sense oligos II, III and IV (SEQ. ID NOS; 7, 8 and 9).

#### **Example 12: Specificity of Oligo I for Adenosine A<sub>2</sub> Receptor (Receptor Binding Studies)**

Tissue from airway smooth muscle was dissected to primary, secondary and tertiary bronchi from rabbits which had been administered 20 mg oligo I (SEQ ID NO: 1) in 4 divided doses over a period of 48 hours as described above. A membrane fraction was prepared according to the method of Ali et al. (Ali, S., et al., Am. J. Resp. Crit. Care Med. 149: 908 (1994), the relevant section relating to the preparation of the membrane fraction is incorporated in its entirety hereby by reference). The protein content was determined by the method of Bradford

and plasma membranes were incubated with 0.2 U/ml adenosine deaminase for 30 minutes at 37°C to remove endogenous adenosine. See, Bradford, M. M. *Anal. Biochem.* 72, 240-254 (1976), the relevant portion of which is hereby incorporated in its entirety by reference. The binding of [<sup>3</sup>H]DPCPX, [<sup>3</sup>H]NPC17731, or [<sup>3</sup>H]CGS-21680 was measured as described by Jarvis et al. See, Jarvis, M.F., et al., *Pharmacol. Exptl. Ther.* 251, 888-893 (1989), the relevant portion of which is fully incorporated herein by reference. The results of this study are shown in Table 8 and discussed in Example 20 below.

**Example 13: Pulmonary Function Measurements (Compliance  $C_{dyn}$  and Resistance)**

At 4 months of age, the immunized animals were anesthetized and relaxed with 1.5 ml of a mixture of ketamine HCl (35 mg/kg) and acepromazine maleate (1.5 mg/kg) administered intramuscularly. After induction of anesthesia, allergic rabbits were comfortably positioned supine on a soft molded animal board. Salve was applied to the eyes to prevent drying, and they were closed. The animals were then intubated with a 4.0 mm intermediate high-low cuffed Murphy 1 endotracheal tube (Mallinckrodt, Glen Falls, NY), as previously described by Zavala and Rhodes. See, Zavala and Rhodes, *Proc. Soc. Exp. Biol. Med.* 144: 509-512 (1973), the relevant portion of which is incorporated herein by reference in its entirety. A polyethylene catheter of OD 2.4 mm (Becton Dickinson, Clay Adams, Parsippany NJ) with an attached thin-walled latex balloon was passed into the esophagus and maintained at the same distance (approximately 16 cm) from the mouth throughout the experiment. The endotracheal tube was attached to a heated Fleisch pneumotach (size 00; DEM Medical, Richmond, VA), and the flow ( $v$ ) measured using a Validyne differential pressure transducer (Model DP-45-16-1927, Validyne Engineering, Northridge, CA), driven by a Gould carrier amplifier (Model 11-4113, Gould Electronics, Cleveland, OH).

An esophageal balloon was attached to one side of the Validyne differential pressure transducer, and the other side was attached to the outflow of the endotracheal tube to obtain transpulmonary pressure ( $P_p$ ). The flow was integrated to yield a continuous tidal volume, and the measurements of total lung resistance ( $R_t$ ) and dynamic compliance ( $C_{dyn}$ ) were made at isovolumetric and zero flow points. The flow, volume and pressure were recorded on an eight channel Gould 2000 W high-frequency recorder and  $C_{dyn}$  was calculated using the total volume and the difference in  $P_p$  at zero flow, and  $R_t$  was calculated as the ratio of  $P_{tp}$  and  $V$  at midtidal lung volumes. These calculations were made automatically with the Buxco automated pulmonary mechanics respiratory analyzer (Model 6, Buxco Electronics, Sharon, CT), as previously described by Giles et al. See, Giles et al., *Arch. Int. Pharmacodyn. Ther.* 194: 213-232 (1971), the relevant portion of which describing these calculations is incorporated in toto hereby by reference. The results obtained upon administration of oligo II on allergic rabbits are shown and discussed in Example 26 below.

**Example 14: Measurement of Bronchial Hyperresponsiveness (BHR)**

Each allergic rabbit was administered histamine by aerosol to determine their baseline hyperresponsiveness. Aerosols of either saline or histamine were generated using a DeVilbiss nebulizer (DeVilbiss, Somerset, PA) for 30 seconds and then for 2 minutes at each dose employed. The ultrasonic nebulizer produced aerosol droplets of which 80% were <5 micron in diameter. The histamine aerosol was administered in increasing concentrations (0.156 to 80 mg/ml) and measurements of pulmonary function were made after each dose. The BHR was then determined by calculating the concentration of histamine (mg/ml) required to reduce the  $C_{dyn}$  50% from baseline ( $PC_{50}$  Histamine).

**Example 15: Cardiovascular Effect of Anti-sense Oligo I**

The measurement of cardiac output and other cardiovascular parameters using CardiomaxJ utilizes the principal of thermal dilution in which the change in temperature of the blood exiting the heart after a venous injection of a known volume of cool saline is monitored. A single rapid injection of cool saline was made into the right atrium via cannulation of the right jugular vein, and the corresponding changes in temperature of the mixed injectate and blood in the aortic arch were recorded via cannulation of the carotid artery by a temperature-sensing miniprobe. Twelve hours after the allergic rabbits had been treated with aerosols of oligo I (EPI 2010; SEQ. ID NO: 1) as described in (d) above, the animals were anesthetized with 0.3 ml/kg of 80% Ketamine and 20% Xylazine. This time point coincides with previous data showing efficacy for SEQ. ID NO: 1, as is clearly shown by Nyce & Metzger, (1997), supra, the pertinent disclosure being incorporated in its entirety here by reference. A therm couple was then inserted into the left carotid artery of each rabbit, and was then advanced 6.5 cm and secured with a silk ligature. The right jugular vein was then cannulated and a length of polyethylene tubing was inserted and secured. A thermodilution curve was then established on a CardiomaxJ II (Columbus Instruments, Ohio) by injecting sterile saline at 20°C to determine the correctness of a portion of the

thermocouple probe. After establishing the correctness of the position of the thermocouple, the femoral artery and vein were isolated. The femoral vein was used as a portal for drug injections, and the femoral artery for blood pressure and heart rate measurements. Once constant baseline cardiovascular parameters were established, CardiomaxJ measurements of blood pressure, heart rate, cardiac output, total peripheral resistance, and cardiac contractility were made.

**Example 16: Duration of Action of Oligo I (SEQ. ID NO: 1)**

Eight allergic rabbits received initially increasing log doses of adenosine by means of a nebulizer via an intra-tracheal tube as described in (f) above, beginning with 0.156 mg/ml until compliance was reduced by 50% ( $PC_{50}$  Adenosine) to establish a baseline. Six of the rabbits then received four 5 mg aerosolized doses of (SEQ. ID NO: 1) as described above. Two rabbits received equivalent amounts of saline vehicle as controls. Beginning 18 hours after the last treatment, the  $PC_{50}$  Adenosine values were tested again. After this point, the measurements were continued for all animals each day, for up to 10 days. The results of this study are discussed in Example 25 below.

**Example 17: Reduction of Adenosine  $A_{2b}$  Receptor Number by Anti-sense Oligo V**

Sprague Dawley rats were administered 2.0 mg respirable anti-sense oligo V (SEQ ID NO:10) three times over two days using an inhalation chamber as described above. Twelve hours after the last administration, lung parenchymal tissue was dissected and assayed for adenosine  $A_{2b}$  receptor binding using [311]-NECA as described by Nyce & Metzger (1997), supra. Controls were conducted by administration of equal volumes of saline. The results are significant at  $p < 0.05$  using Student's paired t test, and are discussed in Example 28 below.

**Example 18: Comparison of Oligo I & Corresponding Phosphodiester Oligo VI (SEQ. ID NO:1681)**

Oligo I (SEQ ID NO:1) countered the effects of adenosine and eliminated sensitivity to it for adenosine amounts up to 20 mg adenosine/5.0 ml (the limit of solubility of adenosine). Oligo VI (SEQ ID NO:1681), the phosphodiester version of the oligonucleotide sequence, was completely ineffective when tested in the same manner. Both compounds have identical sequence, differing only in the presence of phosphorothioate residues in Oligo I (SEQ ID NO:1), and were delivered as an aerosol as described above and in Nyce & Metzger (1997), supra. Significantly different at  $p < 0.001$ , Student's paired t test. The results are discussed in Example 29 below.

**RESULTS OBTAINED FOR ANTI-SENSE OLIGO I (SEQ. ID NO: 1)**

**Example 19: Results of Prior Work**

The nucleotide sequence and other data for anti-sense oligo I (SEQ. ID NO: 1), which is specific for the adenosine  $A_1$  receptor, were provided above. The experimental data showing the effectiveness of oligo I in down regulating the receptor number and activity were also provided above. Further information on the characteristics and activities of anti-sense oligo I is provided in Nyce, J. W. and Metzger, W. J., Nature 385:721 (1997), the relevant parts of which relating to the following results are incorporated in their entireties herein by reference. The Nyce & Metzger (1997) publication provided data showing that the anti-sense oligo I (SEQ. ID NO: 1):

- (1) The anti-sense oligo I reduces the number of adenosine  $A_1$  receptors in the bronchial smooth muscle of allergic rabbits in a dose-dependent manner as may be seen in Table 5.
- (2) Anti-sense Oligo I attenuates adenosine-induced bronchoconstriction and allergen-induced bronchoconstriction.
- (3) The Oligo I attenuates bronchial hyperresponsiveness as measured by  $PC_{50}$  histamine, a standard measurement to assess bronchial hyperresponsiveness. This result clearly demonstrates anti-inflammatory activity of the anti-sense oligo I as is shown in Table 5.
- (4) As expected, because it was designed to target it, the anti-sense oligo I is totally specific for the adenosine  $A_1$  receptor, and has no effect at all at any dose on either the very closely related adenosine  $A_2$  receptor or the related bradykinin  $B_2$  receptor. This is seen in Table 5.
- (5) In contradistinction to the above effects of the Oligo I, the mismatch control molecules MM2 and MM3 (SEQ. ID NO:1682 and SEQ. ID NO:1683) which have identical base composition and molecular weight but differed from the anti-sense oligo I (SEQ ID NO: 1) by 6 and 2 mismatches, respectively. These mismatches, which are the minimum possible while still retaining identical base composition, produced absolutely no effect upon any of the targeted receptors ( $A_1$ ,  $A_2$  or  $B_2$ ).

These results, along with a complete lack of prior art on the use of anti-sense oligonucleotides, such as oligo I, targeted to the adenosine  $A_1$  receptor, are unexpected results. The showings presented in this patent clearly enable and demonstrate the effectiveness, for their intended use, of the claimed agents and method for treating a disease or condition associated with lung airway, such as bronchoconstriction, inflammation, allergy(ies), and the like.



**Example 20: Oligo I Significantly Reduces Response to Adenosine Challenge**

The receptor binding experiment is described in Example 12 above, and the results shown in Table 5 below which shows the binding characteristics of the adenosine A<sub>1</sub>-selective ligand [<sup>3</sup>H]DPCPX and the bradykinin B<sub>2</sub>-selective ligand [<sup>3</sup>H]NPC 17731 in membranes isolated from airway smooth muscle of A<sub>1</sub> adenosine receptor and B<sub>2</sub> bradykinin receptor anti-sense- and mismatch-treated allergic rabbits.

**Table 5: Binding Characteristics of Three Anti-Sense Oligos**

Treatment <sup>1</sup>	A <sub>1</sub> receptor		B <sub>2</sub> receptor	
	Kd	B <sub>max</sub>	Kd	B <sub>max</sub>
<b>Adenosine A<sub>1</sub> Receptor</b>				
20 mg	0.36±0.029 nM	19±1.52 fmoles*	0.39±0.031 nM	14.8±0.99 fmoles
2 mg	0.38±0.030 nM	32±2.56 fmoles*	0.41±0.028 nM	15.5±1.08 fmoles
0.2 mg	0.37±0.030 nM	49±3.43 fmoles	0.34±0.024 nM	15.0±1.06 fmoles
<b>A<sub>1</sub>MM1 (Control)</b>				
20 mg	0.34±0.027 nM	52.0±3.64 fmoles	0.35±0.024 nM	14.0±1.0 fmoles
2 mg	0.37±0.033 nM	51.8±3.88 fmoles	0.38±0.028 nM	14.6±1.02 fmoles
<b>B<sub>2</sub>A (Bradykinin Receptor)</b>				
20 mg	0.36±0.028 nM	45.0±0.15 fmoles	0.38±0.027 nM	8.7±0.62 fmoles*
2 mg	0.39±0.035 nM	44.3±2.90 fmoles	0.34±0.024 nM	11.9±0.76 fmoles**
0.2 mg	0.40±0.028 nM	47.0±3.76 fmoles	0.35±0.028 nM	15.1±1.05 fmoles
<b>B<sub>2</sub>MM (Control)</b>				±
20 mg	0.39±0.031 nM	42.0±2.94 fmoles	0.41±0.029 nM	14.0±0.98 fmoles
2 mg	0.41±0.035 nM	40.0±3.20 fmoles	0.37±0.030 nM	14.8±0.99 fmoles
0.2 mg	0.37±0.029 nM	43.0±3.14 fmoles	0.36±0.025 nM	15.1±1.35 fmoles
Saline Control	0.37±0.041	46.0±5.21	0.39±0.047 nM	14.2±1.35 fmoles

<sup>1</sup> Refers to total oligo administered in four equivalently divided doses over a 48 hour period. Treatments and analyses were performed as described in methods. Significance was determined by repeated-measures analysis of variance (ANOVA), and Tukey's protected t test. n = 4-6 for all groups.

\* Significantly different from mismatch control- and saline-treated groups, p<0.001.

\*\* Significantly different from mismatch control- and saline-treated groups, p<0.05.

**Example 21: Dose-response Effect of Oligo I**

Anti-sense oligo I (SEQ ID NO:1) was found to reduce the effect of adenosine administration to the animal in a dose-dependent manner over the dose range tested as shown in Table 6 below.

**Table 6: Dose-Response Effect of Anti-sense Oligo I**

Total Dose (mg)	PC <sub>50</sub> Adenosine (mg Adenosine)
<b>Anti-sense Oligo I</b>	
0.2	8.32±7.2
2.0	14.0±7.2
20	19.5±0.34
<b>A<sub>1</sub>MM2 oligo (control)</b>	
0.2	2.51±0.46
2.0	3.13±0.71
20	3.25±0.34

The above results were found by the Student's paired t test statistically different,  $p=0.05$

The oligo I (SEQ. ID NO:1), an anti-adenosine A<sub>1</sub> receptor oligo, acts specifically on the adenosine A<sub>1</sub> receptor, but not on the adenosine A<sub>2</sub> receptors. These results stem from the treatment of rabbits with anti-sense oligo I (SEQ. ID NO:1) or mismatch control oligo (SEQ. ID NO:1682; A<sub>1</sub>MM2) as described in Example 9 above and in Nyce & Metzger (1997), supra (four doses of 5 mg spaced 8 to 12 hours apart via nebulizer via endotracheal tube), bronchial smooth muscle tissue excised and the number of adenosine A<sub>1</sub> and adenosine A<sub>2</sub> receptors determined as reported in Nyce & Metzger (1997), supra.

**Example 22: Specificity of Oligo I (SEQ. ID NO:1) for Target Gene Product**

Oligo I (SEQ. ID No:1) is specific for the adenosine A<sub>1</sub> receptor whereas its mismatch controls had no activity. Figure 1 depicts the results obtained from the cross-over experiment described in Example 10 above and in Nyce & Metzger (1997), supra. The two mismatch controls (SEQ. ID NO:1682 and SEQ. ID NO:1683) evidenced no effect on the PC<sub>50</sub> Adenosine value. On the contrary, the administration of anti-sense oligo I (SEQ. ID NO:1) showed a seven-fold increase in the PC<sub>50</sub> Adenosine value. The results clearly indicate that the anti-sense oligo I (SEQ. ID NO: 1) reduces the response (attenuates the sensitivity) to exogenously administered adenosine when compared with a saline control. The results provided in Table 2 above clearly establish that the effect of the anti-sense oligo I is dose dependent (see, column 3 of Table 1). The Oligo I was also shown to be totally specific for the adenosine A<sub>1</sub> receptor, (see, top 3 rows of Table), inducing no activity at either the closely related adenosine A<sub>2</sub> receptor or the bradykinin B<sub>2</sub> receptor (see, lines 8-10 of Table 2 above). In addition, the results shown in Table 2 establish that the anti-sense oligo I (SEQ. ID NO:1) decreases sensitivity to adenosine in a dose dependent manner, and that it does this in an anti-sense oligo-dependent manner since neither of two mismatch control oligonucleotides (A<sub>1</sub>MM2; SEQ. ID NO:1682 and A<sub>1</sub>MM3; SEQ. ID NO:1683) show any effect on PC<sub>50</sub> Adenosine values or on attenuating the number of adenosine A<sub>1</sub> receptors.

**Example 23: Effect on Aeroallergen-induced Bronchoconstriction & Inflammation**

The Oligo I (SEQ. ID NO:1) was shown to significantly reduce the histamine-induced effect in the rabbit model when compared to the mismatch oligos. The effect of the anti-sense Oligo I (SEQ. ID No:1) and the mismatch oligos (A<sub>1</sub>MM2, SEQ. ID NO:1682 and A<sub>1</sub>MM3, SEQ. ID NO:1682) on allergen-induced airway obstruction and bronchial hyperresponsiveness was assessed in allergic rabbits. The effect of the anti-sense oligo I (SEQ. ID NO:1) on allergen-induced airway obstruction was assessed. As calculated from the area under the plotted curve, the anti-sense oligo I significantly inhibited allergen-induced airway obstruction when compared with the mismatched control (55%,  $p<0.05$ ; repeated measures ANOVA, and Tukey's t test). A complete lack of effect was induced by the mismatch oligo A<sub>1</sub>MM2 (Control) on allergen induced airway obstruction. The effect of the anti-sense oligo I (SEQ. ID NO:1) on allergen-induced BHR was determined as above. As calculated from the PC<sub>50</sub> Histamine value, the anti-sense oligo I (SEQ. ID NO:1) significantly inhibited allergen-induced BHR in allergic rabbits when compared to the mismatched control (61%,  $p<0.05$ ; repeated measures ANOVA, Tukey's t test). A complete lack of effect of the A<sub>1</sub>MM mismatch control on allergen-induced BHR was observed. The results indicated that anti-sense oligo I (SEQ. ID NO: 1) is effective to protect against aeroallergen-induced bronchoconstriction (house dust mite). In addition, the anti-sense oligo I (SEQ. ID NO:1) was also found to be a

potent inhibitor of dust mite-induced bronchial hyper responsiveness, as shown by its effects upon histamine sensitivity which indicates anti-inflammatory activity for anti-sense oligo I (SEQ. ID NO:1).

**Example 24:** Anti-sense Oligo I is Free of Deleterious Side Effects

The Oligo I (SEQ. ID NO:1) was shown to be free of side effects that might be toxic to the recipient. No changes in arterial blood pressure, cardiac output, stroke volume, heart rate, total peripheral resistance or heart contractility (dPdT) were observed following administration of 2.0 or 20 mg oligo I (SEQ. ID NO:1). The addition, the results of the measurement of cardiac output (CO), stroke volume (SV), mean arterial pressure (MAP), heart rate (HR), total peripheral resistance (TPR), and contractility (dPdT) with a CardiomaxJ apparatus (Columbus Instruments, Ohio) were assessed. These results evidenced that oligo I (SEQ. ID NO:1) has no detrimental effect upon critical cardiovascular parameters. More particularly, this oligo does not cause hypotension. This finding is of particular importance because other phosphorothioate anti-sense oligonucleotides have been shown in the past to induce hypotension in some model systems. Furthermore, the adenosine A<sub>1</sub> receptor plays an important role in sinoatrial conduction within the heart. Attenuation of the adenosine A<sub>1</sub> receptor by anti-sense oligo I (SEQ. ID NO:1) might be expected to result, therefore, in deleterious extrapulmonary activity in response to the downregulation of the receptor. This is not the case. The anti-sense oligo I (SEQ. ID NO:1) does not produce any deleterious intrapulmonary effects and renders the administration of the low doses of the present anti-sense oligo free of unexpected, undesirable side effects. This demonstrates that when oligo I (SEQ. ID NO:1) is administered directly to the lung, it does not reach the heart in significant quantities to cause deleterious effects. This is in contrast to traditional adenosine receptor antagonists like theophylline which do escape the lung and can cause deleterious, even life-threatening effects outside the lung.

**Example 25:** Long Lasting Effect of Oligo I

The Oligo I (SEQ. ID NO:1) evidenced a long lasting effect as evidenced by the PC<sub>50</sub> and Resistance values obtained upon its administration prior to adenosine challenge. The duration of the effect was measured for with respect to the PC<sub>50</sub> of adenosine anti-sense oligo I when administered in four equal doses of 5 mg each by means of a nebulizer via an endotracheal tube, as described above. The effect of the agent is significant over days 1 to 8 after administration. When the effect of the anti-sense oligo I (SEQ. ID NO:1) had disappeared, the animals were administered saline aerosols (controls), and the PC<sub>50 Adenosine</sub> values for all animals were measured again. Saline-treated animals showed base line PC<sub>50</sub> adenosine values (n=6). The duration of the effect (with respect to Resistance) was measured for six allergic rabbits which were administered 20 mg of anti-sense oligo I (SEQ. ID NO: 1) as described above, upon airway resistance measured as also described above. The mean calculated duration of effect was 8.3 days for both PC<sub>50</sub> adenosine (p<0.05) and resistance (p<0.05). These results show that anti-sense oligo I (SEQ. ID NO:1) has an extremely long duration of action, which is completely unexpected.

**Example 26:** Anti-sense Oligo II

Anti-sense ligo II, targeted to a different regi n of the adenosine A<sub>1</sub> receptor mRNA, was found to be highly active against the adenosine A<sub>1</sub>-mediated effects. The experiment measured the effect f the administration of anti-sense oligo II (SEQ. ID NO:7) upon compliance and resistance. The results showed that 20 mg of anti-sense oligo II (SEQ. ID NO:7) significantly reduced airway resistance and increased compliance.

asthma, and the administration of anti-sense oligos III (SEQ. ID NO:8) and IV (SEQ. ID NO:9) reduced their numbers by 40% and 66%, respectively. Furthermore, anti-sense oligos IV (SEQ. ID NO:9) and III (SEQ. ID NO:8) also reduced the total number of cells in the bronchial lavage fluid by 40% and 80%, respectively. This is also an important indicator of anti-inflammatory activity by the present anti-adenosine A<sub>1</sub> agents of the invention. Inflammation is known to underlie bronchial hyperresponsiveness and allergen-induced bronchoconstriction in asthma. Both anti-sense oligonucleotides III (SEQ. ID NO:8) and IV (SEQ. ID NO:9), which are targeted to the adenosine A<sub>1</sub> receptor, are representative of an important new class of anti-inflammatory agents which may be designed to specifically target the lung receptors of each species.

**Example 28: Anti-sense Oligo V**

The anti-sense oligo V (SEQ. ID NO:10), targeted to the adenosine A<sub>2b</sub> adenosine receptor mRNA was shown to be highly effective at countering adenosine A<sub>2b</sub>-mediated effects and at reducing the number of adenosine A<sub>2b</sub> receptors present to less than half.

**Example 29: Unexpected Superiority of Substituted over Phosphodiester-residue Oligo I-DS (SEQ. ID NO:1681)**

Oligos I (SEQ. ID NO:1) and I-DS (SEQ. ID NO:1681) were separately administered to allergic rabbits as described above, and the rabbits were then challenged with adenosine. The phosphodiester oligo I-DS (SEQ. ID NO:1681) was statistically significantly less effective in countering the effect of adenosine whereas oligo I (SEQ. ID NO:1) showed high effectiveness, evidencing a PC<sub>50</sub> Adenosine of 20 mg.

**Example 30: Anti-sense Oligo VI**

For the present work, I designed an additional anti-sense phosphorothioate oligo targeted to the adenosine A<sub>1</sub> receptor (Oligo VI). This anti-sense oligo was designed for therapy on a selected species as described in the above patent application and is generally specific for that species, unless the segment of the adenosine receptor mRNA of other species elected happens to have a similar sequence. The anti-sense oligos were prepared as described below, and tested in vivo in a rabbit model for bronchoconstriction, inflammation and lung allergy, which have breathing difficulties and impeded lung airways, as is the case in ailments such as asthma, as described in the above-identified application. One additional oligo and its effect in a rabbit model was studied and the results of the study are reported and discussed below. The present oligo (anti-sense oligo VI) was selected for this study to complement the data on SEQ ID NO: 1 (Oligo I), which is anti-sense to the adenosine A<sub>1</sub> receptor mRNA provided in the above-identified patent application. This additional oligo is identified as anti-sense Oligo VI, and is targeted to a different region of the adenosine A<sub>1</sub> receptor mRNA than Oligo I. The design and synthesis of this anti-sense oligo was performed in accordance with the teaching, particularly Example 1, of the above-identified patent application. The anti-sense Oligo VI is a phosphorothioate designed to target the coding region of the rabbit adenosine A<sub>1</sub> receptor mRNA region +964 to +984 relative to the initiation codon (start site). The Oligo VI was prepared as described in the above-indicated application, and is 20 nucleotides long. The Oligo VI is directed to the adenosine A<sub>1</sub> receptor gene, and has the following sequence: 5'-CGC CGG CGG GTG CGG GCC GG-3' (SEQ. ID NO: ). The phosphorothioate anti-sense Oligo VI having the sequence described in (5) above, was synthesized on an Applied Biosystems Model 396 Oligonucleotide Synthesizer, and purified using NENSORB chromatography (DuPont, DE). TETD (tetraethylthiuram disulfide) was used as the sulfurizing agent during the synthesis.

**Example 31: Preparation of Allergic Rabbits**

Neonatal New Zealand white Pasturella-free rabbits were immunized intraperitoneally within 24 hours of birth with 0.5 ml of 312 antigen units/ml house dust mite (*D. farinae*) extract (Berkeley Biologicals, Berkeley, CA) mixed with 10% kaolin as previously described (Metzger, W. J., in Late Phase Allergic Reactions, Dorsch, W., Ed., CRC Handbook, pp 347-362, CRC Press, Boca Raton, 1990; Ali, S. Et al., Am. J. Resp. Crit. Care Med. 149: 908 (1994)). The immunizations were repeated weekly for the first month and then bi-weekly until the animals were 4 months old. These rabbits preferentially produce allergen-specific IgE antibody, typically respond to aeroallergen challenge with both an early and late-phase asthmatic response, and show bronchial hyper responsiveness (BHR). Monthly intraperitoneal administration of allergen (312 units dust mite allergen, as above) continues to stimulate and maintain allergen-specific IgE antibody and BHR. At 4 months of age, sensitized rabbits were prepared for aerosol administration as described by Ali et al. (1994), supra.

**Example 32: Adenosine Aerosol Preparation**

An adenosine aerosol (20 mg/ml) was prepared with an ultrasonic nebulizer (Model 646, DeVilbiss, Somerset, PA), which produced aerosol droplets, 80% of which were smaller than 5 µm in diameter. Equal volumes of the aerosols were administered directly to the lungs via an intratracheal tube to all three rabbits. The animals

were then administered the aerosolized adenosine and Day 1 pre-treatment values for sensitivity to adenosine were calculated as the dose of adenosine causing a 50% loss of compliance ( $PC_{50}$  Adenosine). The animals were then administered the aerosolized anti-sense via the intratracheal tube (5 mg/1.0 ml), for 2 minutes, twice daily for 2 days (total dose, 20 mg). Post-treatment  $PC_{50}$  values were recorded (post-treatment challenge) on the morning of the third day. The results of these studies are provided in (9) below.

**Example 33: Anti-sense Oligo Formulation**

Each one of anti-sense oligos were separately solubilized in an aqueous solution and administered as described for anti-sense oligo I in (e) above, in four 5 mg aliquots (20 mg total dose) by means of a nebulizer via endotracheal tube, as described above.

**Example 34: Oligo VI Reduces Response to Adenosine Challenge as well or Better than Oligo I**

Oligo VI was tested in three allergic rabbits of the characteristics and readied as described in (7) above and in the above-indicated patent application. Oligo VI targets a section of the coding region of the  $A_1$  receptor which is different from Oligo I. Both these target sequences were selected randomly from many possible coding region target sequences. The three rabbits were treated identically as previously indicated for Oligo I. Briefly, 5 mg of Oligo VI were nebulized to the rabbits twice per day at 8 hour intervals, for two days. Thereafter,  $PC_{50}$  adenosine studies were performed on the morning of the third day and compared to pre-treatment  $PC_{50}$  values. This protocol is described in more detail in Nyce and Metzger (Nyce & Metzger, Nature 385: 721-725 (1997)). The results obtained for the three rabbits are shown in Table 1 below.

**Table 1:  $PC_{50}$  Adenosine before & after Aerosolized Adenosine Treatment**

Treatment Time (mg)	$PC_{50}$ Adenosine
Pre-treatment	3.0±2.1
Post-treatment	>20.0*

\* maximum achievable dose due to adenosine insolubility in saline

All three animals treated with Oligo VI completely eliminated sensitivity to adenosine up to the measurable level of the agent shown in Table 1 above. That is, the administration of the Oligo VI abrogated the adenosine-induced bronchoconstriction in the three allergic rabbits. The actual efficacy of Oligo VI is, therefore, greater than could be measured in the experimental system used. By comparing with the previously submitted results for the Oligo I, it may be seen that the Oligo VI was found to be as effective, or more, than Oligo I.

**Example 34: Conclusions**

The work described and results discussed in the examples clearly indicates that all anti-sense oligonucleotides designed in accordance with the teachings of the above-identified application were found to be highly effective at countering or reducing effects mediated by the receptors they are targeted to. That is, each and all of the two anti-sense oligos targeting an adenosine  $A_1$  receptor mRNA, 1 anti-sense oligo targeting an adenosine  $A_{2b}$  receptor mRNA, and the 2 anti-sense oligos targeting an  $A_3$  receptor mRNA were shown capable of countering the effect of exogenously administered adenosine which is mediated by the specific receptor they are targeted to.

## SEQUENCE LISTING

## (1) GENERAL INFORMATION

- (i) APPLICANT: East Carolina University et al.  
(ii) TITLE OF THE INVENTION: LOW ADENOSINE OLIGONUCLEOTIDE AGENT, COMPOSITION, KIT & TREATMENTS  
(iii) NUMBER OF SEQUENCES:  
(iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: ARTER & HADDEN  
(B) STREET: 725 South Figueroa St, # 2400  
(C) CITY: Los Angeles  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 90071  
(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0  
(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: PCT/US99/  
(B) FILING DATE: 3-AUG-1999  
(C) CLASSIFICATION: UNKNOWN  
(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 60/095,212  
(B) FILING DATE: 03-AUG-1998  
(viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Amzel, Viviana  
(B) REGISTRATION NUMBER: 30,930  
(C) REFERENCE/DOCKET NUMBER: EPI-109  
(ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 213-430-3520  
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(C) TELEX:

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cdna

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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21

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- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cdna

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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21

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- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cdna

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTTGTTGGGC ATCTTGCC

18

## (2) INFORMATION FOR SEQ ID NO:4:

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(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cdna

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTACTTGCGG ATCTAGGC

18



- (2) INFORMATION FOR SEQ ID NO:5:  
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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
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(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
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(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
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(D) TOPOLOGY: linear  
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(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
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(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
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- (2) INFORMATION FOR SEQ ID NO:12:  
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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:  
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49

(2) INFORMATION FOR SEQ ID NO:13:  
(i) SEQUENCE CHARACTERISTICS:  
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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:  
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48

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
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47

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(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
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46

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
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45

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(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:  
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44

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:  
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43

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
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42

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(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:  
AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCTGGG C 41
- (2) INFORMATION FOR SEQ ID NO:21:  
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(A) LENGTH: 40 base pairs  
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(D) TOPOLOGY: linear  
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- (2) INFORMATION FOR SEQ ID NO:22:  
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(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
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- (2) INFORMATION FOR SEQ ID NO:25:  
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(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:  
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- (2) INFORMATION FOR SEQ ID NO:26:  
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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:  
GAGATGGAGG GCGGCATGGC GGGCACAGGC TGGGC 35
- (2) INFORMATION FOR SEQ ID NO:27:  
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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:  
AGATGGAGGG CGGCATGGCG GGCACAGGCT GGGC

34

(2) INFORMATION FOR SEQ ID NO:28:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:  
GATGGAGGGC GGCATGGCGG GCACAGGCTG GGC

33

(2) INFORMATION FOR SEQ ID NO:29:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:  
ATGGAGGGCG GCATGGCGGG CACAGGCTGG GC

32

(2) INFORMATION FOR SEQ ID NO:30:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:  
TGGAGGGCGG CATGGCGGGC ACAGGCTGGG C

31

(2) INFORMATION FOR SEQ ID NO:31:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:  
GGAGGGCGGC ATGGCGGGCA CAGGCTGGGC

30

(2) INFORMATION FOR SEQ ID NO:32:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:  
GAGGGCGGCA TGGCGGGCAC AGGCTGGGC

29

(2) INFORMATION FOR SEQ ID NO:33:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:  
AGGGCGGCAT GGCGGGCACA GGCTGGGC

28

(2) INFORMATION FOR SEQ ID NO:34:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:  
GGGCGGCATG GCGGGCACAG GCTGGGC

27

- (2) INFORMATION FOR SEQ ID NO:35:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:  
GGCGGCATGG CGGGCACAGG CTGGGC 26
- (2) INFORMATION FOR SEQ ID NO:36:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:  
GGCGCATGGC GGGCACAGGC TGGGC 25
- (2) INFORMATION FOR SEQ ID NO:37:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:  
CGGCATGGCG GGCACAGGCT GGGC 24
- (2) INFORMATION FOR SEQ ID NO:38:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:  
GGCATGGCGG GCACAGGCTG GGC 23
- (2) INFORMATION FOR SEQ ID NO:39:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:  
GCATGGCGGG CACAGGCTGG GC 22
- (2) INFORMATION FOR SEQ ID NO:40:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:  
CATGGCGGGC ACAGGCTGGG C 21
- (2) INFORMATION FOR SEQ ID NO:41:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:  
ATGGCGGGCA CAGGCTGGGC 20
- (2) INFORMATION FOR SEQ ID NO:42:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:  
TGGCGGGCAC AGGCTGGGC 19

(2) INFORMATION FOR SEQ ID NO:43:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:  
GGCGGGCACCA GGCTGGGC 18

(2) INFORMATION FOR SEQ ID NO:44:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:  
GCGGGCACAG GCTGGGC 17

(2) INFORMATION FOR SEQ ID NO:45:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:  
CGGGCACAGG CTGGGC 16

(2) INFORMATION FOR SEQ ID NO:46:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:  
GGGCACAGGC TGGGC 15

(2) INFORMATION FOR SEQ ID NO:47:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:  
GGCACAGGCT GGGC 14

(2) INFORMATION FOR SEQ ID NO:48:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:  
GCACAGGCTG GGC 13

(2) INFORMATION FOR SEQ ID NO:49:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:  
CACAGGCTGG GC 12



## (2) INFORMATION FOR SEQ ID NO:50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ACAGGCTGGG C

11

## (2) INFORMATION FOR SEQ ID NO:51:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CAGGCTGGGC

10

## (2) INFORMATION FOR SEQ ID NO:52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

AGGCTGGGC

9

## (2) INFORMATION FOR SEQ ID NO:53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCTGGG C

51

## (2) INFORMATION FOR SEQ ID NO:54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCTGGG

50

## (2) INFORMATION FOR SEQ ID NO:55:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCTGG

49

## (2) INFORMATION FOR SEQ ID NO:56:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCTG

48

## (2) INFORMATION FOR SEQ ID NO:57:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:  
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCT 47

(2) INFORMATION FOR SEQ ID NO:58:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:  
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGC 46

(2) INFORMATION FOR SEQ ID NO:59:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 45 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:  
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGG 45

(2) INFORMATION FOR SEQ ID NO:60:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 44 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:  
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAG 44

(2) INFORMATION FOR SEQ ID NO:61:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 43 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:  
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACA 43

(2) INFORMATION FOR SEQ ID NO:62:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:  
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC AC 42

(2) INFORMATION FOR SEQ ID NO:63:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 41 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:  
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC A 41

(2) INFORMATION FOR SEQ ID NO:64:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:  
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC 40

- (2) INFORMATION FOR SEQ ID NO:65:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 39 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:  
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGG 39
- (2) INFORMATION FOR SEQ ID NO:66:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 38 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:  
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGG 38
- (2) INFORMATION FOR SEQ ID NO:67:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 37 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:  
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCG 37
- (2) INFORMATION FOR SEQ ID NO:68:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 36 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:  
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGC 36
- (2) INFORMATION FOR SEQ ID NO:69:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 35 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:  
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGG 35
- (2) INFORMATION FOR SEQ ID NO:70:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 34 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:  
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATG 34
- (2) INFORMATION FOR SEQ ID NO:71:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 33 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:  
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CAT 33
- (2) INFORMATION FOR SEQ ID NO:72:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 32 base pairs  
    (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:  
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CA 32

(2) INFORMATION FOR SEQ ID NO:73:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:  
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG C 31

(2) INFORMATION FOR SEQ ID NO:74:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:  
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG 30

(2) INFORMATION FOR SEQ ID NO:75:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:  
GGCGGCCTGG AAAGCTGAGA TGGAGGGCG 29

(2) INFORMATION FOR SEQ ID NO:76:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:  
GGCGGCCTGG AAAGCTGAGA TGGAGGGC 28

(2) INFORMATION FOR SEQ ID NO:77:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:  
GGCGGCCTGG AAAGCTGAGA TGGAGGG 27

(2) INFORMATION FOR SEQ ID NO:78:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:  
GGCGGCCTGG AAAGCTGAGA TGGAGG 26

(2) INFORMATION FOR SEQ ID NO:79:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:  
GGCGGCCTGG AAAGCTGAGA TGGAG 25

- (2) INFORMATION FOR SEQ ID NO:80:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 24 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:  
GGCGGCCTGG AAAGCTGAGA TGGA 24
- (2) INFORMATION FOR SEQ ID NO:81:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 23 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:  
GGCGGCCTGG AAAGCTGAGA TGG 23
- (2) INFORMATION FOR SEQ ID NO:82:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:  
GGCGGCCTGG AAAGCTGAGA TG 22
- (2) INFORMATION FOR SEQ ID NO:83:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 21 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:  
GGCGGCCTGG AAAGCTGAGA T 21
- (2) INFORMATION FOR SEQ ID NO:84:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:  
GGCGGCCTGG AAAGCTGAGA 20
- (2) INFORMATION FOR SEQ ID NO:85:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 19 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:  
GGCGGCCTGG AAAGCTGAG 19
- (2) INFORMATION FOR SEQ ID NO:86:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 18 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:  
GGCGGCCTGG AAAGCTGA 18
- (2) INFORMATION FOR SEQ ID NO:87:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:  
GGCGGCCTGG AAAGCTG 17

(2) INFORMATION FOR SEQ ID NO:88:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:  
GGCGGCCTGG AAAGCT 16

(2) INFORMATION FOR SEQ ID NO:89:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:  
GGCGGCCTGG AAAGC 15

(2) INFORMATION FOR SEQ ID NO:90:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:  
GGCGGCCTGG AAAG 14

(2) INFORMATION FOR SEQ ID NO:91:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:  
GGCGGCCTGG AAA 13

(2) INFORMATION FOR SEQ ID NO:92:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:  
GGCGGCCTGG AA 12

(2) INFORMATION FOR SEQ ID NO:93:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:  
GGCGGCCTGG A 11

(2) INFORMATION FOR SEQ ID NO:94:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:  
GGCGGCCTGG 10



(2) INFORMATION FOR SEQ ID NO:95:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:  
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGGCTGGGC 50

(2) INFORMATION FOR SEQ ID NO:96:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 49 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:  
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGGCTGGG 49

(2) INFORMATION FOR SEQ ID NO:97:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 48 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:  
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGGCTGG 48

(2) INFORMATION FOR SEQ ID NO:98:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 47 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:  
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGGCTG 47

(2) INFORMATION FOR SEQ ID NO:99:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 46 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:  
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGGCT 46

(2) INFORMATION FOR SEQ ID NO:100:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 45 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:  
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGGC 45

(2) INFORMATION FOR SEQ ID NO:101:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 44 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:  
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGG 44

(2) INFORMATION FOR SEQ ID NO:102:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 43 base pairs  
    (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:  
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAG 43

(2) INFORMATION FOR SEQ ID NO:103:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:  
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CA 42

(2) INFORMATION FOR SEQ ID NO:104:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 41 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:  
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA C 41

(2) INFORMATION FOR SEQ ID NO:105:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:  
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA 40

(2) INFORMATION FOR SEQ ID NO:106:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:  
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGC 39

(2) INFORMATION FOR SEQ ID NO:107:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:  
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGG 38

(2) INFORMATION FOR SEQ ID NO:108:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:  
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGG 37

(2) INFORMATION FOR SEQ ID NO:109:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:  
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCG 36

- (2) INFORMATION FOR SEQ ID NO:110:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 35 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:  
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGC 35
- (2) INFORMATION FOR SEQ ID NO:111:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 34 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:  
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGG 34
- (2) INFORMATION FOR SEQ ID NO:112:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 33 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:  
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATG 33
- (2) INFORMATION FOR SEQ ID NO:113:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 32 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:  
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC AT 32
- (2) INFORMATION FOR SEQ ID NO:114:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 31 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:  
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC A 31
- (2) INFORMATION FOR SEQ ID NO:115:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 30 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:  
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC 30
- (2) INFORMATION FOR SEQ ID NO:116:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 29 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:  
GCGGCCTGGA AAGCTGAGAT GGAGGGCGG 29
- (2) INFORMATION FOR SEQ ID NO:117:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 28 base pairs  
    (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:  
GCGGCCTGGA AAGCTGAGAT GGAGGGCG

28

(2) INFORMATION FOR SEQ ID NO:118:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:  
GCGGCCTGGA AAGCTGAGAT GGAGGGC

27

(2) INFORMATION FOR SEQ ID NO:119:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:  
GCGGCCTGGA AAGCTGAGAT GGAGGG

26

(2) INFORMATION FOR SEQ ID NO:120:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:  
GCGGCCTGGA AAGCTGAGAT GGAGG

25

(2) INFORMATION FOR SEQ ID NO:121:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:  
GCGGCCTGGA AAGCTGAGAT GGAG

24

(2) INFORMATION FOR SEQ ID NO:122:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:  
GCGGCCTGGA AAGCTGAGAT GGA

23

(2) INFORMATION FOR SEQ ID NO:123:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:  
GCGGCCTGGA AAGCTGAGAT GG

22

(2) INFORMATION FOR SEQ ID NO:124:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:  
GCGGCCTGGA AAGCTGAGAT G

21

- (2) INFORMATION FOR SEQ ID NO:125:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:  
GCGGCCTGGA AAGCTGAGAT 20
- (2) INFORMATION FOR SEQ ID NO:126:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:  
GCGGCCTGGA AAGCTGAGA 19
- (2) INFORMATION FOR SEQ ID NO:127:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:  
GCGGCCTGGA AAGCTGAG 18
- (2) INFORMATION FOR SEQ ID NO:128:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:  
GCGGCCTGGA AAGCTGA 17
- (2) INFORMATION FOR SEQ ID NO:129:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:  
GCGGCCTGGA AAGCTG 16
- (2) INFORMATION FOR SEQ ID NO:130:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:  
GCGGCCTGGA AAGCT 15
- (2) INFORMATION FOR SEQ ID NO:131:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:  
GCGGCCTGGA AAGC 14
- (2) INFORMATION FOR SEQ ID NO:132:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:  
GCGGCCTGGA AAG

13

(2) INFORMATION FOR SEQ ID NO:133:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:  
GCGGCCTGGA AA

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(2) INFORMATION FOR SEQ ID NO:134:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:  
GCGGCCTGGA A

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(2) INFORMATION FOR SEQ ID NO:135:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:  
GCGGCCTGGA

10

(2) INFORMATION FOR SEQ ID NO:136:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 49 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:  
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGCTGGGC

49

(2) INFORMATION FOR SEQ ID NO:137:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 48 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:  
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGCTGGG

48

(2) INFORMATION FOR SEQ ID NO:138:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 47 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:  
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGCTGG

47

(2) INFORMATION FOR SEQ ID NO:139:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:  
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGCTG

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- (2) INFORMATION FOR SEQ ID NO:140:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 45 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:  
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGCT 45
- (2) INFORMATION FOR SEQ ID NO:141:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 44 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:  
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGC 44
- (2) INFORMATION FOR SEQ ID NO:142:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 43 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:  
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGG 43
- (2) INFORMATION FOR SEQ ID NO:143:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 42 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:  
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AG 42
- (2) INFORMATION FOR SEQ ID NO:144:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 41 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:  
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGCAC A 41
- (2) INFORMATION FOR SEQ ID NO:145:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 40 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:  
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGCAC 40
- (2) INFORMATION FOR SEQ ID NO:146:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 39 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:  
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGCA 39
- (2) INFORMATION FOR SEQ ID NO:147:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 38 base pairs  
    (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:  
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGC 38

(2) INFORMATION FOR SEQ ID NO:148:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:  
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGG 37

(2) INFORMATION FOR SEQ ID NO:149:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:  
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGG 36

(2) INFORMATION FOR SEQ ID NO:150:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:  
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCG 35

(2) INFORMATION FOR SEQ ID NO:151:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:  
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGC 34

(2) INFORMATION FOR SEQ ID NO:152:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:  
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGG 33

(2) INFORMATION FOR SEQ ID NO:153:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:  
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TG 32

(2) INFORMATION FOR SEQ ID NO:154:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:  
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA T 31

- (2) INFORMATION FOR SEQ ID NO:155:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 30 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:  
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA 30
- (2) INFORMATION FOR SEQ ID NO:156:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 29 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:  
CGGCCTGGAA AGCTGAGATG GAGGGCGGC 29
- (2) INFORMATION FOR SEQ ID NO:157:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 28 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:  
CGGCCTGGAA AGCTGAGATG GAGGGCGG 28
- (2) INFORMATION FOR SEQ ID NO:158:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 27 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:  
CGGCCTGGAA AGCTGAGATG GAGGGCG 27
- (2) INFORMATION FOR SEQ ID NO:159:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 26 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:  
CGGCCTGGAA AGCTGAGATG GAGGGC 26
- (2) INFORMATION FOR SEQ ID NO:160:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 25 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:  
CGGCCTGGAA AGCTGAGATG GAGGG 25
- (2) INFORMATION FOR SEQ ID NO:161:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 24 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:  
CGGCCTGGAA AGCTGAGATG GAGG 24
- (2) INFORMATION FOR SEQ ID NO:162:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 23 base pairs  
    (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:  
CGGCCTGGAA AGCTGAGATG GAG 23

(2) INFORMATION FOR SEQ ID NO:163:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:  
CGGCCTGGAA AGCTGAGATG GA 22

(2) INFORMATION FOR SEQ ID NO:164:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:  
CGGCCTGGAA AGCTGAGATG G 21

(2) INFORMATION FOR SEQ ID NO:165:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:  
CGGCCTGGAA AGCTGAGATG 20

(2) INFORMATION FOR SEQ ID NO:166:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:  
CGGCCTGGAA AGCTGAGAT 19

(2) INFORMATION FOR SEQ ID NO:167:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:  
CGGCCTGGAA AGCTGAGA 18

(2) INFORMATION FOR SEQ ID NO:168:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:  
CGGCCTGGAA AGCTGAG 17

(2) INFORMATION FOR SEQ ID NO:169:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:  
CGGCCTGGAA AGCTGA 16

(2) INFORMATION FOR SEQ ID NO:170:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:  
CGGCCTGGAA AGCTG

15

(2) INFORMATION FOR SEQ ID NO:171:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:  
CGGCCTGGAA AGCT

14

(2) INFORMATION FOR SEQ ID NO:172:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:  
CGGCCTGGAA AGC

13

(2) INFORMATION FOR SEQ ID NO:173:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:  
CGGCCTGGAA AG

12

(2) INFORMATION FOR SEQ ID NO:174:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:  
CGGCCTGGAA A

11

(2) INFORMATION FOR SEQ ID NO:175:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:  
CGGCCTGGAA

10

(2) INFORMATION FOR SEQ ID NO:176:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 48 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:  
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GGCGGGCACA GGCTGGGC

48

(2) INFORMATION FOR SEQ ID NO:177:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 47 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:  
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GCGGGGCACA GGCTGGG

47

(2) INFORMATION FOR SEQ ID NO:178:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:  
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GCGGGGCACA GGCTGG

46

(2) INFORMATION FOR SEQ ID NO:179:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 45 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:  
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GCGGGGCACA GGCTG

45

(2) INFORMATION FOR SEQ ID NO:180:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 44 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:  
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GCGGGGCACA GGCT

44

(2) INFORMATION FOR SEQ ID NO:181:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 43 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:  
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GCGGGGCACA GGC

43

(2) INFORMATION FOR SEQ ID NO:182:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:  
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GCGGGGCACA GG

42

(2) INFORMATION FOR SEQ ID NO:183:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 41 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:  
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GCGGGGCACA G

41

(2) INFORMATION FOR SEQ ID NO:184:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:  
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GCGGGGCACA

40



- (2) INFORMATION FOR SEQ ID NO:185:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 39 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:  
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GCGGGGCAC 39
- (2) INFORMATION FOR SEQ ID NO:186:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 38 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:  
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GCGGGGCA 38
- (2) INFORMATION FOR SEQ ID NO:187:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 37 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:  
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GCGGGGC 37
- (2) INFORMATION FOR SEQ ID NO:188:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 36 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:  
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GCGGGG 36
- (2) INFORMATION FOR SEQ ID NO:189:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 35 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:  
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GCGGG 35
- (2) INFORMATION FOR SEQ ID NO:190:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 34 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:  
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GGCG 34
- (2) INFORMATION FOR SEQ ID NO:191:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 33 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:  
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GGC 33
- (2) INFORMATION FOR SEQ ID NO:192:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 32 base pairs  
    (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:  
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GG

32

(2) INFORMATION FOR SEQ ID NO:193:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:  
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT G

31

(2) INFORMATION FOR SEQ ID NO:194:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:  
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT

30

(2) INFORMATION FOR SEQ ID NO:195:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:  
GGCCTGGAAA GCTGAGATGG AGGGCGGCA

29

(2) INFORMATION FOR SEQ ID NO:196:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:  
GGCCTGGAAA GCTGAGATGG AGGGCGGC

28

(2) INFORMATION FOR SEQ ID NO:197:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:  
GGCCTGGAAA GCTGAGATGG AGGGCGG

27

(2) INFORMATION FOR SEQ ID NO:198:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:  
GGCCTGGAAA GCTGAGATGG AGGGCG

26

(2) INFORMATION FOR SEQ ID NO:199:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:  
GGCCTGGAAA GCTGAGATGG AGGGC

25

- (2) INFORMATION FOR SEQ ID NO:200:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 24 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:  
GGCCTGGAAA GCTGAGATGG AGGG 24
- (2) INFORMATION FOR SEQ ID NO:201:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 23 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:  
GGCCTGGAAA GCTGAGATGG AGG 23
- (2) INFORMATION FOR SEQ ID NO:202:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:  
GGCCTGGAAA GCTGAGATGG AG 22
- (2) INFORMATION FOR SEQ ID NO:203:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 21 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:  
GGCCTGGAAA GCTGAGATGG A 21
- (2) INFORMATION FOR SEQ ID NO:204:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:  
GGCCTGGAAA GCTGAGATGG 20
- (2) INFORMATION FOR SEQ ID NO:205:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 19 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:  
GGCCTGGAAA GCTGAGATG 19
- (2) INFORMATION FOR SEQ ID NO:206:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 18 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:  
GGCCTGGAAA GCTGAGAT 18
- (2) INFORMATION FOR SEQ ID NO:207:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:  
GGCCTGGAAA GCTGAGA 17

(2) INFORMATION FOR SEQ ID NO:208:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:  
GGCCTGGAAA GCTGAG 16

(2) INFORMATION FOR SEQ ID NO:209:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:  
GGCCTGGAAA GCTGA 15

(2) INFORMATION FOR SEQ ID NO:210:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:  
GGCCTGGAAA GCTG 14

(2) INFORMATION FOR SEQ ID NO:211:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:  
GGCCTGGAAA GCT 13

(2) INFORMATION FOR SEQ ID NO:212:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:  
GGCCTGGAAA GC 12

(2) INFORMATION FOR SEQ ID NO:213:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:  
GGCCTGGAAA G 11

(2) INFORMATION FOR SEQ ID NO:214:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:  
GGCCTGGAAA 10

## (2) INFORMATION FOR SEQ ID NO:215:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

GCCTGGAAG CTGAGATGGA GGGCGGCATG GCGGGCACAG GCTGGGC

47

## (2) INFORMATION FOR SEQ ID NO:216:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

GCCTGGAAG CTGAGATGGA GGGCGGCATG GCGGGCACAG GCTGGG

46

## (2) INFORMATION FOR SEQ ID NO:217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GCCTGGAAG CTGAGATGGA GGGCGGCATG GCGGGCACAG GCTGG

45

## (2) INFORMATION FOR SEQ ID NO:218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

GCCTGGAAG CTGAGATGGA GGGCGGCATG GCGGGCACAG GCTG

44

## (2) INFORMATION FOR SEQ ID NO:219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

GCCTGGAAG CTGAGATGGA GGGCGGCATG GCGGGCACAG GCT

43

## (2) INFORMATION FOR SEQ ID NO:220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

GCCTGGAAG CTGAGATGGA GGGCGGCATG GCGGGCACAG GC

42

## (2) INFORMATION FOR SEQ ID NO:221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

GCCTGGAAG CTGAGATGGA GGGCGGCATG GCGGGCACAG G

41

## (2) INFORMATION FOR SEQ ID NO:222:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid

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296

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:  
GCCTGGAAAG CTGAGATGGA GGGCGGCATG GCGGGCACAG 40
- (2) INFORMATION FOR SEQ ID NO:223:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:  
GCCTGGAAAG CTGAGATGGA GGGCGGCATG GCGGGCACA 39
- (2) INFORMATION FOR SEQ ID NO:224:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:  
GCCTGGAAAG CTGAGATGGA GGGCGGCATG GCGGGCAC 38
- (2) INFORMATION FOR SEQ ID NO:225:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:  
GCCTGGAAAG CTGAGATGGA GGGCGGCATG GCGGGCA 37
- (2) INFORMATION FOR SEQ ID NO:226:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:  
GCCTGGAAAG CTGAGATGGA GGGCGGCATG GCGGGC 36
- (2) INFORMATION FOR SEQ ID NO:227:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:  
GCCTGGAAAG CTGAGATGGA GGGCGGCATG GCGGG 35
- (2) INFORMATION FOR SEQ ID NO:228:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:  
GCCTGGAAAG CTGAGATGGA GGGCGGCATG GCGG 34
- (2) INFORMATION FOR SEQ ID NO:229:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:  
GCCTGGAAAG CTGAGATGGA GGGCGGCATG GCG 33



## (2) INFORMATION FOR SEQ ID NO:230:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GCCTGGAAAG CTGAGATGGA GGGCGGCATG GC

32

## (2) INFORMATION FOR SEQ ID NO:231:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

GCCTGGAAAG CTGAGATGGA GGGCGGCATG G

31

## (2) INFORMATION FOR SEQ ID NO:232:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

GCCTGGAAAG CTGAGATGGA GGGCGGCATG

30

## (2) INFORMATION FOR SEQ ID NO:233:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

GCCTGGAAAG CTGAGATGGA GGGCGGCAT

29

## (2) INFORMATION FOR SEQ ID NO:234:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

GCCTGGAAAG CTGAGATGGA GGGCGGCA

28

## (2) INFORMATION FOR SEQ ID NO:235:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

GCCTGGAAAG CTGAGATGGA GGGCGGC

27

## (2) INFORMATION FOR SEQ ID NO:236:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

GCCTGGAAAG CTGAGATGGA GGGCGG

26

## (2) INFORMATION FOR SEQ ID NO:237:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:  
GCCTGGAAAG CTGAGATGGA GGGCG 25
- (2) INFORMATION FOR SEQ ID NO:238:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:  
GCCTGGAAAG CTGAGATGGA GGGC 24
- (2) INFORMATION FOR SEQ ID NO:239:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:  
GCCTGGAAAG CTGAGATGGA GGG 23
- (2) INFORMATION FOR SEQ ID NO:240:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:  
GCCTGGAAAG CTGAGATGGA GG 22
- (2) INFORMATION FOR SEQ ID NO:241:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:  
GCCTGGAAAG CTGAGATGGA G 21
- (2) INFORMATION FOR SEQ ID NO:242:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:  
GCCTGGAAAG CTGAGATGGA 20
- (2) INFORMATION FOR SEQ ID NO:243:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:  
GCCTGGAAAG CTGAGATGG 19
- (2) INFORMATION FOR SEQ ID NO:244:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:  
GCCTGGAAAG CTGAGATG 18

(2) INFORMATION FOR SEQ ID NO:245:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:  
GCCTGGAAAG CTGAGAT

17

(2) INFORMATION FOR SEQ ID NO:246:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 16 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:  
GCCTGGAAAG CTGAGA

16

(2) INFORMATION FOR SEQ ID NO:247:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 15 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:  
GCCTGGAAAG CTGAG

15

(2) INFORMATION FOR SEQ ID NO:248:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:  
GCCTGGAAAG CTGA

14

(2) INFORMATION FOR SEQ ID NO:249:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 13 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:  
GCCTGGAAAG CTG

13

(2) INFORMATION FOR SEQ ID NO:250:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 12 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:  
GCCTGGAAAG CT

12

(2) INFORMATION FOR SEQ ID NO:251:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 11 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:  
GCCTGGAAAG C

11

(2) INFORMATION FOR SEQ ID NO:252:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 10 base pairs  
    (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:  
GCCTGGAAAG 10

(2) INFORMATION FOR SEQ ID NO:253:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:  
CCTGGAAAGC TGAGATGGAG GCGGCATGG CGGGCACAGG CTGGGC 46

(2) INFORMATION FOR SEQ ID NO:254:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 45 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:  
CCTGGAAAGC TGAGATGGAG GCGGCATGG CGGGCACAGG CTGGG 45

(2) INFORMATION FOR SEQ ID NO:255:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 44 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:  
CCTGGAAAGC TGAGATGGAG GCGGCATGG CGGGCACAGG CTGG 44

(2) INFORMATION FOR SEQ ID NO:256:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 43 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:  
CCTGGAAAGC TGAGATGGAG GCGGCATGG CGGGCACAGG CTG 43

(2) INFORMATION FOR SEQ ID NO:257:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:  
CCTGGAAAGC TGAGATGGAG GCGGCATGG CGGGCACAGG CT 42

(2) INFORMATION FOR SEQ ID NO:258:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 41 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:  
CCTGGAAAGC TGAGATGGAG GCGGCATGG CGGGCACAGG C 41

(2) INFORMATION FOR SEQ ID NO:259:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:  
CCTGGAAAGC TGAGATGGAG GCGGCATGG CGGGCACAGG 40

(2) INFORMATION FOR SEQ ID NO:260:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:  
CCTGGAAAGC TGAGATGGAG GCGGCGCATGG CGGGCACAG

39

(2) INFORMATION FOR SEQ ID NO:261:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:  
CCTGGAAAGC TGAGATGGAG GCGGCGCATGG CGGGCACA

38

(2) INFORMATION FOR SEQ ID NO:262:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:  
CCTGGAAAGC TGAGATGGAG GCGGCGCATGG CGGGCAC

37

(2) INFORMATION FOR SEQ ID NO:263:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:  
CCTGGAAAGC TGAGATGGAG GCGGCGCATGG CGGGCA

36

(2) INFORMATION FOR SEQ ID NO:264:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:  
CCTGGAAAGC TGAGATGGAG GCGGCGCATGG CGGGC

35

(2) INFORMATION FOR SEQ ID NO:265:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:  
CCTGGAAAGC TGAGATGGAG GCGGCGCATGG CGGG

34

(2) INFORMATION FOR SEQ ID NO:266:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:  
CCTGGAAAGC TGAGATGGAG GCGGCGCATGG CGG

33

(2) INFORMATION FOR SEQ ID NO:267:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:  
CCTGGAAAGC TGAGATGGAG GCGGCATGG CG 32

(2) INFORMATION FOR SEQ ID NO:268:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:  
CCTGGAAAGC TGAGATGGAG GCGGCATGG C 31

(2) INFORMATION FOR SEQ ID NO:269:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:  
CCTGGAAAGC TGAGATGGAG GCGGCATGG 30

(2) INFORMATION FOR SEQ ID NO:270:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:  
CCTGGAAAGC TGAGATGGAG GCGGCATG 29

(2) INFORMATION FOR SEQ ID NO:271:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:  
CCTGGAAAGC TGAGATGGAG GCGGCAT 28

(2) INFORMATION FOR SEQ ID NO:272:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:  
CCTGGAAAGC TGAGATGGAG GCGGCA 27

(2) INFORMATION FOR SEQ ID NO:273:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:  
CCTGGAAAGC TGAGATGGAG GCGGC 26

(2) INFORMATION FOR SEQ ID NO:274:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:  
CCTGGAAAGC TGAGATGGAG GCGG 25



- (2) INFORMATION FOR SEQ ID NO:275:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 24 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:  
CCTGGAAAGC TGAGATGGAG GGCG 24
- (2) INFORMATION FOR SEQ ID NO:276:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 23 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:  
CCTGGAAAGC TGAGATGGAG GGC 23
- (2) INFORMATION FOR SEQ ID NO:277:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:  
CCTGGAAAGC TGAGATGGAG GG 22
- (2) INFORMATION FOR SEQ ID NO:278:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 21 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:  
CCTGGAAAGC TGAGATGGAG G 21
- (2) INFORMATION FOR SEQ ID NO:279:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:  
CCTGGAAAGC TGAGATGGAG 20
- (2) INFORMATION FOR SEQ ID NO:280:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 19 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:  
CCTGGAAAGC TGAGATGGA 19
- (2) INFORMATION FOR SEQ ID NO:281:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 18 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:  
CCTGGAAAGC TGAGATGG 18
- (2) INFORMATION FOR SEQ ID NO:282:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:  
CCTGGAAAGC TGAGATG 17

(2) INFORMATION FOR SEQ ID NO:283:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:  
CCTGGAAAGC TGAGAT 16

(2) INFORMATION FOR SEQ ID NO:284:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:  
CCTGGAAAGC TGAGA 15

(2) INFORMATION FOR SEQ ID NO:285:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:  
CCTGGAAAGC TGAG 14

(2) INFORMATION FOR SEQ ID NO:286:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:  
CCTGGAAAGC TGA 13

(2) INFORMATION FOR SEQ ID NO:287:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:  
CCTGGAAAGC TG 12

(2) INFORMATION FOR SEQ ID NO:288:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:  
CCTGGAAAGC T 11

(2) INFORMATION FOR SEQ ID NO:289:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:  
CCTGGAAAGC 10

## (2) INFORMATION FOR SEQ ID NO:290:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGGCACAGGC TGGGC

45

## (2) INFORMATION FOR SEQ ID NO:291:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGGCACAGGC TGGG

44

## (2) INFORMATION FOR SEQ ID NO:292:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGGCACAGGC TGG

43

## (2) INFORMATION FOR SEQ ID NO:293:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGGCACAGGC TG

42

## (2) INFORMATION FOR SEQ ID NO:294:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGGCACAGGC T

41

## (2) INFORMATION FOR SEQ ID NO:295:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGGCACAGGC

40

## (2) INFORMATION FOR SEQ ID NO:296:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGGCACAGG

39

## (2) INFORMATION FOR SEQ ID NO:297:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:  
CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGGCACAG 38
- (2) INFORMATION FOR SEQ ID NO:298:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:  
CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGGCACA 37
- (2) INFORMATION FOR SEQ ID NO:299:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:  
CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGGCAC 36
- (2) INFORMATION FOR SEQ ID NO:300:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:  
CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGGCA 35
- (2) INFORMATION FOR SEQ ID NO:301:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:  
CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGGC 34
- (2) INFORMATION FOR SEQ ID NO:302:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:  
CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGG 33
- (2) INFORMATION FOR SEQ ID NO:303:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:  
CTGGAAAGCT GAGATGGAGG GCGGCATGGC GG 32
- (2) INFORMATION FOR SEQ ID NO:304:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:  
CTGGAAAGCT GAGATGGAGG GCGGCATGGC G 31
- (2) INFORMATION FOR SEQ ID NO:305:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:  
CTGGAAAGCT GAGATGGAGG GCGGCATGGC 30
- (2) INFORMATION FOR SEQ ID NO:306:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:  
CTGGAAAGCT GAGATGGAGG GCGGCATGG 29
- (2) INFORMATION FOR SEQ ID NO:307:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:  
CTGGAAAGCT GAGATGGAGG GCGGCATG 28
- (2) INFORMATION FOR SEQ ID NO:308:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:  
CTGGAAAGCT GAGATGGAGG GCGGCAT 27
- (2) INFORMATION FOR SEQ ID NO:309:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:  
CTGGAAAGCT GAGATGGAGG GCGGCA 26
- (2) INFORMATION FOR SEQ ID NO:310:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:  
CTGGAAAGCT GAGATGGAGG GCGGC 25
- (2) INFORMATION FOR SEQ ID NO:311:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:  
CTGGAAAGCT GAGATGGAGG GCGG 24
- (2) INFORMATION FOR SEQ ID NO:312:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:  
CTGGAAAGCT GAGATGGAGG GCG 23
- (2) INFORMATION FOR SEQ ID NO:313:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

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CTGGAAAGCT GAGATGGAGG GC

22

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

CTGGAAAGCT GAGATGGAGG G

21

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

CTGGAAAGCT GAGATGGAGG

20

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

CTGGAAAGCT GAGATGGAG

19

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

CTGGAAAGCT GAGATGGA

18

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

CTGGAAAGCT GAGATGG

17

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

CTGGAAAGCT GAGATG

16

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

CTGGAAAGCT GAGAT

15

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

CTGGAAAGCT GAGA

14

(2) INFORMATION FOR SEQ ID NO:322:



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- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:  
CTGGAAAGCT GAG 13
- (2) INFORMATION FOR SEQ ID NO:323:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:  
CTGGAAAGCT GA 12
- (2) INFORMATION FOR SEQ ID NO:324:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:  
CTGGAAAGCT G 11
- (2) INFORMATION FOR SEQ ID NO:325:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:  
CTGGAAAGCT 10
- (2) INFORMATION FOR SEQ ID NO:326:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 44 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:  
TGGAAAGCTG AGATGGAGGG CGGCATGGCG GGCACAGGCT GGGC 44
- (2) INFORMATION FOR SEQ ID NO:327:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 43 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:  
TGGAAAGCTG AGATGGAGGG CGGCATGGCG GGCACAGGCT GGG 43
- (2) INFORMATION FOR SEQ ID NO:328:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:  
TGGAAAGCTG AGATGGAGGG CGGCATGGCG GGCACAGGCT GG 42
- (2) INFORMATION FOR SEQ ID NO:329:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 41 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:  
TGGAAAGCTG AGATGGAGGG CGGCATGGCG GGCACAGGCT G 41
- (2) INFORMATION FOR SEQ ID NO:330:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:  
TGGAAAGCTG AGATGGAGGG CGGCATGGCG GGCACAGGCT 40

(2) INFORMATION FOR SEQ ID NO:331:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:  
TGGAAAGCTG AGATGGAGGG CGGCATGGCG GGCACAGG 39

(2) INFORMATION FOR SEQ ID NO:332:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:  
TGGAAAGCTG AGATGGAGGG CGGCATGGCG GGCACAGG 38

(2) INFORMATION FOR SEQ ID NO:333:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:  
TGGAAAGCTG AGATGGAGGG CGGCATGGCG GGCACAG 37

(2) INFORMATION FOR SEQ ID NO:334:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:  
TGGAAAGCTG AGATGGAGGG CGGCATGGCG GGCACA 36

(2) INFORMATION FOR SEQ ID NO:335:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:  
TGGAAAGCTG AGATGGAGGG CGGCATGGCG GGCAC 35

(2) INFORMATION FOR SEQ ID NO:336:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:  
TGGAAAGCTG AGATGGAGGG CGGCATGGCG GGCA 34

(2) INFORMATION FOR SEQ ID NO:337:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:  
TGGAAAGCTG AGATGGAGGG CGGCATGGCG GGC 33

(2) INFORMATION FOR SEQ ID NO:338:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

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TGGAAAGCTG AGATGGAGGG CGGCATGGCG GG

32

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

TGGAAAGCTG AGATGGAGGG CGGCATGGCG G

31

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

TGGAAAGCTG AGATGGAGGG CGGCATGGCG

30

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

TGGAAAGCTG AGATGGAGGG CGGCATGGC

29

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

TGGAAAGCTG AGATGGAGGG CGGCATGG

28

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

TGGAAAGCTG AGATGGAGGG CGGCATG

27

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

TGGAAAGCTG AGATGGAGGG CGGCAT

26

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

TGGAAAGCTG AGATGGAGGG CGGCA

25

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

TGGAAAGCTG AGATGGAGGG CGGC

24

(2) INFORMATION FOR SEQ ID NO:347:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:  
TGGAAAGCTG AGATGGAGGG CGG 23
- (2) INFORMATION FOR SEQ ID NO:348:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:  
TGGAAAGCTG AGATGGAGGG CG 22
- (2) INFORMATION FOR SEQ ID NO:349:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:  
TGGAAAGCTG AGATGGAGGG C 21
- (2) INFORMATION FOR SEQ ID NO:350:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:  
TGGAAAGCTG AGATGGAGGG 20
- (2) INFORMATION FOR SEQ ID NO:351:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:  
TGGAAAGCTG AGATGGAGG 19
- (2) INFORMATION FOR SEQ ID NO:352:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:  
TGGAAAGCTG AGATGGAG 18
- (2) INFORMATION FOR SEQ ID NO:353:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:  
TGGAAAGCTG AGATGGA 17
- (2) INFORMATION FOR SEQ ID NO:354:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:  
TGGAAAGCTG AGATGG 16
- (2) INFORMATION FOR SEQ ID NO:355:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:  
TGGAAAGCTG AGATG 15
- (2) INFORMATION FOR SEQ ID NO:356:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:  
TGGAAAGCTG AGAT 14
- (2) INFORMATION FOR SEQ ID NO:357:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:  
TGGAAAGCTG AGA 13
- (2) INFORMATION FOR SEQ ID NO:358:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:  
TGGAAAGCTG AG 12
- (2) INFORMATION FOR SEQ ID NO:359:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:  
TGGAAAGCTG A 11
- (2) INFORMATION FOR SEQ ID NO:360:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:  
TGGAAAGCTG 10
- (2) INFORMATION FOR SEQ ID NO:361:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 43 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:  
GGAAAGCTGA GATGGAGGGC GGCATGGCGG GCACAGGCTG GGC 43
- (2) INFORMATION FOR SEQ ID NO:362:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:  
GGAAAGCTGA GATGGAGGGC GGCATGGCGG GCACAGGCTG GG 42
- (2) INFORMATION FOR SEQ ID NO:363:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 41 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

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GGAAAGCTGA GATGGAGGGC GGCATGGCGG GCACAGGCTG G

41

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

GGAAAGCTGA GATGGAGGGC GGCATGGCGG GCACAGGCTG

40

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

GGAAAGCTGA GATGGAGGGC GGCATGGCGG GCACAGGCT

39

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

GGAAAGCTGA GATGGAGGGC GGCATGGCGG GCACAGGC

38

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 0 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

GGAAAGCTGA GATGGAGGGC GGCATGGCGG GCACAG

36

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

GGAAAGCTGA GATGGAGGGC GGCATGGCGG GCACA

35

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

GGAAAGCTGA GATGGAGGGC GGCATGGCGG GCAC

34

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

GGAAAGCTGA GATGGAGGGC GGCATGGCGG GCA

33

(2) INFORMATION FOR SEQ ID NO:372:



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- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:  
GGAAAGCTGA GATGGAGGGC GGCATGGCGG GC 32
- (2) INFORMATION FOR SEQ ID NO:373:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:  
GGAAAGCTGA GATGGAGGGC GGCATGGCGG G 31
- (2) INFORMATION FOR SEQ ID NO:374:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:  
GGAAAGCTGA GATGGAGGGC GGCATGGCGG 30
- (2) INFORMATION FOR SEQ ID NO:375:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:  
GGAAAGCTGA GATGGAGGGC GGCATGGCG 29
- (2) INFORMATION FOR SEQ ID NO:376:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:  
GGAAAGCTGA GATGGAGGGC GGCATGGC 28
- (2) INFORMATION FOR SEQ ID NO:377:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:  
GGAAAGCTGA GATGGAGGGC GGCATGG 27
- (2) INFORMATION FOR SEQ ID NO:378:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:  
GGAAAGCTGA GATGGAGGGC GGCATG 26
- (2) INFORMATION FOR SEQ ID NO:379:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:  
GGAAAGCTGA GATGGAGGGC GGCAT 25
- (2) INFORMATION FOR SEQ ID NO:380:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:  
GGAAAGCTGA GATGGAGGGC GGCA 24

(2) INFORMATION FOR SEQ ID NO:381:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:  
GGAAAGCTGA GATGGAGGGC GGC 23

(2) INFORMATION FOR SEQ ID NO:382:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:  
GGAAAGCTGA GATGGAGGGC GG 22

(2) INFORMATION FOR SEQ ID NO:383:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:  
GGAAAGCTGA GATGGAGGGC G 21

(2) INFORMATION FOR SEQ ID NO:384:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:  
GGAAAGCTGA GATGGAGGGC 20

(2) INFORMATION FOR SEQ ID NO:385:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:  
GGAAAGCTGA GATGGAGGG 19

(2) INFORMATION FOR SEQ ID NO:386:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:  
GGAAAGCTGA GATGGAGG 18

(2) INFORMATION FOR SEQ ID NO:387:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:  
GGAAAGCTGA GATGGAGG 18

(2) INFORMATION FOR SEQ ID NO:388:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

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GGAAAGCTGA GATGGA

16

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

GGAAAGCTGA GATGG

15

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

GGAAAGCTGA GATG

14

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

GGAAAGCTGA GAT

13

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

GGAAAGCTGA GA

12

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

GGAAAGCTGA G

11

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

GGAAAGCTGA

10

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

GAAAGCTGAG ATGGAGGGCG GCATGGCGGG CACAGGCTGG GC

42

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

GAAAGCTGAG ATGGAGGGCG GCATGGCGGG CACAGGCTGG G

41

(2) INFORMATION FOR SEQ ID NO:397:

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- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:  
GAAAGCTGAG ATGGAGGGCG GCATGGCGGG CACAGGCTGG 40
- (2) INFORMATION FOR SEQ ID NO:398:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:  
GAAAGCTGAG ATGGAGGGCG GCATGGCGGG CACAGGCTG 39
- (2) INFORMATION FOR SEQ ID NO:399:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:  
GAAAGCTGAG ATGGAGGGCG GCATGGCGGG CACAGGCT 38
- (2) INFORMATION FOR SEQ ID NO:400:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:  
GAAAGCTGAG ATGGAGGGCG GCATGGCGGG CACAGGC 37
- (2) INFORMATION FOR SEQ ID NO:401:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:  
GAAAGCTGAG ATGGAGGGCG GCATGGCGGG CACAGG 36
- (2) INFORMATION FOR SEQ ID NO:402:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:  
GAAAGCTGAG ATGGAGGGCG GCATGGCGGG CACAG 35
- (2) INFORMATION FOR SEQ ID NO:403:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:  
GAAAGCTGAG ATGGAGGGCG GCATGGCGGG CACA 34
- (2) INFORMATION FOR SEQ ID NO:404:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:  
GAAAGCTGAG ATGGAGGGCG GCATGGCGGG CACA 34
- (2) INFORMATION FOR SEQ ID NO:405:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:  
GAAAGCTGAG ATGGAGGGCG GCATGGCGGG CA 32

(2) INFORMATION FOR SEQ ID NO:406:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:  
GAAAGCTGAG ATGGAGGGCG GCATGGCGGG C 31

(2) INFORMATION FOR SEQ ID NO:407:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:  
GAAAGCTGAG ATGGAGGGCG GCATGGCGGG 30

(2) INFORMATION FOR SEQ ID NO:408:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:  
GAAAGCTGAG ATGGAGGGCG GCATGGCGG 29

(2) INFORMATION FOR SEQ ID NO:409:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:  
GAAAGCTGAG ATGGAGGGCG GCATGGCG 28

(2) INFORMATION FOR SEQ ID NO:410:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:  
GAAAGCTGAG ATGGAGGGCG GCATGGC 27

(2) INFORMATION FOR SEQ ID NO:411:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:  
GAAAGCTGAG ATGGAGGGCG GCATGG 26

(2) INFORMATION FOR SEQ ID NO:412:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:  
GAAAGCTGAG ATGGAGGGCG GCATG 25

(2) INFORMATION FOR SEQ ID NO:413:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

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GAAAGCTGAG ATGGAGGGCG GCAT

24

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

GAAAGCTGAG ATGGAGGGCG GCA

23

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

GAAAGCTGAG ATGGAGGGCG GC

22

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

GAAAGCTGAG ATGGAGGGCG G

21

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

GAAAGCTGAG ATGGAGGGCG

20

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

GAAAGCTGAG ATGGAGGGC

19

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

GAAAGCTGAG ATGGAGGG

18

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

GAAAGCTGAG ATGGAGG

17

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

GAAAGCTGAG ATGGAG

16

(2) INFORMATION FOR SEQ ID NO:422:

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- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 15 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:  
GAAAGCTGAG ATGGA 15
- (2) INFORMATION FOR SEQ ID NO:423:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:  
GAAAGCTGAG ATGG 14
- (2) INFORMATION FOR SEQ ID NO:424:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 13 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:  
GAAAGCTGAG ATG 13
- (2) INFORMATION FOR SEQ ID NO:425:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 12 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:  
GAAAGCTGAG AT 12
- (2) INFORMATION FOR SEQ ID NO:426:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 11 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:  
GAAAGCTGAG A 11
- (2) INFORMATION FOR SEQ ID NO:427:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 10 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:  
GAAAGCTGAG 10
- (2) INFORMATION FOR SEQ ID NO:428:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 41 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:  
AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCTGGG C 41
- (2) INFORMATION FOR SEQ ID NO:429:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 40 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:  
AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCTGGG 40
- (2) INFORMATION FOR SEQ ID NO:430:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 39 base pairs  
    (B) TYPE: nucleic acid



(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:  
AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCTGG 39

(2) INFORMATION FOR SEQ ID NO:431:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:  
AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCTG 38

(2) INFORMATION FOR SEQ ID NO:432:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:  
AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCT 37

(2) INFORMATION FOR SEQ ID NO:433:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:  
AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGC 36

(2) INFORMATION FOR SEQ ID NO:434:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:  
AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGG 35

(2) INFORMATION FOR SEQ ID NO:435:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:  
AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAG 34

(2) INFORMATION FOR SEQ ID NO:436:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:  
AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACA 33

(2) INFORMATION FOR SEQ ID NO:437:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:  
AAAGCTGAGA TGGAGGGCGG CATGGCGGGC AC 32

(2) INFORMATION FOR SEQ ID NO:438:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

AAAGCTGAGA TGGAGGGCGG CATGGCGGGC A

31

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

AAAGCTGAGA TGGAGGGCGG CATGGCGGGC

30

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

AAAGCTGAGA TGGAGGGCGG CATGGCGGG

29

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

AAAGCTGAGA TGGAGGGCGG CATGGCGG

28

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

AAAGCTGAGA TGGAGGGCGG CATGGCG

27

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

AAAGCTGAGA TGGAGGGCGG CATGGC

26

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

AAAGCTGAGA TGGAGGGCGG CATGG

25

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

AAAGCTGAGA TGGAGGGCGG CATG

24

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

AAAGCTGAGA TGGAGGGCGG CAT

23

(2) INFORMATION FOR SEQ ID NO:447:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:  
 AAAGCTGAGA TGGAGGGCGG CA 22
- (2) INFORMATION FOR SEQ ID NO:448:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:  
 AAAGCTGAGA TGGAGGGCGG C 21
- (2) INFORMATION FOR SEQ ID NO:449:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:  
 AAAGCTGAGA TGGAGGGCGG 20
- (2) INFORMATION FOR SEQ ID NO:450:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:  
 AAAGCTGAGA TGGAGGGCG 19
- (2) INFORMATION FOR SEQ ID NO:451:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:  
 AAAGCTGAGA TGGAGGGC 18
- (2) INFORMATION FOR SEQ ID NO:452:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:  
 AAAGCTGAGA TGGAGGG 17
- (2) INFORMATION FOR SEQ ID NO:453:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 16 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:  
 AAAGCTGAGA TGGAGG 16
- (2) INFORMATION FOR SEQ ID NO:454:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:  
 AAAGCTGAGA TGGAG 15
- (2) INFORMATION FOR SEQ ID NO:455:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 14 base pairs  
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:  
AAAGCTGAGA TGGA 14
- (2) INFORMATION FOR SEQ ID NO:456:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:  
AAAGCTGAGA TGG 13
- (2) INFORMATION FOR SEQ ID NO:457:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:  
AAAGCTGAGA TG 12
- (2) INFORMATION FOR SEQ ID NO:458:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:  
AAAGCTGAGA T 11
- (2) INFORMATION FOR SEQ ID NO:459:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:  
AAAGCTGAGA 10
- (2) INFORMATION FOR SEQ ID NO:460:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:  
AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGGCTGGGC 40
- (2) INFORMATION FOR SEQ ID NO:461:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:  
AAAGCTGAGA T 11
- (2) INFORMATION FOR SEQ ID NO:462:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:  
AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGGCTGG 38
- (2) INFORMATION FOR SEQ ID NO:463:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

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AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGGCTG

37

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGGCT

36

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGGC

35

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGG

34

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAG

33

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CA

32

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA C

31

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA

30

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

AAGCTGAGAT GGAGGGCGGC ATGGCGGGC

29

(2) INFORMATION FOR SEQ ID NO:472:

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- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:  
AAGCTGAGAT GGAGGGCGGC ATGGCGGG 28
- (2) INFORMATION FOR SEQ ID NO:473:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:  
AAGCTGAGAT GGAGGGCGGC ATGGCGG 27
- (2) INFORMATION FOR SEQ ID NO:474:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:  
AAGCTGAGAT GGAGGGCGGC ATGGCG 26
- (2) INFORMATION FOR SEQ ID NO:475:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:  
AAGCTGAGAT GGAGGGCGGC ATGGC 25
- (2) INFORMATION FOR SEQ ID NO:476:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:  
AAGCTGAGAT GGAGGGCGGC ATGG 24
- (2) INFORMATION FOR SEQ ID NO:477:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:  
AAGCTGAGAT GGAGGGCGGC ATG 23
- (2) INFORMATION FOR SEQ ID NO:478:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:  
AAGCTGAGAT GGAGGGCGGC AT 22
- (2) INFORMATION FOR SEQ ID NO:479:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:  
AAGCTGAGAT GGAGGGCGGC A 21
- (2) INFORMATION FOR SEQ ID NO:480:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:  
AAGCTGAGAT GGAGGGCGGC 20

(2) INFORMATION FOR SEQ ID NO:481:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:  
AAGCTGAGAT GGAGGGCGG 19

(2) INFORMATION FOR SEQ ID NO:482:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:  
AAGCTGAGAT GGAGGGCG 18

(2) INFORMATION FOR SEQ ID NO:483:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:  
AAGCTGAGAT GGAGGGC 17

(2) INFORMATION FOR SEQ ID NO:484:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:  
AAGCTGAGAT GGAGGG 16

(2) INFORMATION FOR SEQ ID NO:485:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:  
AAGCTGAGAT GGAGG 15

(2) INFORMATION FOR SEQ ID NO:486:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:  
AAGCTGAGAT GGAG 14

(2) INFORMATION FOR SEQ ID NO:487:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:  
AAGCTGAGAT GGA 13

(2) INFORMATION FOR SEQ ID NO:488:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:



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AAGCTGAGAT GG

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(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

AAGCTGAGAT G

11

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

AAGCTGAGAT

10

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGCTGGG

39

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGCTGGG

38

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGCTGG

37

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGCTG

36

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGCT

35

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGC

34

(2) INFORMATION FOR SEQ ID NO:497:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:  
AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGG 33
- (2) INFORMATION FOR SEQ ID NO:498:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:  
AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AG 32
- (2) INFORMATION FOR SEQ ID NO:499:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:  
AGCTGAGATG GAGGGCGGCA TGGCGGGCAC A 31
- (2) INFORMATION FOR SEQ ID NO:500:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:  
AGCTGAGATG GAGGGCGGCA TGGCGGGCAC 30
- (2) INFORMATION FOR SEQ ID NO:501:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:  
AGCTGAGATG GAGGGCGGCA TGGCGGGCA 29
- (2) INFORMATION FOR SEQ ID NO:502:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:  
AGCTGAGATG GAGGGCGGCA TGGCGGGC 28
- (2) INFORMATION FOR SEQ ID NO:503:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:  
AGCTGAGATG GAGGGCGGCA TGGCGGG 27
- (2) INFORMATION FOR SEQ ID NO:504:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:  
AGCTGAGATG GAGGGCGGCA TGGCGG 26
- (2) INFORMATION FOR SEQ ID NO:505:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:  
AGCTGAGATG GAGGGCGGCA TGGCG 25

(2) INFORMATION FOR SEQ ID NO:506:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:  
AGCTGAGATG GAGGGCGGCA TGGC 24

(2) INFORMATION FOR SEQ ID NO:507:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:  
AGCTGAGATG GAGGGCGGCA TGG 23

(2) INFORMATION FOR SEQ ID NO:508:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:  
AGCTGAGATG GAGGGCGGCA TG 22

(2) INFORMATION FOR SEQ ID NO:509:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:  
AGCTGAGATG GAGGGCGGCA T 21

(2) INFORMATION FOR SEQ ID NO:510:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:  
AGCTGAGATG GAGGGCGGCA 20

(2) INFORMATION FOR SEQ ID NO:511:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:  
AGCTGAGATG GAGGGCGGC 19

(2) INFORMATION FOR SEQ ID NO:512:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:  
AGCTGAGATG GAGGGCGG 18

(2) INFORMATION FOR SEQ ID NO:513:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

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AGCTGAGATG GAGGGCG

17

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

AGCTGAGATG GAGGGC

16

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

AGCTGAGATG GAGGG

15

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

AGCTGAGATG GAGG

14

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

AGCTGAGATG GAG

13

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

AGCTGAGATG GA

12

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

AGCTGAGATG G

11

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

AGCTGAGATG

10

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

GCTGAGATGG AGGGCGGCAT GCGGGGCACA GGCTGGGC

38

(2) INFORMATION FOR SEQ ID NO:522:

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- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:  
GCTGAGATGG AGGGCGGCAT GCGGGGCACA GGCTGGG 37
- (2) INFORMATION FOR SEQ ID NO:523:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:  
GCTGAGATGG AGGGCGGCAT GCGGGGCACA GGCTGG 36
- (2) INFORMATION FOR SEQ ID NO:524:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:  
GCTGAGATGG AGGGCGGCAT GCGGGGCACA GGCTG 35
- (2) INFORMATION FOR SEQ ID NO:525:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:  
GCTGAGATGG AGGGCGGCAT GCGGGGCACA GGCT 34
- (2) INFORMATION FOR SEQ ID NO:526:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:  
GCTGAGATGG AGGGCGGCAT GCGGGGCACA GGC 33
- (2) INFORMATION FOR SEQ ID NO:527:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:  
GCTGAGATGG AGGGCGGCAT GCGGGGCACA GG 32
- (2) INFORMATION FOR SEQ ID NO:528:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:  
GCTGAGATGG AGGGCGGCAT GCGGGGCACA G 31
- (2) INFORMATION FOR SEQ ID NO:529:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:  
GCTGAGATGG AGGGCGGCAT GCGGGGCACA 30
- (2) INFORMATION FOR SEQ ID NO:530:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:  
GCTGAGATGG AGGGCGGCAT GCGGGGCAC 29
- (2) INFORMATION FOR SEQ ID NO:531:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:  
GCTGAGATGG AGGGCGGCAT GCGGGGCA 28
- (2) INFORMATION FOR SEQ ID NO:532:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:  
GCTGAGATGG AGGGCGGCAT GCGGGC 27
- (2) INFORMATION FOR SEQ ID NO:533:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:  
GCTGAGATGG AGGGCGGCAT GCGGG 26
- (2) INFORMATION FOR SEQ ID NO:534:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:  
GCTGAGATGG AGGGCGGCAT GCGG 25
- (2) INFORMATION FOR SEQ ID NO:535:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:  
GCTGAGATGG AGGGCGGCAT GCGG 24
- (2) INFORMATION FOR SEQ ID NO:536:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:  
GCTGAGATGG AGGGCGGCAT GGC 23
- (2) INFORMATION FOR SEQ ID NO:537:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:  
GCTGAGATGG AGGGCGGCAT GG 22
- (2) INFORMATION FOR SEQ ID NO:538:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

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GCTGAGATGG AGGGCGGCAT G

21

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

GCTGAGATGG AGGGCGGCAT

20

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

GCTGAGATGG AGGGCGGCA

19

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

GCTGAGATGG AGGGCGGC

18

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

GCTGAGATGG AGGGCGG

17

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

GCTGAGATGG AGGGCG

16

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

GCTGAGATGG AGGGC

15

(2) INFORMATION FOR SEQ ID NO:545:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

GCTGAGATGG AGGG

14

(2) INFORMATION FOR SEQ ID NO:546:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

GCTGAGATGG AGG

13

(2) INFORMATION FOR SEQ ID NO:547:



- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:  
GCTGAGATGG AG 12
- (2) INFORMATION FOR SEQ ID NO:548:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:  
GCTGAGATGG A 11
- (2) INFORMATION FOR SEQ ID NO:549:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:  
GCTGAGATGG 10
- (2) INFORMATION FOR SEQ ID NO:550:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:  
CTGAGATGGA GGGCGGCATG GCGGGCACAG GCTGGG 37
- (2) INFORMATION FOR SEQ ID NO:551:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:  
CTGAGATGGA GGGCGGCATG GCGGGCACAG GCTGG 36
- (2) INFORMATION FOR SEQ ID NO:552:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:  
CTGAGATGGA GGGCGGCATG GCGGGCACAG GCTGG 35
- (2) INFORMATION FOR SEQ ID NO:553:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:  
CTGAGATGGA GGGCGGCATG GCGGGCACAG GCTG 34
- (2) INFORMATION FOR SEQ ID NO:554:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:  
CTGAGATGGA GGGCGGCATG GCGGGCACAG GCT 33
- (2) INFORMATION FOR SEQ ID NO:555:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:  
CTGAGATGGA GGGCGGCATG GCGGGCACAG GC 32
- (2) INFORMATION FOR SEQ ID NO:556:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:  
CTGAGATGGA GGGCGGCATG GCGGGCACAG G 31
- (2) INFORMATION FOR SEQ ID NO:557:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:  
CTGAGATGGA GGGCGGCATG GCGGGCACAG 30
- (2) INFORMATION FOR SEQ ID NO:558:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:  
CTGAGATGGA GGGCGGCATG GCGGGCACA 29
- (2) INFORMATION FOR SEQ ID NO:559:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:  
CTGAGATGGA GGGCGGCATG GCGGGCAC 28
- (2) INFORMATION FOR SEQ ID NO:560:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:  
CTGAGATGGA GGGCGGCATG GCGGGCA 27
- (2) INFORMATION FOR SEQ ID NO:561:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:  
CTGAGATGGA GGGCGGCATG GCGGGC 26
- (2) INFORMATION FOR SEQ ID NO:562:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:  
CTGAGATGGA GGGCGGCATG GCGGG 25
- (2) INFORMATION FOR SEQ ID NO:563:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

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CTGAGATGGA GGGCGGCATG GCGG

24

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

CTGAGATGGA GGGCGGCATG GCG

23

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

CTGAGATGGA GGGCGGCATG GC

22

(2) INFORMATION FOR SEQ ID NO:566:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

CTGAGATGGA GGGCGGCATG G

21

(2) INFORMATION FOR SEQ ID NO:567:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

CTGAGATGGA GGGCGGCATG

20

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

CTGAGATGGA GGGCGGCAT

19

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

CTGAGATGGA GGGCGGCA

18

(2) INFORMATION FOR SEQ ID NO:570:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

CTGAGATGGA GGGCGGC

17

(2) INFORMATION FOR SEQ ID NO:571:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

CTGAGATGGA GGGCGG

16

(2) INFORMATION FOR SEQ ID NO:572:

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- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 15 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:  
CTGAGATGGA GGGCG 15
- (2) INFORMATION FOR SEQ ID NO:573:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:  
CTGAGATGGA GGGC 14
- (2) INFORMATION FOR SEQ ID NO:574:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 13 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:  
CTGAGATGGA GGG 13
- (2) INFORMATION FOR SEQ ID NO:575:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 12 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:  
CTGAGATGGA GG 12
- (2) INFORMATION FOR SEQ ID NO:576:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 11 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:  
CTGAGATGGA G 11
- (2) INFORMATION FOR SEQ ID NO:577:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 10 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:  
CTGAGATGGA 10
- (2) INFORMATION FOR SEQ ID NO:578:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 36 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:  
TGAGATGGAG GCGGCATGG CGGGCACAGG CTGGG 36
- (2) INFORMATION FOR SEQ ID NO:579:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 35 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:  
TGAGATGGAG GCGGCATGG CGGGCACAGG CTGGG 35
- (2) INFORMATION FOR SEQ ID NO:580:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 34 base pairs  
    (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:  
TGAGATGGAG GCGGCGCATGG CGGGCACAGG CTGG 34

(2) INFORMATION FOR SEQ ID NO:581:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:  
TGAGATGGAG GCGGCGCATGG CGGGCACAGG CTG 33

(2) INFORMATION FOR SEQ ID NO:582:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:  
TGAGATGGAG GCGGCGCATGG CGGGCACAGG CT 32

(2) INFORMATION FOR SEQ ID NO:583:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:  
TGAGATGGAG GCGGCGCATGG CGGGCACAGG C 31

(2) INFORMATION FOR SEQ ID NO:584:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:  
TGAGATGGAG GCGGCGCATGG CGGGCACAGG 30

(2) INFORMATION FOR SEQ ID NO:585:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:  
TGAGATGGAG GCGGCGCATGG CGGGCACAG 29

(2) INFORMATION FOR SEQ ID NO:586:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:  
TGAGATGGAG GCGGCGCATGG CGGGCACA 28

(2) INFORMATION FOR SEQ ID NO:587:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:  
TGAGATGGAG GCGGCGCATGG CGGGCAC 27

(2) INFORMATION FOR SEQ ID NO:588:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

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TGAGATGGAG GCGGGCATGG CGGGCA

26

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

TGAGATGGAG GCGGGCATGG CGGGC

25

(2) INFORMATION FOR SEQ ID NO:590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

TGAGATGGAG GCGGGCATGG CGGG

24

(2) INFORMATION FOR SEQ ID NO:591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

TGAGATGGAG GCGGGCATGG CGG

23

(2) INFORMATION FOR SEQ ID NO:592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

TGAGATGGAG GCGGGCATGG CG

22

(2) INFORMATION FOR SEQ ID NO:593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

TGAGATGGAG GCGGGCATGG C

21

(2) INFORMATION FOR SEQ ID NO:594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

TGAGATGGAG GCGGGCATGG

20

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

TGAGATGGAG GCGGGCATG

19

(2) INFORMATION FOR SEQ ID NO:596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

TGAGATGGAG GCGGGCAT

18

(2) INFORMATION FOR SEQ ID NO:597:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:  
TGAGATGGAG GCGGCA 17
- (2) INFORMATION FOR SEQ ID NO:598:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:  
TGAGATGGAG GCGGGC 16
- (2) INFORMATION FOR SEQ ID NO:599:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:  
TGAGATGGAG GCGGG 15
- (2) INFORMATION FOR SEQ ID NO:600:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:  
TGAGATGGAG GGCG 14
- (2) INFORMATION FOR SEQ ID NO:601:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:  
TGAGATGGAG GGC 13
- (2) INFORMATION FOR SEQ ID NO:602:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:  
TGAGATGGAG GG 12
- (2) INFORMATION FOR SEQ ID NO:603:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:  
TGAGATGGAG G 11
- (2) INFORMATION FOR SEQ ID NO:604:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:  
TGAGATGGAG 10
- (2) INFORMATION FOR SEQ ID NO:605:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid



- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:  
GAGATGGAGG GCGGCATGGC GGGCACAGGC TGGGC 35
- (2) INFORMATION FOR SEQ ID NO:606:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:  
GAGATGGAGG GCGGCATGGC GGGCACAGGC TGGG 34
- (2) INFORMATION FOR SEQ ID NO:607:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:  
GAGATGGAGG GCGGCATGGC GGGCACAGGC TGG 33
- (2) INFORMATION FOR SEQ ID NO:608:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:  
GAGATGGAGG GCGGCATGGC GGGCACAGGC TG 32
- (2) INFORMATION FOR SEQ ID NO:609:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:  
GAGATGGAGG GCGGCATGGC GGGCACAGGC T 31
- (2) INFORMATION FOR SEQ ID NO:610:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:  
GAGATGGAGG GCGGCATGGC GGGCACAGG 29
- (2) INFORMATION FOR SEQ ID NO:611:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:  
GAGATGGAGG GCGGCATGGC GGGCACAGG 29
- (2) INFORMATION FOR SEQ ID NO:612:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:  
GAGATGGAGG GCGGCATGGC GGGCACAG 28
- (2) INFORMATION FOR SEQ ID NO:613:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

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GAGATGGAGG GCGGCATGGC GGGCACA

27

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

GAGATGGAGG GCGGCATGGC GGGCAC

26

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

GAGATGGAGG GCGGCATGGC GGGCA

25

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

GAGATGGAGG GCGGCATGGC GGGC

24

(2) INFORMATION FOR SEQ ID NO:617:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

GAGATGGAGG GCGGCATGGC GGG

23

(2) INFORMATION FOR SEQ ID NO:618:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

GAGATGGAGG GCGGCATGGC GG

22

(2) INFORMATION FOR SEQ ID NO:619:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

GAGATGGAGG GCGGCATGGC G

21

(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

GAGATGGAGG GCGGCATGGC

20

(2) INFORMATION FOR SEQ ID NO:621:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

GAGATGGAGG GCGGCATGG

19

(2) INFORMATION FOR SEQ ID NO:622:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 18 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:  
GAGATGGAGG GCGGCATG 18
- (2) INFORMATION FOR SEQ ID NO:623:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:  
GAGATGGAGG GCGGCAT 17
- (2) INFORMATION FOR SEQ ID NO:624:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 16 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:  
GAGATGGAGG GCGGCA 16
- (2) INFORMATION FOR SEQ ID NO:625:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 15 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:  
GAGATGGAGG GCGGC 15
- (2) INFORMATION FOR SEQ ID NO:626:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:  
GAGATGGAGG GCGG 14
- (2) INFORMATION FOR SEQ ID NO:627:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 13 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:  
GAGATGGAGG GCG 13
- (2) INFORMATION FOR SEQ ID NO:628:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 12 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:  
GAGATGGAGG GC 12
- (2) INFORMATION FOR SEQ ID NO:629:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 11 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:  
GAGATGGAGG G 11
- (2) INFORMATION FOR SEQ ID NO:630:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 10 base pairs  
    (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:  
GAGATGGAGG 10

(2) INFORMATION FOR SEQ ID NO:631:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:  
AGATGGAGGG CGGCATGGCG GGCACAGGCT GGGC 34

(2) INFORMATION FOR SEQ ID NO:632:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:  
AGATGGAGGG CGGCATGGCG GGCACAGGCT GGG 33

(2) INFORMATION FOR SEQ ID NO:633:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:  
AGATGGAGGG CGGCATGGCG GGCACAGGCT GG 32

(2) INFORMATION FOR SEQ ID NO:634:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:  
AGATGGAGGG CGGCATGGCG GGCACAGGCT G 31

(2) INFORMATION FOR SEQ ID NO:635:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:  
AGATGGAGGG CGGCATGGCG GGCACAGGCT 30

(2) INFORMATION FOR SEQ ID NO:636:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:  
AGATGGAGGG CGGCATGGCG GGCACAGGC 29

(2) INFORMATION FOR SEQ ID NO:637:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:  
AGATGGAGGG CGGCATGGCG GGCACAGG 28

(2) INFORMATION FOR SEQ ID NO:638:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

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AGATGGAGGG CGGCATGGCG GGCACAG

27

(2) INFORMATION FOR SEQ ID NO:639:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

AGATGGAGGG CGGCATGGCG GGCACA

26

(2) INFORMATION FOR SEQ ID NO:640:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

AGATGGAGGG CGGCATGGCG GGCAC

25

(2) INFORMATION FOR SEQ ID NO:641:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

AGATGGAGGG CGGCATGGCG GGCA

24

(2) INFORMATION FOR SEQ ID NO:642:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

AGATGGAGGG CGGCATGGCG GGC

23

(2) INFORMATION FOR SEQ ID NO:643:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

AGATGGAGGG CGGCATGGCG GG

22

(2) INFORMATION FOR SEQ ID NO:644:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

AGATGGAGGG CGGCATGGCG G

21

(2) INFORMATION FOR SEQ ID NO:645:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

AGATGGAGGG CGGCATGGCG

20

(2) INFORMATION FOR SEQ ID NO:646:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

AGATGGAGGG CGGCATGGC

19

(2) INFORMATION FOR SEQ ID NO:647:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:  
AGATGGAGGG CGGCATGG 18
- (2) INFORMATION FOR SEQ ID NO:648:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:  
AGATGGAGGG CGGCATG 17
- (2) INFORMATION FOR SEQ ID NO:649:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:  
AGATGGAGGG CGGCAT 16
- (2) INFORMATION FOR SEQ ID NO:650:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:  
AGATGGAGGG CGGCA 15
- (2) INFORMATION FOR SEQ ID NO:651:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:  
AGATGGAGGG CGGC 14
- (2) INFORMATION FOR SEQ ID NO:652:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:  
AGATGGAGGG CGG 13
- (2) INFORMATION FOR SEQ ID NO:653:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:  
AGATGGAGGG CG 12
- (2) INFORMATION FOR SEQ ID NO:654:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:  
AGATGGAGGG C 11
- (2) INFORMATION FOR SEQ ID NO:655:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:  
AGATGGAGGG 10
- (2) INFORMATION FOR SEQ ID NO:656:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:  
GATGGAGGGC GGCATGGCGG GCACAGGCTG GGC 33
- (2) INFORMATION FOR SEQ ID NO:657:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:  
GATGGAGGGC GGCATGGCGG GCACAGGCTG GG 32
- (2) INFORMATION FOR SEQ ID NO:658:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:  
GATGGAGGGC GGCATGGCGG GCACAGGCTG G 31
- (2) INFORMATION FOR SEQ ID NO:659:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:  
GATGGAGGGC GGCATGGCGG GCACAGGCTG 30
- (2) INFORMATION FOR SEQ ID NO:660:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:  
GATGGAGGGC GGCATGGCGG GCACAGGCT 29
- (2) INFORMATION FOR SEQ ID NO:661:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:  
GATGGAGGGC GGCATGGCGG GCACAGGC 28
- (2) INFORMATION FOR SEQ ID NO:662:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:  
GATGGAGGGC GGCATGGCGG GCACAGG 27
- (2) INFORMATION FOR SEQ ID NO:663:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:



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GATGGAGGGC GGCATGGCGG GCACAG

26

(2) INFORMATION FOR SEQ ID NO:664:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

GATGGAGGGC GGCATGGCGG GCACA

25

(2) INFORMATION FOR SEQ ID NO:665:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

GATGGAGGGC GGCATGGCGG GCAC

24

(2) INFORMATION FOR SEQ ID NO:666:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

GATGGAGGGC GGCATGGCGG GCA

23

(2) INFORMATION FOR SEQ ID NO:667:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

GATGGAGGGC GGCATGGCGG GC

22

(2) INFORMATION FOR SEQ ID NO:668:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

GATGGAGGGC GGCATGGCGG G

21

(2) INFORMATION FOR SEQ ID NO:669:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

GATGGAGGGC GGCATGGCGG

20

(2) INFORMATION FOR SEQ ID NO:670:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

GATGGAGGGC GGCATGGCG

19

(2) INFORMATION FOR SEQ ID NO:671:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

GATGGAGGGC GGCATGGC

18

(2) INFORMATION FOR SEQ ID NO:672:

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- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:  
GATGGAGGGC GGCATGG 17
- (2) INFORMATION FOR SEQ ID NO:673:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:  
GATGGAGGGC GGCATG 16
- (2) INFORMATION FOR SEQ ID NO:674:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:  
GATGGAGGGC GGCAT 15
- (2) INFORMATION FOR SEQ ID NO:675:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:  
GATGGAGGGC GGCA 14
- (2) INFORMATION FOR SEQ ID NO:676:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:  
GATGGAGGGC GGC 13
- (2) INFORMATION FOR SEQ ID NO:677:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:  
GATGGAGGGC GG 12
- (2) INFORMATION FOR SEQ ID NO:678:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:  
GATGGAGGGC G 11
- (2) INFORMATION FOR SEQ ID NO:679:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:  
GATGGAGGGC 10
- (2) INFORMATION FOR SEQ ID NO:680:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:  
ATGGAGGGCG GCATGGCGGG CACAGGCTGG GC 32

(2) INFORMATION FOR SEQ ID NO:681:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:  
ATGGAGGGCG GCATGGCGGG CACAGGCTGG G 31

(2) INFORMATION FOR SEQ ID NO:682:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:  
ATGGAGGGCG GCATGGCGGG CACAGGCTGG 30

(2) INFORMATION FOR SEQ ID NO:683:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:  
ATGGAGGGCG GCATGGCGGG CACAGGCTG 29

(2) INFORMATION FOR SEQ ID NO:684:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:  
ATGGAGGGCG GCATGGCGGG CACAGGCT 28

(2) INFORMATION FOR SEQ ID NO:685:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:  
ATGGAGGGCG GCATGGCGGG CACAGGC 27

(2) INFORMATION FOR SEQ ID NO:686:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:  
ATGGAGGGCG GCATGGCGGG CACAGG 26

(2) INFORMATION FOR SEQ ID NO:687:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:  
ATGGAGGGCG GCATGGCGGG CACAG 25

(2) INFORMATION FOR SEQ ID NO:688:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

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ATGGAGGGCG GCATGGCGGG CACA

24

(2) INFORMATION FOR SEQ ID NO:689:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

ATGGAGGGCG GCATGGCGGG CAC

23

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

ATGGAGGGCG GCATGGCGGG CA

22

(2) INFORMATION FOR SEQ ID NO:691:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

ATGGAGGGCG GCATGGCGGG C

21

(2) INFORMATION FOR SEQ ID NO:692:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

ATGGAGGGCG GCATGGCGGG

20

(2) INFORMATION FOR SEQ ID NO:693:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

ATGGAGGGCG GCATGGCGG

19

(2) INFORMATION FOR SEQ ID NO:694:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

ATGGAGGGCG GCATGGCG

18

(2) INFORMATION FOR SEQ ID NO:695:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

ATGGAGGGCG GCATGGC

17

(2) INFORMATION FOR SEQ ID NO:696:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

ATGGAGGGCG GCATGG

16

(2) INFORMATION FOR SEQ ID NO:697:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:  
ATGGAGGGCG GCATG 15
- (2) INFORMATION FOR SEQ ID NO:698:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:  
ATGGAGGGCG GCAT 14
- (2) INFORMATION FOR SEQ ID NO:699:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:  
ATGGAGGGCG GCA 13
- (2) INFORMATION FOR SEQ ID NO:700:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:  
ATGGAGGGCG GC 12
- (2) INFORMATION FOR SEQ ID NO:701:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:  
ATGGAGGGCG G 11
- (2) INFORMATION FOR SEQ ID NO:702:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:  
ATGGAGGGCG 10
- (2) INFORMATION FOR SEQ ID NO:703:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:  
TGGAGGGCGG CATGGCGGC ACAGGCTGGG C 31
- (2) INFORMATION FOR SEQ ID NO:704:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:  
TGGAGGGCGG CATGGCGGC ACAGGCTGGG 30
- (2) INFORMATION FOR SEQ ID NO:705:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:  
TGGAGGGCGG CATGGCGGGC ACAGGCTGG 29
- (2) INFORMATION FOR SEQ ID NO:706:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:  
TGGAGGGCGG CATGGCGGGC ACAGGCTG 28
- (2) INFORMATION FOR SEQ ID NO:707:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:  
TGGAGGGCGG CATGGCGGGC ACAGGCT 27
- (2) INFORMATION FOR SEQ ID NO:708:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:  
TGGAGGGCGG CATGGCGGGC ACAGGC 26
- (2) INFORMATION FOR SEQ ID NO:709:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:  
TGGAGGGCGG CATGGCGGGC ACAGG 25
- (2) INFORMATION FOR SEQ ID NO:710:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:  
TGGAGGGCGG CATGGCGGGC ACAG 24
- (2) INFORMATION FOR SEQ ID NO:711:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:  
TGGAGGGCGG CATGGCGGGC ACA 23
- (2) INFORMATION FOR SEQ ID NO:712:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:  
TGGAGGGCGG CATGGCGGGC AC 22
- (2) INFORMATION FOR SEQ ID NO:713:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

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TGGAGGGCGG CATGGCGGGC A

21

## (2) INFORMATION FOR SEQ ID NO:714:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

TGGAGGGCGG CATGGCGGGC

20

## (2) INFORMATION FOR SEQ ID NO:715:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

TGGAGGGCGG CATGGCGGG

19

## (2) INFORMATION FOR SEQ ID NO:716:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

TGGAGGGCGG CATGGCGG

18

## (2) INFORMATION FOR SEQ ID NO:717:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

TGGAGGGCGG CATGGCG

17

## (2) INFORMATION FOR SEQ ID NO:718:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

TGGAGGGCGG CATGGC

16

## (2) INFORMATION FOR SEQ ID NO:719:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

TGGAGGGCGG CATGG

15

## (2) INFORMATION FOR SEQ ID NO:720:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

TGGAGGGCGG CATG

14

## (2) INFORMATION FOR SEQ ID NO:721:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

TGGAGGGCGG CAT

13

## (2) INFORMATION FOR SEQ ID NO:722:



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- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:  
TGGAGGGCGG CA 12
- (2) INFORMATION FOR SEQ ID NO:723:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:  
TGGAGGGCGG C 11
- (2) INFORMATION FOR SEQ ID NO:724:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:  
TGGAGGGCGG 10
- (2) INFORMATION FOR SEQ ID NO:725:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:  
GGAGGGCGGC ATGGCGGGCA CAGGCTGGGC 30
- (2) INFORMATION FOR SEQ ID NO:726:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:  
GGAGGGCGGC ATGGCGGGCA CAGGCTGGG 29
- (2) INFORMATION FOR SEQ ID NO:727:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:  
GGAGGGCGGC ATGGCGGGCA CAGGCTGG 28
- (2) INFORMATION FOR SEQ ID NO:728:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:  
GGAGGGCGGC ATGGCGGGCA CAGGCTG 27
- (2) INFORMATION FOR SEQ ID NO:729:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:  
GGAGGGCGGC ATGGCGGGCA CAGGCT 26
- (2) INFORMATION FOR SEQ ID NO:730:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:  
GGAGGGCGGC ATGGCGGGCA CAGGC 25
- (2) INFORMATION FOR SEQ ID NO:731:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:  
GGAGGGCGGC ATGGCGGGCA CAGG 24
- (2) INFORMATION FOR SEQ ID NO:732:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:  
GGAGGGCGGC ATGGCGGGCA CAG 23
- (2) INFORMATION FOR SEQ ID NO:733:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:  
GGAGGGCGGC ATGGCGGGCA CA 22
- (2) INFORMATION FOR SEQ ID NO:734:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:  
GGAGGGCGGC ATGGCGGGCA C 21
- (2) INFORMATION FOR SEQ ID NO:735:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:  
GGAGGGCGGC ATGGCGGGCA 20
- (2) INFORMATION FOR SEQ ID NO:736:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:  
GGAGGGCGGC ATGGCGGGC 19
- (2) INFORMATION FOR SEQ ID NO:737:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:  
GGAGGGCGGC ATGGCGGG 18
- (2) INFORMATION FOR SEQ ID NO:738:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

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GGAGGGCGGC ATGGCGG

17

(2) INFORMATION FOR SEQ ID NO:739:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

GGAGGGCGGC ATGGCG

16

(2) INFORMATION FOR SEQ ID NO:740:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

GGAGGGCGGC ATGGC

15

(2) INFORMATION FOR SEQ ID NO:741:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

GGAGGGCGGC ATGG

14

(2) INFORMATION FOR SEQ ID NO:742:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

GGAGGGCGGC ATG

13

(2) INFORMATION FOR SEQ ID NO:743:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

GGAGGGCGGC AT

12

(2) INFORMATION FOR SEQ ID NO:744:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

GGAGGGCGGC A

11

(2) INFORMATION FOR SEQ ID NO:745:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

GGAGGGCGGC

10

(2) INFORMATION FOR SEQ ID NO:746:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:

GAGGGCGGCA TGGCGGGCAC AGGCTGGGC

29

(2) INFORMATION FOR SEQ ID NO:747:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:  
GAGGGCGGCA TGGCGGGCAC AGGCTGGG 28
- (2) INFORMATION FOR SEQ ID NO:748:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:  
GAGGGCGGCA TGGCGGGCAC AGGCTGG 27
- (2) INFORMATION FOR SEQ ID NO:749:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:  
GAGGGCGGCA TGGCGGGCAC AGGCTG 26
- (2) INFORMATION FOR SEQ ID NO:750:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:  
GAGGGCGGCA TGGCGGGCAC AGGCT 25
- (2) INFORMATION FOR SEQ ID NO:751:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:  
GAGGGCGGCA TGGCGGGCAC AGGC 24
- (2) INFORMATION FOR SEQ ID NO:752:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:  
GAGGGCGGCA TGGCGGGCAC AGG 23
- (2) INFORMATION FOR SEQ ID NO:753:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:  
GAGGGCGGCA TGGCGGGCAC AG 22
- (2) INFORMATION FOR SEQ ID NO:754:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:  
GAGGGCGGCA TGGCGGGCAC A 21
- (2) INFORMATION FOR SEQ ID NO:755:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:  
GAGGGCGGCA TGGCGGGCAC 20

(2) INFORMATION FOR SEQ ID NO:756:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:  
GAGGGCGGCA TGGCGGGCA 19

(2) INFORMATION FOR SEQ ID NO:757:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:  
GAGGGCGGCA TGGCGGGC 18

(2) INFORMATION FOR SEQ ID NO:758:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:  
GAGGGCGGCA TGGCGGG 17

(2) INFORMATION FOR SEQ ID NO:759:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:  
GAGGGCGGCA TGGCGG 16

(2) INFORMATION FOR SEQ ID NO:760:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:  
GAGGGCGGCA TGGCG 15

(2) INFORMATION FOR SEQ ID NO:761:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:  
GAGGGCGGCA TGGC 14

(2) INFORMATION FOR SEQ ID NO:762:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:  
GAGGGCGGCA TGG 13

(2) INFORMATION FOR SEQ ID NO:763:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

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GAGGGCGGCA TG

12

(2) INFORMATION FOR SEQ ID NO:764:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

GAGGGCGGCA T

11

(2) INFORMATION FOR SEQ ID NO:765:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:

AGGGCGGCA

10

(2) INFORMATION FOR SEQ ID NO:766:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

AGGGCGGCAT GCGGGCACA GGCTGGGC

28

(2) INFORMATION FOR SEQ ID NO:767:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

AGGGCGGCAT GCGGGCACA GGCTGGG

27

(2) INFORMATION FOR SEQ ID NO:768:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

AGGGCGGCAT GCGGGCACA GGCTGG

26

(2) INFORMATION FOR SEQ ID NO:769:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

AGGGCGGCAT GCGGGCACA GGCTG

25

(2) INFORMATION FOR SEQ ID NO:770:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

AGGGCGGCAT GCGGGCACA GGCT

24

(2) INFORMATION FOR SEQ ID NO:771:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

AGGGCGGCAT GCGGGCACA GGC

23

(2) INFORMATION FOR SEQ ID NO:772:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:  
AGGGCGGCAT GGCGGGCACA GG 22
- (2) INFORMATION FOR SEQ ID NO:773:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 21 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:  
AGGGCGGCAT GGCGGGCACA G 21
- (2) INFORMATION FOR SEQ ID NO:774:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:  
AGGGCGGCAT GGCGGGCACA 20
- (2) INFORMATION FOR SEQ ID NO:775:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 19 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:  
AGGGCGGCAT GGCGGGCAC 19
- (2) INFORMATION FOR SEQ ID NO:776:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 18 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:  
AGGGCGGCAT GGCGGGCA 18
- (2) INFORMATION FOR SEQ ID NO:777:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:  
AGGGCGGCAT GGCGGGC 17
- (2) INFORMATION FOR SEQ ID NO:778:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 16 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:  
AGGGCGGCAT GGCGGG 16
- (2) INFORMATION FOR SEQ ID NO:779:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 15 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:  
AGGGCGGCAT GGCGG 15
- (2) INFORMATION FOR SEQ ID NO:780:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid



(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:  
AGGGCGGCAT GGCG 14

(2) INFORMATION FOR SEQ ID NO:781:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:  
AGGGCGGCAT GGC 13

(2) INFORMATION FOR SEQ ID NO:782:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:  
AGGGCGGCAT GG 12

(2) INFORMATION FOR SEQ ID NO:783:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:  
AGGGCGGCAT G 11

(2) INFORMATION FOR SEQ ID NO:784:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:  
AGGGCGGCAT 10

(2) INFORMATION FOR SEQ ID NO:785:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:  
GGGCGGCATG GCGGGCACAG GCTGGGC 27

(2) INFORMATION FOR SEQ ID NO:786:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:  
GGGCGGCATG GCGGGCACAG GCTGGG 26

(2) INFORMATION FOR SEQ ID NO:787:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:  
GGGCGGCATG GCGGGCACAG GCTGG 25

(2) INFORMATION FOR SEQ ID NO:788:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

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GGGCGGCATG GCGGGCACAG GCTG

24

(2) INFORMATION FOR SEQ ID NO:789:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

GGGCGGCATG GCGGGCACAG GCT

23

(2) INFORMATION FOR SEQ ID NO:790:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

GGGCGGCATG GCGGGCACAG GC

22

(2) INFORMATION FOR SEQ ID NO:791:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

GGGCGGCATG GCGGGCACAG G

21

(2) INFORMATION FOR SEQ ID NO:792:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

GGGCGGCATG GCGGGCACAG

20

(2) INFORMATION FOR SEQ ID NO:793:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

GGGCGGCATG GCGGGCAC

19

(2) INFORMATION FOR SEQ ID NO:794:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

GGGCGGCATG GCGGGCAC

18

(2) INFORMATION FOR SEQ ID NO:795:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

GGGCGGCATG GCGGGCA

17

(2) INFORMATION FOR SEQ ID NO:796:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

GGGCGGCATG GCGGGC

16

(2) INFORMATION FOR SEQ ID NO:797:

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- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:  
GGGCGGCATG GCGGG 15
- (2) INFORMATION FOR SEQ ID NO:798:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:  
GGGCGGCATG GCGG 14
- (2) INFORMATION FOR SEQ ID NO:799:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:  
GGGCGGCATG GCG 13
- (2) INFORMATION FOR SEQ ID NO:800:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:  
GGGCGGCATG GC 12
- (2) INFORMATION FOR SEQ ID NO:801:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:  
GGGCGGCATG G 11
- (2) INFORMATION FOR SEQ ID NO:802:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:  
GGGCGGCATG 10
- (2) INFORMATION FOR SEQ ID NO:803:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:  
GGCGGCATGG CGGGCACAGG CTGGG 26
- (2) INFORMATION FOR SEQ ID NO:804:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:  
GGCGGCATGG CGGGCACAGG CTGGG 25
- (2) INFORMATION FOR SEQ ID NO:805:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:  
GGCGGCATGG CGGGCACAGG CTGG 24
- (2) INFORMATION FOR SEQ ID NO:806:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:  
GGCGGCATGG CGGGCACAGG CTG 23
- (2) INFORMATION FOR SEQ ID NO:807:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:  
GGCGGCATGG CGGGCACAGG CT 22
- (2) INFORMATION FOR SEQ ID NO:808:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:  
GGCGGCATGG CGGGCACAGG C 21
- (2) INFORMATION FOR SEQ ID NO:809:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:  
GGCGGCATGG CGGGCACAGG 20
- (2) INFORMATION FOR SEQ ID NO:810:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:  
GGCGGCATGG CGGGCACAG 19
- (2) INFORMATION FOR SEQ ID NO:811:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:  
GGCGGCATGG CGGGCACA 18
- (2) INFORMATION FOR SEQ ID NO:812:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:  
GGCGGCATGG CGGGCAC 17
- (2) INFORMATION FOR SEQ ID NO:813:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

GGCGGCATGG CGGGCA

16

## (2) INFORMATION FOR SEQ ID NO:814:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

GGCGGCATGG CGGGC

15

## (2) INFORMATION FOR SEQ ID NO:815:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:

GGCGGCATGG CGGG

14

## (2) INFORMATION FOR SEQ ID NO:816:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

GGCGGCATGG CGG

13

## (2) INFORMATION FOR SEQ ID NO:817:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

GGCGGCATGG CG

12

## (2) INFORMATION FOR SEQ ID NO:818:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:

GGCGGCATGG C

11

## (2) INFORMATION FOR SEQ ID NO:819:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:

GGCGGCATGG

10

## (2) INFORMATION FOR SEQ ID NO:820:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:

GCGGCATGGC GGGCACAGGC TGGGC

25

## (2) INFORMATION FOR SEQ ID NO:821:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

GCGGCATGGC GGGCACAGGC TGGG

24

## (2) INFORMATION FOR SEQ ID NO:822:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:  
GCGGCATGGC GGGCACAGGC TGG 23
- (2) INFORMATION FOR SEQ ID NO:823:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:  
GCGGCATGGC GGGCACAGGC TG 22
- (2) INFORMATION FOR SEQ ID NO:824:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:  
GCGGCATGGC GGGCACAGGC T 21
- (2) INFORMATION FOR SEQ ID NO:825:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:  
GCGGCATGGC GGGCACAGGC 20
- (2) INFORMATION FOR SEQ ID NO:826:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:  
GCGGCATGGC GGGCACAGG 19
- (2) INFORMATION FOR SEQ ID NO:827:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:  
GCGGCATGGC GGGCACAG 18
- (2) INFORMATION FOR SEQ ID NO:828:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:  
GCGGCATGGC GGGCAC 17
- (2) INFORMATION FOR SEQ ID NO:829:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:  
GCGGCATGGC GGGCAC 16
- (2) INFORMATION FOR SEQ ID NO:830:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:  
GCGGCATGGC GGGCA 15

(2) INFORMATION FOR SEQ ID NO:831:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:  
GCGGCATGGC GGGC 14

(2) INFORMATION FOR SEQ ID NO:832:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:  
GCGGCATGGC GGG 13

(2) INFORMATION FOR SEQ ID NO:833:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:  
GCGGCATGGC GG 12

(2) INFORMATION FOR SEQ ID NO:834:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:  
GCGGCATGGC G 11

(2) INFORMATION FOR SEQ ID NO:835:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:  
GCGGCATGGC 10

(2) INFORMATION FOR SEQ ID NO:836:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:  
CGGCATGGCG GGCACAGGCT GGGC 24

(2) INFORMATION FOR SEQ ID NO:837:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:  
CGGCATGGCG GGCACAGGCT GGG 23

(2) INFORMATION FOR SEQ ID NO:838:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:



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CGGCATGGCG GGCACAGGCT GG

22

(2) INFORMATION FOR SEQ ID NO:839:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

CGGCATGGCG GGCACAGGCT G

21

(2) INFORMATION FOR SEQ ID NO:840:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

CGGCATGGCG GGCACAGGCT

20

(2) INFORMATION FOR SEQ ID NO:841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

CGGCATGGCG GGCACAGG

19

(2) INFORMATION FOR SEQ ID NO:842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

CGGCATGGCG GGCACAGG

18

(2) INFORMATION FOR SEQ ID NO:843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:

CGGCATGGCG GGCACAG

17

(2) INFORMATION FOR SEQ ID NO:844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:

CGGCATGGCG GGCACA

16

(2) INFORMATION FOR SEQ ID NO:845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:

CGGCATGGCG GGCAC

15

(2) INFORMATION FOR SEQ ID NO:846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:

CGGCATGGCG GGCA

14

(2) INFORMATION FOR SEQ ID NO:847:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:  
CGGCATGGCG GGC 13
- (2) INFORMATION FOR SEQ ID NO:848:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:  
CGGCATGGCG GG 12
- (2) INFORMATION FOR SEQ ID NO:849:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:  
CGGCATGGCG G 11
- (2) INFORMATION FOR SEQ ID NO:850:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:  
CGGCATGGCG 10
- (2) INFORMATION FOR SEQ ID NO:851:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:  
GGCATGGCGG GCACAGGCTG GGC 23
- (2) INFORMATION FOR SEQ ID NO:852:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:  
GGCATGGCGG GCACAGGCTG GG 22
- (2) INFORMATION FOR SEQ ID NO:853:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:  
GGCATGGCGG GCACAGGCTG G 21
- (2) INFORMATION FOR SEQ ID NO:854:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:  
GGCATGGCGG GCACAGGCTG 20
- (2) INFORMATION FOR SEQ ID NO:855:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:  
GGCATGGCGG GCACAGGCT 19
- (2) INFORMATION FOR SEQ ID NO:856:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:  
GGCATGGCGG GCACAGGC 18
- (2) INFORMATION FOR SEQ ID NO:857:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:  
GGCATGGCGG GCACAGG 17
- (2) INFORMATION FOR SEQ ID NO:858:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:  
GGCATGGCGG GCACAG 16
- (2) INFORMATION FOR SEQ ID NO:859:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:  
GGCATGGCGG GCACA 15
- (2) INFORMATION FOR SEQ ID NO:860:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:  
GGCATGGCGG GCAC 14
- (2) INFORMATION FOR SEQ ID NO:861:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:  
GGCATGGCGG GCA 13
- (2) INFORMATION FOR SEQ ID NO:862:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:  
GGCATGGCGG GC 12
- (2) INFORMATION FOR SEQ ID NO:863:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:

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GGCATGGCGG G

11

## (2) INFORMATION FOR SEQ ID NO:864:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:

GGCATGGCGG

10

## (2) INFORMATION FOR SEQ ID NO:865:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

GCATGGCGGG CACAGGCTGG GC

22

## (2) INFORMATION FOR SEQ ID NO:866:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:

GCATGGCGGG CACAGGCTGG G

21

## (2) INFORMATION FOR SEQ ID NO:867:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:

GCATGGCGGG CACAGGCTGG

20

## (2) INFORMATION FOR SEQ ID NO:868:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

GCATGGCGGG CACAGGCTG

19

## (2) INFORMATION FOR SEQ ID NO:869:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

GCATGGCGGG CACAGGCT

18

## (2) INFORMATION FOR SEQ ID NO:870:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

GCATGGCGGG CACAGGC

17

## (2) INFORMATION FOR SEQ ID NO:871:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

GCATGGCGGG CACAGG

16

## (2) INFORMATION FOR SEQ ID NO:872:

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- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 15 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:  
GCATGGCGGG CACAG 15
- (2) INFORMATION FOR SEQ ID NO:873:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:  
GCATGGCGGG CACA 14
- (2) INFORMATION FOR SEQ ID NO:874:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 13 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:  
GCATGGCGGG CAC 13
- (2) INFORMATION FOR SEQ ID NO:875:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 12 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:  
GCATGGCGGG CA 12
- (2) INFORMATION FOR SEQ ID NO:876:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 11 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:  
GCATGGCGGG C 11
- (2) INFORMATION FOR SEQ ID NO:877:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 10 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:  
GCATGGCGGG 10
- (2) INFORMATION FOR SEQ ID NO:878:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 21 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:  
CATGGCGGGC ACAGGCTGGG C 21
- (2) INFORMATION FOR SEQ ID NO:879:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:  
CATGGCGGGC ACAGGCTGGG 20
- (2) INFORMATION FOR SEQ ID NO:880:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 19 base pairs  
    (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:  
CATGGCGGGC ACAGGCTGG 19

(2) INFORMATION FOR SEQ ID NO:881:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:  
CATGGCGGGC ACAGGCTG 18

(2) INFORMATION FOR SEQ ID NO:882:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:  
CATGGCGGGC ACAGGCT 17

(2) INFORMATION FOR SEQ ID NO:883:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:  
CATGGCGGGC ACAGGC 16

(2) INFORMATION FOR SEQ ID NO:884:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:  
CATGGCGGGC ACAGG 15

(2) INFORMATION FOR SEQ ID NO:885:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:  
CATGGCGGGC ACAG 14

(2) INFORMATION FOR SEQ ID NO:886:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:  
CATGGCGGGC ACA 13

(2) INFORMATION FOR SEQ ID NO:887:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:  
CATGGCGGGC AC 12

(2) INFORMATION FOR SEQ ID NO:888:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

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CATGGCGGGC A

11

(2) INFORMATION FOR SEQ ID NO:889:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:

CATGGCGGGC

10

(2) INFORMATION FOR SEQ ID NO:890:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:

ATGGCGGGCA CAGGCTGGGC

20

(2) INFORMATION FOR SEQ ID NO:891:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:

ATGGCGGGCA CAGGCTGGG

19

(2) INFORMATION FOR SEQ ID NO:892:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:

ATGGCGGGCA CAGGCTGG

18

(2) INFORMATION FOR SEQ ID NO:893:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:

ATGGCGGGCA CAGGCTG

17

(2) INFORMATION FOR SEQ ID NO:894:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:

ATGGCGGGCA CAGGCT

16

(2) INFORMATION FOR SEQ ID NO:895:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

ATGGCGGGCA CAGGC

15

(2) INFORMATION FOR SEQ ID NO:896:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

ATGGCGGGCA CAGG

14

(2) INFORMATION FOR SEQ ID NO:897:



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- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:  
ATGGCGGGCA CAG 13
- (2) INFORMATION FOR SEQ ID NO:898:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:  
ATGGCGGGCA CA 12
- (2) INFORMATION FOR SEQ ID NO:899:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:  
ATGGCGGGCA C 11
- (2) INFORMATION FOR SEQ ID NO:900:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:  
ATGGCGGGCA 10
- (2) INFORMATION FOR SEQ ID NO:901:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:  
TGGCGGGCAC AGGCTGGGC 19
- (2) INFORMATION FOR SEQ ID NO:902:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:  
TGGCGGGCAC AGGCTGGG 18
- (2) INFORMATION FOR SEQ ID NO:903:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:  
TGGCGGGCAC AGGCTGG 17
- (2) INFORMATION FOR SEQ ID NO:904:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:  
TGGCGGGCAC AGGCTG 16
- (2) INFORMATION FOR SEQ ID NO:905:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:  
TGGCGGGCAC AGGCT 15
- (2) INFORMATION FOR SEQ ID NO:906:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:  
TGGCGGGCAC AGGC 14
- (2) INFORMATION FOR SEQ ID NO:907:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:  
TGGCGGGCAC AGG 13
- (2) INFORMATION FOR SEQ ID NO:908:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:  
TGGCGGGCAC AG 12
- (2) INFORMATION FOR SEQ ID NO:909:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:  
TGGCGGGCAC A 11
- (2) INFORMATION FOR SEQ ID NO:910:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:  
TGGCGGGCAC 10
- (2) INFORMATION FOR SEQ ID NO:911:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:  
GGCGGGCACA GGCTGGGC 18
- (2) INFORMATION FOR SEQ ID NO:912:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:  
GGCGGGCACA GGCTGGG 17
- (2) INFORMATION FOR SEQ ID NO:913:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:

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GGCGGGCACA GGCTGG

16

(2) INFORMATION FOR SEQ ID NO:914:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:

GGCGGGCACA GGCTG

15

(2) INFORMATION FOR SEQ ID NO:915:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:915:

GGCGGGCACA GGCT

14

(2) INFORMATION FOR SEQ ID NO:916:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:

GGCGGGCACA GGC

13

(2) INFORMATION FOR SEQ ID NO:917:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:917:

GGCGGGCACA GG

12

(2) INFORMATION FOR SEQ ID NO:918:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:

GGCGGGCACA G

11

(2) INFORMATION FOR SEQ ID NO:919:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:

GGCGGGCACA

10

(2) INFORMATION FOR SEQ ID NO:920:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:

GCGGGCACAG GCTGGGC

17

(2) INFORMATION FOR SEQ ID NO:921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:

GCGGGCACAG GCTGGG

16

(2) INFORMATION FOR SEQ ID NO:922:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:  
GCGGGCACAG GCTGG 15
- (2) INFORMATION FOR SEQ ID NO:923:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:  
GCGGGCACAG GCTG 14
- (2) INFORMATION FOR SEQ ID NO:924:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:  
GCGGGCACAG GCT 13
- (2) INFORMATION FOR SEQ ID NO:925:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:  
GCGGGCACAG GC 12
- (2) INFORMATION FOR SEQ ID NO:926:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:  
GCGGGCACAG G 11
- (2) INFORMATION FOR SEQ ID NO:927:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:  
GCGGGCACAG 10
- (2) INFORMATION FOR SEQ ID NO:928:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:  
CGGGCACAGG CTGGGC 16
- (2) INFORMATION FOR SEQ ID NO:929:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:  
GGGCACAGGC TGGG 14
- (2) INFORMATION FOR SEQ ID NO:930:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:  
CGGGCACAGG CTGG 14

(2) INFORMATION FOR SEQ ID NO:931:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:  
CGGGCACAGG CTG 13

(2) INFORMATION FOR SEQ ID NO:932:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:932:  
CGGGCACAGG CT 12

(2) INFORMATION FOR SEQ ID NO:933:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:  
CGGGCACAGG C 11

(2) INFORMATION FOR SEQ ID NO:934:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:934:  
CGGGCACAGG 10

(2) INFORMATION FOR SEQ ID NO:935:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:935:  
GGGCACAGGC TGGGC 15

(2) INFORMATION FOR SEQ ID NO:936:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:936:  
GGGCACAGGC TGGG 14

(2) INFORMATION FOR SEQ ID NO:937:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:  
GGGCACAGGC TGG 13

(2) INFORMATION FOR SEQ ID NO:938:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:  
GGGCACAGGC TG

12

(2) INFORMATION FOR SEQ ID NO:939:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:939:  
GGGCACAGGC T

11

(2) INFORMATION FOR SEQ ID NO:940:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:940:  
GGGCACAGGC

10

(2) INFORMATION FOR SEQ ID NO:941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:941:  
GGCACAGGCT GGGC

14

(2) INFORMATION FOR SEQ ID NO:942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:  
GGCACAGGCT GGG

13

(2) INFORMATION FOR SEQ ID NO:943:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:  
GGCACAGGCT GG

12

(2) INFORMATION FOR SEQ ID NO:944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:  
GGCACAGGCT G

11

(2) INFORMATION FOR SEQ ID NO:945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:  
GGCACAGGCT

10

(2) INFORMATION FOR SEQ ID NO:946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:946:  
GCACAGGCTG GGC

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(2) INFORMATION FOR SEQ ID NO:947:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 12 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:  
GCACAGGCTG GG 12

(2) INFORMATION FOR SEQ ID NO:948:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 11 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:  
GCACAGGCTG G 11

(2) INFORMATION FOR SEQ ID NO:949:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 10 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:  
GCACAGGCTG 10

(2) INFORMATION FOR SEQ ID NO:950:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 12 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:  
CACAGGCTGG GC 12

(2) INFORMATION FOR SEQ ID NO:951:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 11 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:  
CACAGGCTGG G 11

(2) INFORMATION FOR SEQ ID NO:952:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 10 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:  
CACAGGCTGG 10

(2) INFORMATION FOR SEQ ID NO:953:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 11 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:  
ACAGGCTGGG C 11

(2) INFORMATION FOR SEQ ID NO:954:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 10 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:  
ACAGGCTGGG 10

(2) INFORMATION FOR SEQ ID NO:955:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 10 base pairs



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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:  
CAGGCTGGGC

10

(2) INFORMATION FOR SEQ ID NO:956:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:  
TTTTCCTTCC TTTGTCTCTC TTC

23

(2) INFORMATION FOR SEQ ID NO:957:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:957:  
GCTCCCGGCT GCCTG

15

(2) INFORMATION FOR SEQ ID NO:958:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:  
CTCGGCCGTG CGGCTCTGTC GCTCCCGT

29

(2) INFORMATION FOR SEQ ID NO:959:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:  
CCGCCGCCCT CCGGGGGGTC

20

(2) INFORMATION FOR SEQ ID NO:960:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:  
TGCTGCCGTT GGCTGCCC

18

(2) INFORMATION FOR SEQ ID NO:961:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:  
CTTCTGCGGG TCGCCG

17

(2) INFORMATION FOR SEQ ID NO:962:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:  
TGCTGGGCTT GTGGC

15

(2) INFORMATION FOR SEQ ID NO:963:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:963: GGCCTCTCTT CTGGG	15
(2) INFORMATION FOR SEQ ID NO:964: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 14 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:964: CCTGGTCCCT CCGT	14
(2) INFORMATION FOR SEQ ID NO:965: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 14 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:965: GGTGGCTCCT CTGC	14
(2) INFORMATION FOR SEQ ID NO:966: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:966: GCTTGGTCCT GGGGCTGC	18
(2) INFORMATION FOR SEQ ID NO:967: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:967: TGCTCTCCTC TCCTT	15
(2) INFORMATION FOR SEQ ID NO:968: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:968: TGCTTTTCTT TTCTGGGCCT C	21
(2) INFORMATION FOR SEQ ID NO:969: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:969: TGTGGTCTGT TTTTCTTG	19
(2) INFORMATION FOR SEQ ID NO:970: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:970: GCCCTGCTGG GCGCTCTCC	20
(2) INFORMATION FOR SEQ ID NO:971: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:971: GCCGCCGCC TGGCTCCC	18

- (2) INFORMATION FOR SEQ ID NO:972:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 21 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:  
GGBGCCCBTG BTGGGCBTGC C 21
- (2) INFORMATION FOR SEQ ID NO:973:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 24 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:  
GTGGTTCTTG CCCTCCTTG GCTG 24
- (2) INFORMATION FOR SEQ ID NO:974:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 18 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:  
CCGTGCCCCG TCCCCGGC 18
- (2) INFORMATION FOR SEQ ID NO:975:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:  
CTCCTGGCGG GTGGCCGTTG 20
- (2) INFORMATION FOR SEQ ID NO:976:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 18 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:  
GGCCCCGTGT CCCTGCGG 18
- (2) INFORMATION FOR SEQ ID NO:977:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:  
GCCTGGGGCT CCCTTCTCTC 20
- (2) INFORMATION FOR SEQ ID NO:978:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 19 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:  
GCCCTTCTTG CTGGGCCTC 19
- (2) INFORMATION FOR SEQ ID NO:979:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 25 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:  
TGCTGCTGCT GGTGCTGTGG CCCCC 25
- (2) INFORMATION FOR SEQ ID NO:980:  
(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:  
GTACACCGAG GAGCCCATGA TGGGCATGCC ACAGACGACA GGC

43

(2) INFORMATION FOR SEQ ID NO:981:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:  
GTBCBCCGBG GBGCCCCBTGB TGGGCBTGCC BCBGBCGBCB GGC

43

(2) INFORMATION FOR SEQ ID NO:982:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:  
GGCGCCGTGC CGCGTCTTGG TGGCGGCGG

29

(2) INFORMATION FOR SEQ ID NO:983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:  
GTTCCGCGCCC GCGCGGGGCC CCTCCGGTCC

30

(2) INFORMATION FOR SEQ ID NO:984:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:  
GTTCCGCGCCC GCGCGGGGCC CCTCCGGTCC

30

(2) INFORMATION FOR SEQ ID NO:985:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:  
CGGGTCGGGG CCCCCCGGG CC

22

(2) INFORMATION FOR SEQ ID NO:986:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:  
GCCTCGGGGC TGGGGCGCTG GTGGCCGGG

29

(2) INFORMATION FOR SEQ ID NO:987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:  
CCGCGCCTCC GCCTGCCGCT TCTG

24

(2) INFORMATION FOR SEQ ID NO:988:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:  
GCTGGGCCCC GGGGCCCCC T 21

(2) INFORMATION FOR SEQ ID NO:989:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:  
CCCCTCTTGC TCGGGTCCCC GTG 23

(2) INFORMATION FOR SEQ ID NO:990:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 48 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:  
ACAGCGCGTC CTGTGTCTCC AGCAGCATGG CCGGGCCAGC TGGGCCCC 48

(2) INFORMATION FOR SEQ ID NO:991:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 48 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:  
BCBGC GGCTC CTGTGTCTCC BGCBCBTGG CCGGGCCBGC TGGGCCCC 48

(2) INFORMATION FOR SEQ ID NO:992:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:  
ACAGAGCATG CTGTTGTTGG GCATCTTGCC TTCCAGGG 39

(2) INFORMATION FOR SEQ ID NO:993:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:  
BCBGBGCBTG CTGTTGTTGG GCBTCTTGCC TTCCBGGG 39

(2) INFORMATION FOR SEQ ID NO:994:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:  
CCCTTTTCTG GTGGGGTG 18

(2) INFORMATION FOR SEQ ID NO:995:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:  
GTGCTGTTGT TGGGC 15

(2) INFORMATION FOR SEQ ID NO:996:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:  
TTTCTTCTGT TCCC 14

(2) INFORMATION FOR SEQ ID NO:997:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:  
CCCTTTTCTG GTGGGGTG 18

(2) INFORMATION FOR SEQ ID NO:998:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:998:  
GTGCTGTTGT TGGGC 15

(2) INFORMATION FOR SEQ ID NO:999:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:999:  
TTTCTTCTGT TCCC 14

(2) INFORMATION FOR SEQ ID NO:1000:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:  
TTTCCCCTGG GTCTTCC 17

(2) INFORMATION FOR SEQ ID NO:1001:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:  
CTCCTGCTCT TTTTTC 16

(2) INFORMATION FOR SEQ ID NO:1002:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002:  
ATTTGCTCTC CTATTACTTT CTGTGTCCAT TTTTTCATTA ACCGAGCTGT 50

(2) INFORMATION FOR SEQ ID NO:1003:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003:  
BTTTGCTCTC CTBTBCTTT CTGTGTCCBT TTTTTCBTTB BCCGBGCTGT 50

(2) INFORMATION FOR SEQ ID NO:1004:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:

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GCCTGTGTCT GTCCTCCT

18

(2) INFORMATION FOR SEQ ID NO:1005:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:

GCTTCGTTC TCTCGTTC

18

(2) INFORMATION FOR SEQ ID NO:1006:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:

CTGCTTGGTG CCCTTGCCG

19

(2) INFORMATION FOR SEQ ID NO:1007:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:

GTCCTGCTCC TCCGGGCTGT GG

22

(2) INFORMATION FOR SEQ ID NO:1008:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:

GTCGTGGCCC TGGCTCCGGC TGGTGGGCTC CCCTGG

36

(2) INFORMATION FOR SEQ ID NO:1009:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:

CCTTCGCTGG CTGGCGGCGT GC

22

(2) INFORMATION FOR SEQ ID NO:1010:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:

GGGTCTTGCT CTGGGCTGG CTGT

24

(2) INFORMATION FOR SEQ ID NO:1011:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:

GGCCGTGGTT GGGGTCTTC

20

(2) INFORMATION FOR SEQ ID NO:1012:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:

GCTGCCTCCG TTTGGGTGGC

20

(2) INFORMATION FOR SEQ ID NO:1013:



(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:  
TCTCTGAATA TTGACCTTCC TCCATGGCGG TCCTGCTTGG ATTCTCCCGA 50

(2) INFORMATION FOR SEQ ID NO:1014:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:  
TCTCTGBBTB TTGBCCTTCC TCCBTGGCGG TCCTGCTTGG BTTCTCCCGB 50

(2) INFORMATION FOR SEQ ID NO:1015:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:  
GCCTTTCCTG GTTCTCTGT TGTTTTGGG GTTTGGCTT 39

(2) INFORMATION FOR SEQ ID NO:1016:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:  
ACAGTAGAGT AGGGGATTCC ATGGCAGGAG CCATCTTCTT CATGGACTCC 50

(2) INFORMATION FOR SEQ ID NO:1017:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:  
TTCAAGGAGA CCTTAGGTTT CTGAGGGACT GCTAACACGC CATCTGGAGC 50

(2) INFORMATION FOR SEQ ID NO:1018:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 77 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:  
BCBGTBGBGT BGGGGBTTCC BTGGCBGBG CCBTCTTCTT CBTGBBCTCC TTCBBGGBG 60  
CCTTBGGTTT CTGBGGG 77

(2) INFORMATION FOR SEQ ID NO:1019:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:  
BCTGCTBBCB CGCCBTCTGG BGC 23

(2) INFORMATION FOR SEQ ID NO:1020:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020:  
GTTGTTTTG GGGTTTGGCT T 21

- (2) INFORMATION FOR SEQ ID NO:1021:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 18 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:  
GCCTTTCCTG GTTCTCTT 18
- (2) INFORMATION FOR SEQ ID NO:1022:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:  
BCBGTBGBGT BGGGGBTTCC BTGGCBGGBG CCBTCTTCTT CBTGGBCTCC 50
- (2) INFORMATION FOR SEQ ID NO:1023:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:  
TTCBBGGBGB CCTTBGGTTT CTGBGGGBCT GCTBBCBGC CBTCTGGBGC 50
- (2) INFORMATION FOR SEQ ID NO:1024:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 18 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024:  
GCCTGTGTCT GTCCTCCT 18
- (2) INFORMATION FOR SEQ ID NO:1025:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 18 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025:  
GCTTCGTTC TCTCGTTC 18
- (2) INFORMATION FOR SEQ ID NO:1026:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 19 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:  
CTGCTTG TG G C C C T T G C C G 19
- (2) INFORMATION FOR SEQ ID NO:1027:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:  
GTCCTGTCC TCCGGGCTGT GG 22
- (2) INFORMATION FOR SEQ ID NO:1028:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 36 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:  
GTCCTCGCCC TGGCTCCGCG TGGTGGGCTC CCCTGG 36
- (2) INFORMATION FOR SEQ ID NO:1029:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029:  
CCTTCGCTGG CTGGCGGCGT GC 22
- (2) INFORMATION FOR SEQ ID NO:1030:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 24 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030:  
CCCBGBBCGB GBCCCGBCC GBCB 24
- (2) INFORMATION FOR SEQ ID NO:1031:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031:  
GGCCGTGGTT GGGGTCTTC 20
- (2) INFORMATION FOR SEQ ID NO:1032:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032:  
GCTGCCTCCG TTTGGGTGGC 20
- (2) INFORMATION FOR SEQ ID NO:1033:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 40 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033:  
GBTCTCTGBB TBTGBCCTT CCBTGGCGGT CCTGCTTGGB 40
- (2) INFORMATION FOR SEQ ID NO:1034:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 26 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:  
TCTCCCTTGG GCTCTGGCTC CTTCTC 26
- (2) INFORMATION FOR SEQ ID NO:1035:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 21 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:  
TCTCTCTCCC TCTCTCTCTG T 21
- (2) INFORMATION FOR SEQ ID NO:1036:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 32 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:  
CGCCTCCGCC CTGGCTGCTG GGGTGGTGT GC 32
- (2) INFORMATION FOR SEQ ID NO:1037:  
(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:  
TTTTGTTCTT CCTTGCTGCC

20

(2) INFORMATION FOR SEQ ID NO:1038:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:  
GCCCCGCTGC TTGTCTTCCT CG

22

(2) INFORMATION FOR SEQ ID NO:1039:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:  
CTCTGTCCTT CTCTCTGT BCTCCTCBGG CTCBCBCTC TCCCTTGGGC

50

(2) INFORMATION FOR SEQ ID NO:1040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040:  
CTTGCTCCTG GGGGCCTCCT G

21

(2) INFORMATION FOR SEQ ID NO:1041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:  
GTCCCTCCGG GTGTTCCCG C

21

(2) INFORMATION FOR SEQ ID NO:1042:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042:  
GGGCCTGGCC TGGGCBGGG GCCGCTBGG CGCGGCTCGC CBGGBCGGGC BGCGCCBGC  
GCBGCBGTT CBGCBCTCTG C

60

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(2) INFORMATION FOR SEQ ID NO:1043:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:  
CTTGCTCCTG GGGGCCTCCT G

21

(2) INFORMATION FOR SEQ ID NO:1044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:  
GTCCCTCTGG CTGTTCCCG C

21

(2) INFORMATION FOR SEQ ID NO:1045:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 90 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:  
CCTGGBCTGG GGCBBGGGCC GCGTBGGCGC GGCTCGCCBG GBCGGGCBGC GCCBGCBCBG 60  
GCBGGCTCBG CBTCTGGCC BCGBBTTC 90

(2) INFORMATION FOR SEQ ID NO:1046:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:  
GGTGTGCGGG GCCTGGTGCC 20

(2) INFORMATION FOR SEQ ID NO:1047:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:  
CCTGGGCCTC GGGTGCTGCC TGT 23

(2) INFORMATION FOR SEQ ID NO:1048:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:  
GCGCTGCCTT CTTCTCTGG 20

(2) INFORMATION FOR SEQ ID NO:1049:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:  
GTCCTCGCCG GGGCCCTTGC TGCCCTGGCT GT 32

(2) INFORMATION FOR SEQ ID NO:1050:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:  
GCCCTGGGGG TCTGGGTTG GCTGT 25

(2) INFORMATION FOR SEQ ID NO:1051:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:  
CCCCBGCBBG BCCBGTCBCCB TCCBCBGCCT GTGBTGBGTB GCCBTTCTCC TGCBGCCBG 60

(2) INFORMATION FOR SEQ ID NO:1052:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:  
GGGCGCGGGC GBGCBTCGC 19

(2) INFORMATION FOR SEQ ID NO:1053:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053:  
TTTGGGCTTT TCTCCTTGG TT 22
- (2) INFORMATION FOR SEQ ID NO:1054:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:  
TGBGCGCCBG GBCCGCGCBC BGCBCBGGG CGCGGGCGBG CBTGCBGCG GCGGGCBGGG 60
- (2) INFORMATION FOR SEQ ID NO:1055:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:  
GCCCTGCTGC TCTTTCTGCT 20
- (2) INFORMATION FOR SEQ ID NO:1056:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056:  
TCCCTTGCTG GGTGGGCC 19
- (2) INFORMATION FOR SEQ ID NO:1057:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057:  
TTGCTGCCCC TTCTGTCCC 19
- (2) INFORMATION FOR SEQ ID NO:1058:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058:  
TTGCTGCCCC TTCTGTCCC 19
- (2) INFORMATION FOR SEQ ID NO:1059:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:  
TGTTTGCTGG TGTCTGCGC 19
- (2) INFORMATION FOR SEQ ID NO:1060:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:  
CCCCBBGBG BGBBGBGBC BBTTTGGGB BGTGBBGBGT TTTGGBBCCB TGTTTCCTGT 60
- (2) INFORMATION FOR SEQ ID NO:1061:  
(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061:  
GCGCTCGGCC TGGTCCCGG 19
- (2) INFORMATION FOR SEQ ID NO:1062:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062:  
GGGTCTCTC TTGTTGTTGC 20
- (2) INFORMATION FOR SEQ ID NO:1063:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:  
TTGCGCCTCC TGCTGGGGGT CC 22
- (2) INFORMATION FOR SEQ ID NO:1064:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:  
CTCTGTTCTT GTTTGGGGG C 21
- (2) INFORMATION FOR SEQ ID NO:1065:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:  
GGCCCCGGCC GTTGTCTTG 19
- (2) INFORMATION FOR SEQ ID NO:1066:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:  
GTTTGGGGGT TTCCGTTG 18
- (2) INFORMATION FOR SEQ ID NO:1067:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:  
GGGTTCTCCT GGCCCCGGCC TGCCCC 26
- (2) INFORMATION FOR SEQ ID NO:1068:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:  
GGCCGTGGTC CCGGCTTCGT TGC 23
- (2) INFORMATION FOR SEQ ID NO:1069:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single



- (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:  
CCTGTCTCCG TCTCGGCTCT TCTG 24
- (2) INFORMATION FOR SEQ ID NO:1070:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070:  
GGGCCTTGCG CTGTCTTTGG TG 22
- (2) INFORMATION FOR SEQ ID NO:1071:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071:  
GCBCCGTCCB GTGTGGTGC GGTBCTGTG GCTGCBGCGC TCGGCCTGGT CCCGGBGBGC 60
- (2) INFORMATION FOR SEQ ID NO:1072:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072:  
GCGCGGGCCG GGGGCTGCTG GG 22
- (2) INFORMATION FOR SEQ ID NO:1073:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:  
GGTTGGCCCG GGGTGCCCC 19
- (2) INFORMATION FOR SEQ ID NO:1074:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074:  
GCCGCTGGGT GCCCTCGTCC TCTGCGGTC 29
- (2) INFORMATION FOR SEQ ID NO:1075:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075:  
GTGTCTCCTG GCTCTGGTTC CCC 23
- (2) INFORMATION FOR SEQ ID NO:1076:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076:  
GCTGCGCCCG TTGTCCTCTG GGGTGGCCTT C 31
- (2) INFORMATION FOR SEQ ID NO:1077:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:

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400

GCTCCCGGGT CTGGTTCTTG TGT

23

## (2) INFORMATION FOR SEQ ID NO:1078:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:

TGGGGGTCCC TTTTGGGCC TGTGT

26

## (2) INFORMATION FOR SEQ ID NO:1079:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:

GGCGTGGCTT GTGTGTCGG TTTC

24

## (2) INFORMATION FOR SEQ ID NO:1080:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:

TGCCCTGTCC TCCGGCGTCC C

21

## (2) INFORMATION FOR SEQ ID NO:1081:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081:

CGGBGCCTCC CCGGGGCBGG BTGBCTTTTG BGGGGBCBC BGBTGTCTGG GCBTTGCCBG  
GTCCTGGGBB CBGBGCCCG BCBGBGCCB GGBGTGCGG CBGCGCGGC CGGGGGCTGC  
TGGGBGCCBT BGCGBGGCTG BG

60

120

142

## (2) INFORMATION FOR SEQ ID NO:1082:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082:

CCTCTTTTCT GTTTTCCC

19

## (2) INFORMATION FOR SEQ ID NO:1083:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083:

CTCTGCCTTT GTTGGGTTC G

21

## (2) INFORMATION FOR SEQ ID NO:1084:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:

CTTCCTTTCT GCTTCTTC

19

## (2) INFORMATION FOR SEQ ID NO:1085:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:

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401

CTGTGTCTCC TGTCTCCGCT TTTTCTTC

29

## (2) INFORMATION FOR SEQ ID NO:1086:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:

GTCTTTGTTG TTTTCTCTTC CTTG

24

## (2) INFORMATION FOR SEQ ID NO:1087:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:

CTGBGCBBGB TBTCTBGBTT CTGGGGTGGT CTCGBTTTB BBBGCTTGBG BBGCTGCBBB  
CBTBTCCBB BGTBTBTTG BGGCTCCBBG GBTBCBCC BTCTCCCBG GCBTTTTBBG  
TTGCTGTCGT

60

120

130

## (2) INFORMATION FOR SEQ ID NO:1088:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:

GTTCTTGGCT TCTTCTGTC

19

## (2) INFORMATION FOR SEQ ID NO:1089:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:

CGTTGGCTTC TC GTTGTCCC

20

## (2) INFORMATION FOR SEQ ID NO:1090:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:

TGTGGGCTTC TC GTTGTCCC

20

## (2) INFORMATION FOR SEQ ID NO:1091:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:

CCCTTCGGGG GCTGGTGG

18

## (2) INFORMATION FOR SEQ ID NO:1092:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:

GGCTGGTGG

9

## (2) INFORMATION FOR SEQ ID NO:1093:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:

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402

GGCCGTCCTT GCCTGCTGG

19

(2) INFORMATION FOR SEQ ID NO:1094:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:

TTTTCTCTTT CGCTTTCTTT TCGTCTCCTG TTCTCCTTT T

41

(2) INFORMATION FOR SEQ ID NO:1095:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:

TTGCTGTTTT TTCTCCTTCT TCTCTCCTTT CTTTC

36

(2) INFORMATION FOR SEQ ID NO:1096:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:

TTTTCTCTTT CGCTTTCTTT TCGTCTCCTG TTCTCCTTT T

41

(2) INFORMATION FOR SEQ ID NO:1097:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:

TTGCTGTTTT TTCTCCTTCT TCTCTCCTTT CTTTC

36

(2) INFORMATION FOR SEQ ID NO:1098:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:

CTCTGTCTTG TTCTGGTCCT TCGTGGGGCT CTG

33

(2) INFORMATION FOR SEQ ID NO:1099:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:

TGTCGCGTGG GTGCGGCCGT GGCC

24

(2) INFORMATION FOR SEQ ID NO:1100:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:

GGCGGBCCBG GBGTTGGBGC BGGBCBGBB CGGGCBGGCG GTCBTGTTT GGBTCGGCBG  
GBGGCBCTC

60

69

(2) INFORMATION FOR SEQ ID NO:1101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:

TCTGGGGTGT CTG

14

## (2) INFORMATION FOR SEQ ID NO:1102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:

GCCTTCGTGG TTCC

14

## (2) INFORMATION FOR SEQ ID NO:1103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:

TCTTCCTTCG TTTGC

15

## (2) INFORMATION FOR SEQ ID NO:1104:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:

GGCTGCGCTC CTGCCCCGC

19

## (2) INFORMATION FOR SEQ ID NO:1105:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:

GGCTGCGCTC CTGCCCCGC

19

## (2) INFORMATION FOR SEQ ID NO:1106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106:

CTCTTTCCCG GGCTCTT

17

## (2) INFORMATION FOR SEQ ID NO:1107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107:

GCGCTGGGGG GTGCTCC

17

## (2) INFORMATION FOR SEQ ID NO:1108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:

CGTGTGTTTG CGCCCTCCTC CTGGTCGC

28

## (2) INFORMATION FOR SEQ ID NO:1109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:

GCTTGTCGTT TTGG

14

## (2) INFORMATION FOR SEQ ID NO:1110:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:  
GGCCGGCTTT GCCCGCTCC C 21

(2) INFORMATION FOR SEQ ID NO:1111:  
(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 16 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:  
GGCGCTGGC CCGGCC 16

(2) INFORMATION FOR SEQ ID NO:1112:  
(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:  
TTCCTGGGCT GCGTGCGC 18

(2) INFORMATION FOR SEQ ID NO:1113:  
(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:  
GTTCTGTTCT TCTCCTGGC 20

(2) INFORMATION FOR SEQ ID NO:1114:  
(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 78 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:  
GCBGGBGBCB GGGCBGGGCG BTCBGGBCB GCGTGBGCCB BBGGBGBCC BTCGGGBBCG 60  
CBGCTCCGGB BCGCBGGB 78

(2) INFORMATION FOR SEQ ID NO:1115:  
(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115:  
CTCTGGTTGG CTTCTTC 18

(2) INFORMATION FOR SEQ ID NO:1116:  
(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116:  
GCCGGCBGBT GCTBGCBBG BGGBCBGBGG GGGBBGCBGT TGGGBGGTGB GBCCCBTTBB 60  
TBGGTGTGCB 70

(2) INFORMATION FOR SEQ ID NO:1117:  
(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:  
TCTGCGCGCC CCTGCTCC 18

- (2) INFORMATION FOR SEQ ID NO:1118:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:  
CGCCCCGGCTT CTCT 14
- (2) INFORMATION FOR SEQ ID NO:1119:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:  
CGTGTGGGCT TCGG 14
- (2) INFORMATION FOR SEQ ID NO:1120:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 21 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:  
CCCCGCGCCT CCGTTGTTCT C 21
- (2) INFORMATION FOR SEQ ID NO:1121:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 15 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:  
TGCTCGCTGG GCTTG 15
- (2) INFORMATION FOR SEQ ID NO:1122:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 23 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:  
GGTTTCCTGG GGCCCTGGGT TTC 23
- (2) INFORMATION FOR SEQ ID NO:1123:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:  
TCTGCCGGGT CGTTTC 17
- (2) INFORMATION FOR SEQ ID NO:1124:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:  
GGGTGCTGGC TGCG 14
- (2) INFORMATION FOR SEQ ID NO:1125:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:  
CTTGGTGCTG GGGCTCC 17
- (2) INFORMATION FOR SEQ ID NO:1126:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:  
GGCGGCTGCG GGCTGGGTG GG 22

(2) INFORMATION FOR SEQ ID NO:1127:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:  
CTTGGCTGGT TCCTGGCCTC GGG 23

(2) INFORMATION FOR SEQ ID NO:1128:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:  
CCTCCTCCTC CTCCTCGCTC CCTTTTCTT CCTCT 35

(2) INFORMATION FOR SEQ ID NO:1129:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:  
TCCCTGCTGC TCTC 14

(2) INFORMATION FOR SEQ ID NO:1130:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:  
TGCCCTCCCT TCCTCCTGG 20

(2) INFORMATION FOR SEQ ID NO:1131:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:  
GGTGCCCTCCT TGGGCCCTGC 20

(2) INFORMATION FOR SEQ ID NO:1132:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:  
GGCTGCTCCT TGCCCC 16

(2) INFORMATION FOR SEQ ID NO:1133:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:  
CTCTGGGTGCG GGCTGGC 17

(2) INFORMATION FOR SEQ ID NO:1134:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear



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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134:  
GGGGCGTCTC TGTGC

15

(2) INFORMATION FOR SEQ ID NO:1135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135:  
CTGGCCTGGG TGCC

14

(2) INFORMATION FOR SEQ ID NO:1136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136:  
GCCTCTCCTG GGGGGTGGC TCCCTGTCC

29

(2) INFORMATION FOR SEQ ID NO:1137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137:  
CCTTTTCCCC CGGCTCC

17

(2) INFORMATION FOR SEQ ID NO:1138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:  
GTGGGGGCTT TGGC

14

(2) INFORMATION FOR SEQ ID NO:1139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:  
GGGGGTCTGT GGCTGCTCC TGGGG

25

(2) INFORMATION FOR SEQ ID NO:1140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140:  
AGGGGTCTGG GGCCCTC

17

(2) INFORMATION FOR SEQ ID NO:1141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141:  
TTTTGGGGGT CTGGCTTG

18

(2) INFORMATION FOR SEQ ID NO:1142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:  
GCCTGGCTGC CTTCC

15

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- (2) INFORMATION FOR SEQ ID NO:1143:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143:  
GGGGCCTGCC GTGGGGC 17
- (2) INFORMATION FOR SEQ ID NO:1144:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144:  
TGTCCTCTGT TGCTCCCCTT 20
- (2) INFORMATION FOR SEQ ID NO:1145:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:  
TGCTGCTGT CTGG 14
- (2) INFORMATION FOR SEQ ID NO:1146:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 16 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:  
GGTCCCGCC TTCCCT 16
- (2) INFORMATION FOR SEQ ID NO:1147:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 100 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:  
GTTCCCGAG CTTGCCACCT GCAGCAGGAC CAGGCAGCTC ACAGGGAACA GGAGCCCAGA 60  
GCAAAGCCAC CCCATTGGGA GATGCCAAGG CACCAGGCTG 100
- (2) INFORMATION FOR SEQ ID NO:1148:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 100 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:  
GTTCCCBGBG CTTGCCBCCT GCBGCBGGBC CBGGCBGCTC BCBGGGBBCB GGBGCCCBGB 60  
GCBGBGCCBC CCCBTGGGB GTGCCBBGG CBCCBGGCTG 100
- (2) INFORMATION FOR SEQ ID NO:1149:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 18 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:  
TCCCTGTTT CCCCTTT 18
- (2) INFORMATION FOR SEQ ID NO:1150:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 21 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:  
CGTTCTGCGT TTGCCTTTGG C 21

(2) INFORMATION FOR SEQ ID NO:1151:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:  
GTTTTTTGTT TGTTTTCT 18

(2) INFORMATION FOR SEQ ID NO:1152:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152:  
CTCTCCGTCT TTCTTCTCC 19

(2) INFORMATION FOR SEQ ID NO:1153:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153:  
CCTCCTGCCT GTGTCCTGC TCCCC 25

(2) INFORMATION FOR SEQ ID NO:1154:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154:  
GAGGGTTTCT GGCTTCTCT CT 22

(2) INFORMATION FOR SEQ ID NO:1155:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155:  
TGTCTCTCTG TCCTTTTGT 20

(2) INFORMATION FOR SEQ ID NO:1156:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156:  
TGTGTGCGG CCTGGTGCTG CCCTGCCCCG GG 32

(2) INFORMATION FOR SEQ ID NO:1157:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 89 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1157:  
GTGGGBBTTT CTGTGGGGBT GGCBTBCBG TBGGCBGCTC CBBGBGCTBG CBBBCTCBBB 60  
TGCBBBGC B TCTCBTGGC TCTGBBBCG 89

(2) INFORMATION FOR SEQ ID NO:1158:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158:  
GTGTGTCTTT GCTGT 15

(2) INFORMATION FOR SEQ ID NO:1159:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1159:  
TTCCTTTGCT CTTG 14
- (2) INFORMATION FOR SEQ ID NO:1160:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1160:  
GTGTGTCTTT GCTGT 15
- (2) INFORMATION FOR SEQ ID NO:1161:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161:  
GCCCTGCCTC TCTGC 15
- (2) INFORMATION FOR SEQ ID NO:1162:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162:  
GGGGGTGGCT TCCTGCC 17
- (2) INFORMATION FOR SEQ ID NO:1163:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1163:  
CGGTCTCTGG GCCGTCCC 18
- (2) INFORMATION FOR SEQ ID NO:1164:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1164:  
GTCCCTCGGC CCCGCGCCGC GCTCGGCTCC TCTCCC 36
- (2) INFORMATION FOR SEQ ID NO:1165:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1165:  
TCTGGCCCCG CTC 13
- (2) INFORMATION FOR SEQ ID NO:1166:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1166:  
GGGGCGGGGC GGGGCGGTGG GCGGGC 26
- (2) INFORMATION FOR SEQ ID NO:1167:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1167:  
GGCGCTGCCC TGCGC 15
- (2) INFORMATION FOR SEQ ID NO:1168:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1168:  
TGCTGGCCGT CGGCTGCGCG CTGCTGGCTG CCCT 34
- (2) INFORMATION FOR SEQ ID NO:1169:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1169:  
TGCTGGCCGT CGGCTGCGCG CTGCTGGCTG CCCT 34
- (2) INFORMATION FOR SEQ ID NO:1170:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1170:  
GCTGGCCGCG CCGGG 15
- (2) INFORMATION FOR SEQ ID NO:1171:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171:  
GCCTGTCCGC CTCTGCGGG 19
- (2) INFORMATION FOR SEQ ID NO:1172:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1172:  
CGCTGTCTCC TGGC 14
- (2) INFORMATION FOR SEQ ID NO:1173:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1173:  
TTGTCTCCG GCTCT 15
- (2) INFORMATION FOR SEQ ID NO:1174:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174:  
TCTGCTGGGG TGGG 14
- (2) INFORMATION FOR SEQ ID NO:1175:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175:

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GCTGGGCGGC CGGCCCGGT

19

(2) INFORMATION FOR SEQ ID NO:1176:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176:

GCTGGGGCTC CTCGGGGG

19

(2) INFORMATION FOR SEQ ID NO:1177:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1177:

GGGGGCTCTT CCGG

14

(2) INFORMATION FOR SEQ ID NO:1178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178:

GCTGTCTCCC TCCGGG

16

(2) INFORMATION FOR SEQ ID NO:1179:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179:

GCGGGGGTTT CTGGCC

16

(2) INFORMATION FOR SEQ ID NO:1180:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1180:

GTGGGGGTCT TGCC

14

(2) INFORMATION FOR SEQ ID NO:1181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1181:

TGGCCTCCGG GCTCC

15

(2) INFORMATION FOR SEQ ID NO:1182:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1182:

TGCTTGCTT GCCTTCCTC

20

(2) INFORMATION FOR SEQ ID NO:1183:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1183:

TCTGGTCGGT TGTGGCTCG

19

(2) INFORMATION FOR SEQ ID NO:1184:

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- (1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1184:  
GGGCTCCGTG GGTCCCTGGC 20
- (2) INFORMATION FOR SEQ ID NO:1185:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1185:  
GCCCCGTTTGT GTTTTGTC 18
- (2) INFORMATION FOR SEQ ID NO:1186:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1186:  
TTTTCCCTG GCGT 14
- (2) INFORMATION FOR SEQ ID NO:1187:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187:  
CCCTGTGCC CTCTCCTCTC CTCCTCTGC TTCTC 35
- (2) INFORMATION FOR SEQ ID NO:1188:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188:  
GCTCTCCTTT GTGGG 15
- (2) INFORMATION FOR SEQ ID NO:1189:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189:  
GCCCTCCCTG CTGCT 15
- (2) INFORMATION FOR SEQ ID NO:1190:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190:  
CTTGGTTTTG GGCT 14
- (2) INFORMATION FOR SEQ ID NO:1191:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1191:  
TTTTTCTCT TCCTCCTTT TC 22
- (2) INFORMATION FOR SEQ ID NO:1192:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1192:  
GTGCGTGGGC CTCC

14

(2) INFORMATION FOR SEQ ID NO:1193:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1193:  
CCCGGGCGC

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(2) INFORMATION FOR SEQ ID NO:1194:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 150 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1194:  
GCACGCCTCT TGCCACCTCC TGCGCAGGGC AGCGCCTTGG GGCCAGCGCC GCTCCCGGCG  
CGGCCAGCAG GGCAGCCAGC AGCGCGCAGC CGACGGCCAG CATGCTTCCT CCTCGGCTAC  
CACTCCATGG TCCCGCAGAG GCGGACAGGC

60  
120  
150

(2) INFORMATION FOR SEQ ID NO:1195:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195:  
GGCCBGCBBG

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(2) INFORMATION FOR SEQ ID NO:1196:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 150 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196:  
GCBGCGCTCT TGCCBCCTCC TGCGCBGGGC BGCGCCTTGG GGCCBGC GCC GCTCCCGGCG  
CGGCCBGCBG GGCBCGCBGC BGCGCGCBGC CGBGCGCCBG CBTGCTTCCT CCTCGGCTBC  
CBCTCCBTGG TCCCGCBGBG GCGGBCBGGC

60  
120  
150

(2) INFORMATION FOR SEQ ID NO:1197:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1197:  
GCTTCTCTTT CGTTCCCGGT GGGCTCG

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(2) INFORMATION FOR SEQ ID NO:1198:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1198:  
GTGGCTGTCT GTGTGGGGCG GCT

23

(2) INFORMATION FOR SEQ ID NO:1199:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1199:  
GTGCCTCTTT GCTGCTTC

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- (2) INFORMATION FOR SEQ ID NO:1200:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1200:  
GATTCTTTGC CTTTTTCTGC 20
- (2) INFORMATION FOR SEQ ID NO:1201:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1201:  
GCTTGCTGTGC TCTGCTGTCT CT 22
- (2) INFORMATION FOR SEQ ID NO:1202:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1202:  
TGGTTCCTTC CGGTGGTTC TTCCTGGCTC TTGTCCT 37
- (2) INFORMATION FOR SEQ ID NO:1203:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1203:  
TTCTCTTGGC CCTTGGC 17
- (2) INFORMATION FOR SEQ ID NO:1204:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1204:  
TGGTGGGGCT GGGGCTCCGG GGTCTGTGCC CCTCCGTGC 39
- (2) INFORMATION FOR SEQ ID NO:1205:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1205:  
CGCGTGGGGC CGCGCTCGCC GGCCCCC 28
- (2) INFORMATION FOR SEQ ID NO:1206:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1206:  
CCTGCCGGGT GGGCTCCGC CGCG 24
- (2) INFORMATION FOR SEQ ID NO:1207:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1207:  
CGCCGGCCTG CCGGCCCTC 20
- (2) INFORMATION FOR SEQ ID NO:1208:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1208:  
GTGGGTCCTG CTGGCCGGGT CCGGGTCCCG GGGGTGGGG

39

(2) INFORMATION FOR SEQ ID NO:1209:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1209:  
CGCGBGTCGG CGGCCBGGG TC

22

(2) INFORMATION FOR SEQ ID NO:1210:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1210:  
GGCCTCCBCC BGGGBCBTG

19

(2) INFORMATION FOR SEQ ID NO:1211:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1211:  
GTCCTTCTTG TCCGCTGCC

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(2) INFORMATION FOR SEQ ID NO:1212:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1212:  
TCTCTGGGGT TTTCGGTCTG GGTGG

25

(2) INFORMATION FOR SEQ ID NO:1213:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1213:  
GCTTTCCTCC TGGGGCTGCT GCTG

24

(2) INFORMATION FOR SEQ ID NO:1214:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214:  
GGCTCTTCTT TTTGTTCTG GCCTGGTG

28

(2) INFORMATION FOR SEQ ID NO:1215:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215:  
CTCTCTCGTG CCCTTTCC

18

(2) INFORMATION FOR SEQ ID NO:1216:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1216:  
CTTGGGTGTC TTGTTTTTGT 20

(2) INFORMATION FOR SEQ ID NO:1217:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 bas pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1217:  
GGCCTCCBCC BGGGBCBTG 19

(2) INFORMATION FOR SEQ ID NO:1218:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1218:  
GTGGGGCCTG CTCTCCCGGC CTCCG 25

(2) INFORMATION FOR SEQ ID NO:1219:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1219:  
TGTGTTGCTG GGTGTTTTCC CGTCTCTGG 29

(2) INFORMATION FOR SEQ ID NO:1220:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1220:  
TCTGCCTTCG GGGGTCGT 18

(2) INFORMATION FOR SEQ ID NO:1221:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1221:  
GGGTCCTCBT GGCTGGGG 18

(2) INFORMATION FOR SEQ ID NO:1222:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1222:  
GCCTGGGCCT GCBGGGCC 18

(2) INFORMATION FOR SEQ ID NO:1223:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1223:  
GCTCTGCTCCT GGBGTGGCTC 20

(2) INFORMATION FOR SEQ ID NO:1224:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1224:  
GCCCCBGBGTC TTCCTGGT

19

(2) INFORMATION FOR SEQ ID NO:1225:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1225:  
GGGTCCTCBT GGCTGGGGTC

20

(2) INFORMATION FOR SEQ ID NO:1226:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226:  
CCTCTCTCCC GTCCT

15

(2) INFORMATION FOR SEQ ID NO:1227:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227:  
GTCTTTGTTT CTGGGCTCGT GCC

23

(2) INFORMATION FOR SEQ ID NO:1228:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228:  
CCBTCCCGGC TTCTCTCTGG TTCC

24

(2) INFORMATION FOR SEQ ID NO:1229:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1229:  
GTCTCTGTG GTGTTTG

18

(2) INFORMATION FOR SEQ ID NO:1230:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1230:  
CCCTGCTTCC TTTGCTGT T

21

(2) INFORMATION FOR SEQ ID NO:1231:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 85 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1231:  
GAGGGGGCAG CAGTTGGGCC CCAAAGGCCC TCTCGTTCAC CTTCTGGCAC GGAGTTGCAT  
CCCATAGTC AAACCTCTGTG GTCGT

60  
85

(2) INFORMATION FOR SEQ ID NO:1232:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1232:  
GTCATAGTCC TCTGTGGTGT TTGGAGTTTC CATCCCGGCT TCTCTCTGGT TCCAAGGGA 59
- (2) INFORMATION FOR SEQ ID NO:1233:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 86 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1233:  
GBGGGGGCBG CBGTTGGGCC CCBBBGGCCC TCTCGTTCBC CTTCTGGCBC GGBGTTGCBT 60  
CCCCBTBGTG BBBCTCTGTG GTCGTG 86
- (2) INFORMATION FOR SEQ ID NO:1234:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234:  
TCBTBGTCTT CTGTGGTGTG TGGBTGTTCC BTCCCGGCTT CTCTCTGGTT CCBBGGGB 58
- (2) INFORMATION FOR SEQ ID NO:1235:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 84 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1235:  
GGGCBGCGGG CBGTGGGCGG GCBTGTBGG CBBBGBGCB GGGTGTGGTG TCCGBGGBBT 60  
BTGGGGBGCG BGBTGCBGGB GCGC 84
- (2) INFORMATION FOR SEQ ID NO:1236:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 78 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236:  
BGBGGGCBGT BGCBTGBGG BTGBCBGCGB GGCCTGCCGC GGBGBCCTTC BTGGTBCCTG 60  
TGGBGGBGGCT GTCGGBGG 78
- (2) INFORMATION FOR SEQ ID NO:1237:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1237:  
GGGTGTGGTG TCCGCTTGGC GGTCTTTTCG GGTGTTTCTT CTCTGGGTTG GCCTGCTGCT 60  
CGTCGTGGTC 70
- (2) INFORMATION FOR SEQ ID NO:1238:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 71 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1238:  
GCTCCGCTCC CGGGTTCGTC TCGCTCTGTC GCCCCTTCCT TCCTTGTCGT GTTCCTCCCT 60  
TCCTTGCCCTC T 71
- (2) INFORMATION FOR SEQ ID NO:1239:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1239:  
GGGTGTGGTG TCCG

14

- (2) INFORMATION FOR SEQ ID NO:1240:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1240:  
CTTGGCGGTT CTTTCGGGTG

20

- (2) INFORMATION FOR SEQ ID NO:1241:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1241:  
TTTCTTCTCT GGGTTGGC

18

- (2) INFORMATION FOR SEQ ID NO:1242:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242:  
CTGCTGCTCG TCGTGGTC

18

- (2) INFORMATION FOR SEQ ID NO:1243:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243:  
GCTCCGCTCC CGGGTTC

17

- (2) INFORMATION FOR SEQ ID NO:1244:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1244:  
GTCTCGCTCT GTCGCCC

17

- (2) INFORMATION FOR SEQ ID NO:1245:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245:  
CTTCCTTCT TGTC

14

- (2) INFORMATION FOR SEQ ID NO:1246:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246:  
GTGTTCTCC CTTCTTGCC TCT

23

- (2) INFORMATION FOR SEQ ID NO:1247:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247:  
GTTCTGGTG GCTBGGTGGG GC

22

- (2) INFORMATION FOR SEQ ID NO:1248:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 26 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248:  
GCTGCCCCGGC GGGGTGTGCG CTTGGC 26
- (2) INFORMATION FOR SEQ ID NO:1249:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 30 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249:  
GCTCCCGTGC TCGGTTCTCT GTCTCCCGGT 30
- (2) INFORMATION FOR SEQ ID NO:1250:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250:  
CCCCCTTTGC CTGGCGTCTC GG 22
- (2) INFORMATION FOR SEQ ID NO:1251:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 29 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1251:  
GCCTTCGTCC TCTTCCTCTT CTTCTTCC 29
- (2) INFORMATION FOR SEQ ID NO:1252:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 43 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252:  
GCTCCGTGGG GGCTGCTTGG TGGGGGCCTG TGCCTCGGGG TCC 43
- (2) INFORMATION FOR SEQ ID NO:1253:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253:  
CGGGGCTTCT GGCCCTTGCC 20
- (2) INFORMATION FOR SEQ ID NO:1254:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254:  
GTTTCATGGTG GCTAGGTGGG GC 22
- (2) INFORMATION FOR SEQ ID NO:1255:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 24 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255:  
GGGGTGGGTB GGCCGTGTCT GGGG 24
- (2) INFORMATION FOR SEQ ID NO:1256:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1256:  
GTTGGCCBTG TTGTTGCC

19

(2) INFORMATION FOR SEQ ID NO:1257:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1257:  
TCTTGGTGGT GCGCCGGG

19

(2) INFORMATION FOR SEQ ID NO:1258:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 47 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1258:  
GCGTCTTGGC TTTCTTCTCC TCGGGCCCT CGGGCCGGTG CTTGTGG

47

(2) INFORMATION FOR SEQ ID NO:1259:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1259:  
GCTCCTCCCG GCGGCCTCC CCGGCGGGG GCTTCTTG

38

(2) INFORMATION FOR SEQ ID NO:1260:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1260:  
GCGCTGGCGG GGGGGCTCC TCC

23

(2) INFORMATION FOR SEQ ID NO:1261:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1261:  
GCTCTGTGGC TGGCGTTCC TTGGTGTCT GGGTGGC

37

(2) INFORMATION FOR SEQ ID NO:1262:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262:  
TGGCGGGCGT GGTGGCCTCT GTGGTGG

27

(2) INFORMATION FOR SEQ ID NO:1263:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1263:  
GGGCCCCGCG CTGCBGGG

19

(2) INFORMATION FOR SEQ ID NO:1264:  
(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1264:  
TTGCCTGTCT GCTTCGTC

18

- (2) INFORMATION FOR SEQ ID NO:1265:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265:  
CTTTGCGCTC CCGGGCCGCC

20

- (2) INFORMATION FOR SEQ ID NO:1266:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 24 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266:  
GGGGTGGGTA GGCCGTGTCT GGGG

24

- (2) INFORMATION FOR SEQ ID NO:1267:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 19 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267:  
GTTGGCCATG TTGTTGCC

19

- (2) INFORMATION FOR SEQ ID NO:1268:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 19 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268:  
GGGCCCCGGG CTGCAGGGG

19

- (2) INFORMATION FOR SEQ ID NO:1269:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 17 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1269:  
CGGTTTCCTT TCGGTC

17

- (2) INFORMATION FOR SEQ ID NO:1270:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 19 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270:  
TTGGCCCCGGG CTCCGGTG

19

- (2) INFORMATION FOR SEQ ID NO:1271:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 23 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271:  
CCCCCCCCGC CGCCGGCCGC CGC

23

- (2) INFORMATION FOR SEQ ID NO:1272:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 27 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1272:  
CCCGCCGGGC TGTCCCCGCC CCGCCCC 27

(2) INFORMATION FOR SEQ ID NO:1273:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1273:  
GGCCCCGGGC GCGGGG 17

(2) INFORMATION FOR SEQ ID NO:1274:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1274:  
CGGCCCTCCC GCCCTCTGG 20

(2) INFORMATION FOR SEQ ID NO:1275:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1275:  
CGCGGCGCGG GCGTCGG 17

(2) INFORMATION FOR SEQ ID NO:1276:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276:  
CCGCTCGCGC CTGGGGTTCC CTCTCCTCCC CCTGTGC 37

(2) INFORMATION FOR SEQ ID NO:1277:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277:  
GCCTGCCTCT TGCTCTTC 18

(2) INFORMATION FOR SEQ ID NO:1278:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1278:  
TGCGTCCGCT GCCTTCTCCC 20

(2) INFORMATION FOR SEQ ID NO:1279:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279:  
CTCTCCTCGG CCGTTGCTG TGC 23

(2) INFORMATION FOR SEQ ID NO:1280:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1280:  
TGTCCGTCCT GTCGCCCTTC CGTGGTGC 28

- (2) INFORMATION FOR SEQ ID NO:1281:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281:  
TGTTGTCTCT TCTGCCCTC 19
- (2) INFORMATION FOR SEQ ID NO:1282:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1282:  
GGTGTGCTGG TGCTGGTGGT GGTG 24
- (2) INFORMATION FOR SEQ ID NO:1283:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283:  
CCTCTGCCCG TGCTCGCC 18
- (2) INFORMATION FOR SEQ ID NO:1284:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284:  
CTGCCCTGGGC TGGCCTCTTC GGGT 24
- (2) INFORMATION FOR SEQ ID NO:1285:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1285:  
GTGGCTTTGG GGCTCTTTG GTGCCCTTT 30
- (2) INFORMATION FOR SEQ ID NO:1286:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1286:  
CTTCTCGTGG TGCCTCTCCT CCCTGGCTTG GTCGT 35
- (2) INFORMATION FOR SEQ ID NO:1287:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287:  
TGTCTGGGGT GGTGCTCCTC TCCC 24
- (2) INFORMATION FOR SEQ ID NO:1288:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1288:  
TTTCCCTGCT GGCCGTTTGT 20
- (2) INFORMATION FOR SEQ ID NO:1289:  
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1289:  
CCTGTTTCT GTCTTCCTCT 20
- (2) INFORMATION FOR SEQ ID NO:1290:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1290:  
TTCTCTCTGT TTCTCCGT 18
- (2) INFORMATION FOR SEQ ID NO:1291:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291:  
TTGGCTTGCT GCTTGCGGG CTGTCTCC 28
- (2) INFORMATION FOR SEQ ID NO:1292:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1292:  
CTTGCCCTG TGGCTTTCC C 21
- (2) INFORMATION FOR SEQ ID NO:1293:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1293:  
TGGTCCGGTC TTCTCCTTG GGGTC 25
- (2) INFORMATION FOR SEQ ID NO:1294:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1294:  
GCCCTTCTTG GTGGGCTG 18
- (2) INFORMATION FOR SEQ ID NO:1295:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1295:  
GCTCGTCTGT CTTTTCTT CC 22
- (2) INFORMATION FOR SEQ ID NO:1296:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296:  
TGGGGGTGGC CGTTGTGGC GGTGTGGTCC GCCT 34
- (2) INFORMATION FOR SEQ ID NO:1297:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297:  
TGCCTCTGCT GGTCTTTC 18
- (2) INFORMATION FOR SEQ ID NO:1298:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298:  
GTGCTCCGGT GGCTTTTT 18
- (2) INFORMATION FOR SEQ ID NO:1299:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1299:  
GCTTGTGTGC TCTGCTGTCT CTG 23
- (2) INFORMATION FOR SEQ ID NO:1300:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1300:  
TTCCTTCCGG TGGTTTCTTC CTGGCTCTTG TCCT 34
- (2) INFORMATION FOR SEQ ID NO:1301:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1301:  
TTCTCTTGGC CCTTGGCCC 19
- (2) INFORMATION FOR SEQ ID NO:1302:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1302:  
TGGCTCGGTG CTTCTGCCCC 20
- (2) INFORMATION FOR SEQ ID NO:1303:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1303:  
TGTTGTTGCG GCGCTC 16
- (2) INFORMATION FOR SEQ ID NO:1304:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1304:  
GGTTGGTGTG GCCCCTG 17
- (2) INFORMATION FOR SEQ ID NO:1305:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1305:  
TGGTGCTTCG TTCC 15

- (2) INFORMATION FOR SEQ ID NO:1306:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1306:  
CCCTCTTTCT CTTTGTTTC 18
- (2) INFORMATION FOR SEQ ID NO:1307:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1307:  
GGGGGTTCTT GTGGC 15
- (2) INFORMATION FOR SEQ ID NO:1308:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1308:  
GGGCTGCTTG TCTCGTTCC 19
- (2) INFORMATION FOR SEQ ID NO:1309:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1309:  
GGTCCBGCCB TGGGTCTGGG 20
- (2) INFORMATION FOR SEQ ID NO:1310:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1310:  
GGCTGGGCTG CBGGCTCCGG 20
- (2) INFORMATION FOR SEQ ID NO:1311:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1311:  
GCGGGCGGGT GCGGGCTGCG TGCTGGG 27
- (2) INFORMATION FOR SEQ ID NO:1312:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1312:  
GGCTGCCCGG CAGGCCCTGC 20
- (2) INFORMATION FOR SEQ ID NO:1313:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 115 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1313:  
GCBCCGCGCTG GBGCCCTGGG GCCCCCTGT CTCTTGGGG BCGGCCTCCT CGGCCBGCTC 60

CBGCTCCCGG BTCBTGCTTT CBGTGCTCBT GGTGTCCTTT CCBGGGGGBG GBGGG

115

(2) INFORMATION FOR SEQ ID NO:1314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1314:

GCTGGTCCTC	TGCTGTCCTT	GCTGGTGCTC	BTGGTGTCTT	TTCCGCCCTG	GGGCCCCCTT	60
GTCTTCTTGG	GGCCTCTTCC	CTCTGGGGGC	CGTCTCTCTC	CCTCTCTTGC	GTCTCTCTCT	120
TTCTCTCTCT	CTCTTCCCTT	TTCCCGCTCT	TTCTGTCTCG	GTGTCTGGTT	TTCTCTCTCC	180
GCTGGCTGCC	TGTCTGGCCT	GCGCTCTTGG	CCTGTGCTGT	TCCTCCTCCG	GTTCTGTCC	240
TCTCTGTCTG	TCGCCCCCTC	TGGGGTCTCC	CTCTGGCGTG	GTGGTCTTGT	TGCTTGGGCT	300
GGGCTCCGTG	TCTCCBTGC	TCTGGGTGTC				331

(2) INFORMATION FOR SEQ ID NO:1315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1315:

GCTGBGGGBG	CGTCTGCTGG	CGCTGGTCCT	CTGCTGTCCT	TGCTGGTGCT	CBTGGTGTCC	60
TTTCCGCCCT	GGGCCCCCCC	TGTCTTCTTG	GGGCCTCTTC	CCTCTGGGGG	CCGTCTCTCT	120
CCCTCTCTTG	CGTCTCTCTC	TTTCTCTCTC	TCTCTTCCCC	TTTCCCGCTC	TTTCTGTCTC	180
GGTGTCTGGT	TTTCTCTCTC	CGCTGGCTGC	CTGTCTGGCC	TGCGCTCTTG	GCCTGTGCTG	240
TTCTCTCTCC	GGTTCCTGTC	CTCTCTGTCT	GTGCCCCCTT	CTGGGGTCTC	CCTCTGGGCT	300
GGTGTCTTGG	TTGCTTGGGC	TGGGCTCCGT	GTCTCCBTGC	CTCBTGGTGT	CCGCTGBGGG	360
BGGCTCTGCT	GGC					373

(2) INFORMATION FOR SEQ ID NO:1316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316:

GCCCCGTCTG	CTGCTCCTCG	TGCCG	25
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(2) INFORMATION FOR SEQ ID NO:1317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1317:

CCTCGTCCTT	CATGGTACCG	TCGGTGTGGT	GGC	33
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(2) INFORMATION FOR SEQ ID NO:1318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1318:

CTCGGGTGGG	CCGGTGGTG	19
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(2) INFORMATION FOR SEQ ID NO:1319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1319:

GGGCGCGCGC	GCTCGCGT	18
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(2) INFORMATION FOR SEQ ID NO:1320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1320:  
GGCTCCGGCT CTTCTTTCCC GGCTCCGTCG GCCCGGGGGC CTTGGTCTC

49

(2) INFORMATION FOR SEQ ID NO:1321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321:  
CCTCGTCCTT CBTGGTBCCG

20

(2) INFORMATION FOR SEQ ID NO:1322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1322:  
CCCGTTCGCC TGGCGC

16

(2) INFORMATION FOR SEQ ID NO:1323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1323:  
GCGCTCGGGG TTCCTC

16

(2) INFORMATION FOR SEQ ID NO:1324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1324:  
GTGGGTTTCT CCCC GCCGTT CTC

23

(2) INFORMATION FOR SEQ ID NO:1325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1325:  
CGGTCTGTTG CCTTTGTGGG

20

(2) INFORMATION FOR SEQ ID NO:1326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326:  
CTTCTTGTCT TTTTGGCT

18

(2) INFORMATION FOR SEQ ID NO:1327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:  
GTTCTTTTCC TGCTTGGC

18

(2) INFORMATION FOR SEQ ID NO:1328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1328:  
GTCTTTTCCT TTCTT

15



- (2) INFORMATION FOR SEQ ID NO:1329:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1329:  
TGTGCTCGGT TGTGGGTC 18
- (2) INFORMATION FOR SEQ ID NO:1330:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1330:  
CGCTGGTCCT TTGCC 15
- (2) INFORMATION FOR SEQ ID NO:1331:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1331:  
CTGTGTGTTT CTGCTG 16
- (2) INFORMATION FOR SEQ ID NO:1332:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1332:  
CCCCGTCGCC TGGCGC 16
- (2) INFORMATION FOR SEQ ID NO:1333:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1333:  
GCGCTGCGGG TTCCTC 16
- (2) INFORMATION FOR SEQ ID NO:1334:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1334:  
GTGGGTTTCT CCCC GCCGTT CTC 23
- (2) INFORMATION FOR SEQ ID NO:1335:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1335:  
CGGTCTGTTG CCTTTGTGGG 20
- (2) INFORMATION FOR SEQ ID NO:1336:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1336:  
CTTCTGTCT TTTGGCT 18
- (2) INFORMATION FOR SEQ ID NO:1337:  
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1337:  
GTTCTTTTCC TGCTGGC 18
- (2) INFORMATION FOR SEQ ID NO:1338:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1338:  
GTCTTTTCCT TTCTT 15
- (2) INFORMATION FOR SEQ ID NO:1339:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1339:  
TGTGCTCGGT TGTGGGTC 18
- (2) INFORMATION FOR SEQ ID NO:1340:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1340:  
CGCTGGTCCT TTGCC 15
- (2) INFORMATION FOR SEQ ID NO:1341:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1341:  
CTGTGTGTTT CTGCTG 16
- (2) INFORMATION FOR SEQ ID NO:1342:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342:  
GCGTCCGGTG GCCGCCGC 18
- (2) INFORMATION FOR SEQ ID NO:1343:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1343:  
GCCTCTCTCC TCTCCCC 17
- (2) INFORMATION FOR SEQ ID NO:1344:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1344:  
GTGGCCCTGT CGGGCGGG 18
- (2) INFORMATION FOR SEQ ID NO:1345:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1345:  
TCCTGCCGTC CTGTCTCCTT T 21
- (2) INFORMATION FOR SEQ ID NO:1346:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1346:  
TCTTTTGCTG TCTTGT 16
- (2) INFORMATION FOR SEQ ID NO:1347:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1347:  
CTTCCCGTCT CTGCTTT 17
- (2) INFORMATION FOR SEQ ID NO:1348:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1348:  
GTCTGTCTC CCCGTCTCCT CCC 23
- (2) INFORMATION FOR SEQ ID NO:1349:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349:  
ACTGCTTCTC CCGGGG 16
- (2) INFORMATION FOR SEQ ID NO:1350:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1350:  
GCTTCCCCGG CTTC 14
- (2) INFORMATION FOR SEQ ID NO:1351:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1351:  
GGGTGGCCGG TGTCCGGGC TCCGGCGCGG CGGC 34
- (2) INFORMATION FOR SEQ ID NO:1352:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1352:  
GGCTTCGGCT GC 12
- (2) INFORMATION FOR SEQ ID NO:1353:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1353:  
GGGTGGGTGG CGCGG 15

- (2) INFORMATION FOR SEQ ID NO:1354:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1354:  
GCTGCCGGGT CCGCGCGGCG CCTGGGCC 28
- (2) INFORMATION FOR SEQ ID NO:1355:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1355:  
CTTGTGCTGC TTTT 14
- (2) INFORMATION FOR SEQ ID NO:1356:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1356:  
TGCTTGTTCC GTTC 14
- (2) INFORMATION FOR SEQ ID NO:1357:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1357:  
TGGCTGCTCC GGTCTGTGTT GTGGTTGTTT TG 32
- (2) INFORMATION FOR SEQ ID NO:1358:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1358:  
TTTCTTCTTG GGTGTGGG 18
- (2) INFORMATION FOR SEQ ID NO:1359:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1359:  
CCTTGCGGTT TTGG 14
- (2) INFORMATION FOR SEQ ID NO:1360:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1360:  
CTGTGGGCC TTTG 14
- (2) INFORMATION FOR SEQ ID NO:1361:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1361:  
GGGCCTTGGC TTCTGGCTC 19
- (2) INFORMATION FOR SEQ ID NO:1362:  
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1362:  
CATCCACATG ATTGCTTAGA TTTGTGCTGT ATCTCTCAGG ATTATCACTG ATTACACATC 60  
CAACCAAGTGC CAGCCAAAAG GATGCCCTGA GGCAAAGGT TTCCATCTTG AGGCAAATTT 120  
GAGGA 125

(2) INFORMATION FOR SEQ ID NO:1363:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 125 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1363:  
CBTCCBCBTG BTTGCTTBGB TTTGTGCTGT BTCTCTCBGG BTTBTCBCTG BTTBCBCBTC 60  
CBCCBGTGC CBGCCBBBG GBTGCCCTGB GGCBGGGGT TTCCBTCTTG BGGCBBBTTT 120  
GBGG 125

(2) INFORMATION FOR SEQ ID NO:1364:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1364:  
CGTGGTCGCT CCGC 14

(2) INFORMATION FOR SEQ ID NO:1365:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1365:  
GTTTCTCTGG TTCCTCCG 18

(2) INFORMATION FOR SEQ ID NO:1366:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1366:  
GTCCCGCGGG GTGCTG 16

(2) INFORMATION FOR SEQ ID NO:1367:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1367:  
TCTGGTCGCT GTCGT 15

(2) INFORMATION FOR SEQ ID NO:1368:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1368:  
GGCTTGGGTC TCCGGGCG 18

(2) INFORMATION FOR SEQ ID NO:1369:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1369:  
GTTTCCTTCC TTTTCCGC 18

- (2) INFORMATION FOR SEQ ID NO:1370:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1370:  
GTCCTGTCGT GCGCCTGGG GCTC 24
- (2) INFORMATION FOR SEQ ID NO:1371:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1371:  
TTCTTTTGTG GGCT 14
- (2) INFORMATION FOR SEQ ID NO:1372:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1372:  
CTTTGGTGGC TGTGGCTG 18
- (2) INFORMATION FOR SEQ ID NO:1373:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1373:  
TGGTCTCTGT GGTG 15
- (2) INFORMATION FOR SEQ ID NO:1374:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1374:  
CTGCCCTGGG TCTGG 15
- (2) INFORMATION FOR SEQ ID NO:1375:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1375:  
GGGTGTGGCC TTGGGGCCGT CCTCTGGCTC CTCCTCGTGG GCCCCC 46
- (2) INFORMATION FOR SEQ ID NO:1376:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 265 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1376:  
GGGCTAAGAT GATCCACATC ACTACCACGT TGCCCAACAC AGAGGTCACC ACAATGACCG 60  
TGTAGGCAGC TGCCCAAAGG ACAATTTGCC AGGCTGGTTG CACGAAGTGA TTGGGTTCCG 120  
AGGTGTTAGT GGAGATGTTT GGGGAGAGGT CTGAGTCCAC CGGGAGGACG TTATCCATTT 180  
CGAAGCTAGG CGGTAAAGCC CTACTATCTG TACACAACCC CCCTCTGCAG CAGAGTCCTG 240  
TCGTGGCGCC TGGGGCTCAG GGTCC 265
- (2) INFORMATION FOR SEQ ID NO:1377:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 265 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1377:

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GGGCTBBGBT	GBTCCBCBTC	BCTBCCBCGT	TGCCCBCBC	BGBGGTCBCC	BCBBTGBCCG	60
TGTBGGCBGC	TGCCCCBBBG	BCBBTTTGCC	BGGCTGGTTG	CBCGBBCTGB	TTGGGTTCCG	120
BGGTGTBTGT	GGGBGTGTTT	GGGGBGGGT	CTGBGTCCBC	CGGGBGGBCG	TTBTCCBTTT	180
CGBBGCTBGG	CGGTBBBGCC	CTBCTBTCTG	TBCBCBCCCC	CCCTCTGCBG	CBGBGTCCTG	240
TCGTGGCGCC	TGGGGCTCBG	GGTCC				265

## (2) INFORMATION FOR SEQ ID NO:1378:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1378:

CGTTTTCTTC TCTC

14

## (2) INFORMATION FOR SEQ ID NO:1379:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1379:

GCTGGTTTTC CTTTCC

16

## (2) INFORMATION FOR SEQ ID NO:1380:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1380:

TGGCAGTGGG TGGGGGTGGG GGTGGGTGG C

31

## (2) INFORMATION FOR SEQ ID NO:1381:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1381:

TTCCTTGTTT CTGGGGGTGT CCT

23

## (2) INFORMATION FOR SEQ ID NO:1382:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1382:

CTTGCTCTGG GCTTTTCT

18

## (2) INFORMATION FOR SEQ ID NO:1383:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1383:

CCCCTTTTC TTCC

14

## (2) INFORMATION FOR SEQ ID NO:1384:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1384:

TGTCTGTTTT CTGGGG

17

## (2) INFORMATION FOR SEQ ID NO:1385:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1385:  
CTCTCCTCTG TCTCTGTGT

19

(2) INFORMATION FOR SEQ ID NO:1386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1386:  
CCTTGCCCTG GCCC

14

(2) INFORMATION FOR SEQ ID NO:1387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1387:  
TCTTCCCTCT CCTGTCTCT GT

22

(2) INFORMATION FOR SEQ ID NO:1388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1388:  
CCCTGTGTTC CGCCC

15

(2) INFORMATION FOR SEQ ID NO:1389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1389:  
GTCTTCCCTC TCCTG

15

(2) INFORMATION FOR SEQ ID NO:1390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1390:  
ACCTCCTTTT CCTCCG

16

(2) INFORMATION FOR SEQ ID NO:1391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1391:  
CTGGGTGGGG CCCTG

15

(2) INFORMATION FOR SEQ ID NO:1392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1392:  
CCTGTTCTCT GCTCCC

16

(2) INFORMATION FOR SEQ ID NO:1393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1393:  
TGGCTTGGGG TTTCTTCTG

19



- (2) INFORMATION FOR SEQ ID NO:1394:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 19 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1394:  
TGTGTCTTCT TCCTCTGTT 19
- (2) INFORMATION FOR SEQ ID NO:1395:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1395:  
GGCTGGCTTT CTCCTTC 17
- (2) INFORMATION FOR SEQ ID NO:1396:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 15 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1396:  
TTTTGTCTTC CTGGG 15
- (2) INFORMATION FOR SEQ ID NO:1397:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1397:  
TGCCCCCTTCT TCCTTCTTG GG 22
- (2) INFORMATION FOR SEQ ID NO:1398:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1398:  
TCCTTGGTGC TTGGGCTGGG 20
- (2) INFORMATION FOR SEQ ID NO:1399:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 19 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1399:  
CTGTGCGTCC GTCTGCTGG 19
- (2) INFORMATION FOR SEQ ID NO:1400:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 31 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1400:  
GGGGCCGGGG TGGCTGGGCC CTGCTGCCG C 31
- (2) INFORMATION FOR SEQ ID NO:1401:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 21 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1401:  
ACGACCCCGG GCCGACCCGA G 21
- (2) INFORMATION FOR SEQ ID NO:1402:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 31 base pairs

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1402:  
GCTCGGGGGG CTGTGTTCTG GCGCTGGTGG G 31
- (2) INFORMATION FOR SEQ ID NO:1403:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1403:  
CTTGGGCCCC TCTGGGGGCT GGGTT 25
- (2) INFORMATION FOR SEQ ID NO:1404:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1404:  
TCCTGCTGCG CCTGGGCGCT G 21
- (2) INFORMATION FOR SEQ ID NO:1405:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1405:  
GCGTCTTGGG GTGC 14
- (2) INFORMATION FOR SEQ ID NO:1406:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1406:  
GGGGCCGGGG GGCCGGGGG 19
- (2) INFORMATION FOR SEQ ID NO:1407:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1407:  
GCCGCTGTTC GTGGGCTGG G 21
- (2) INFORMATION FOR SEQ ID NO:1408:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408:  
GGTGCCTGTG GCTGCC 16
- (2) INFORMATION FOR SEQ ID NO:1409:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1409:  
GGTTGCCCCG GTTGTGGC 19
- (2) INFORMATION FOR SEQ ID NO:1410:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1410:  
GCCGTCCTGC TGCCGGT

17

(2) INFORMATION FOR SEQ ID NO:1411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1411:  
CGTTGGCTGG GTCCCCCGC

20

(2) INFORMATION FOR SEQ ID NO:1412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1412:  
CCGTTTCCTG GGGTCC

16

(2) INFORMATION FOR SEQ ID NO:1413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1413:  
GCGTGGGGTG CTCC

14

(2) INFORMATION FOR SEQ ID NO:1414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1414:  
GGTTCCTCGT GCCG

14

(2) INFORMATION FOR SEQ ID NO:1415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1415:  
CTGCTGCCTT GTCTTTCC

18

(2) INFORMATION FOR SEQ ID NO:1416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1416:  
GGCCGTGGCG GCGTGGTGGT CC

22

(2) INFORMATION FOR SEQ ID NO:1417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1417:  
GCCCCCCTG GCCTTCTGCT C

21

(2) INFORMATION FOR SEQ ID NO:1418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1418:  
GGGGTCTGGC TGGT

14

- (2) INFORMATION FOR SEQ ID NO:1419:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 19 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1419:  
TGCCCGGTGCC CTTGGCGGC 19
- (2) INFORMATION FOR SEQ ID NO:1420:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 16 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1420:  
GGTCTTCTTC CTGGTG 16
- (2) INFORMATION FOR SEQ ID NO:1421:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 23 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1421:  
GCTCTGGGCC CGGCCGTCT CGG 23
- (2) INFORMATION FOR SEQ ID NO:1422:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1422:  
CGGTCTCGTG TTCG 14
- (2) INFORMATION FOR SEQ ID NO:1423:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1423:  
CTCTTGCTGT GTCCGCCG 20
- (2) INFORMATION FOR SEQ ID NO:1424:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1424:  
CTCCTTCCTC TTCCGCCG 20
- (2) INFORMATION FOR SEQ ID NO:1425:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1425:  
GCCGCTCCCC GCCC 14
- (2) INFORMATION FOR SEQ ID NO:1426:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1426:  
GCTCGTCGCC CTGGCC 17
- (2) INFORMATION FOR SEQ ID NO:1427:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1427:  
GGCCTCCTCC TGGCCGC 17
- (2) INFORMATION FOR SEQ ID NO:1428:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1428:  
TGTCTCGGGC GCGGCCTTG GC 22
- (2) INFORMATION FOR SEQ ID NO:1429:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1429:  
GCTCCGTTG GGGCTG 16
- (2) INFORMATION FOR SEQ ID NO:1430:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1430:  
CCTCTGGCGC TTCC 14
- (2) INFORMATION FOR SEQ ID NO:1431:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1431:  
GGCCTCGGC CTGGGCGCTC 20
- (2) INFORMATION FOR SEQ ID NO:1432:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1432:  
TCTTCGCCT GTGC 14
- (2) INFORMATION FOR SEQ ID NO:1433:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1433:  
TGGTGGCCCT CGTGG 15
- (2) INFORMATION FOR SEQ ID NO:1434:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1434:  
GCCCCCTCTG GCCTCCGTG TCC 23
- (2) INFORMATION FOR SEQ ID NO:1435:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1435:  
TGTGGTCCCC CGGCTGGT

18

(2) INFORMATION FOR SEQ ID NO:1436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1436:  
GGCCGGGCGG GTGGGCGGG C

21

(2) INFORMATION FOR SEQ ID NO:1437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1437:  
GTGGGCGCGG GCGGGTCCTC C

21

(2) INFORMATION FOR SEQ ID NO:1438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1438:  
GGGCTGCCCT TCTCC

15

(2) INFORMATION FOR SEQ ID NO:1439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1439:  
GCCGGGGGTC CCGC

14

(2) INFORMATION FOR SEQ ID NO:1440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1440:  
GCTCCTGCTG TTCCCTGGGC TCTCTGCC

29

(2) INFORMATION FOR SEQ ID NO:1441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1441:  
TCTCTCCTGG GTGGGTGCTG GGTGCCG

27

(2) INFORMATION FOR SEQ ID NO:1442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1442:  
GGGTCTCCGG GCTTG

15

(2) INFORMATION FOR SEQ ID NO:1443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1443:  
CCCCGCGCTG CTGGGCGTTC TGC

23

- (2) INFORMATION FOR SEQ ID NO:1444:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 15 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1444:  
GGTCTTGGGG TTGTC 15
- (2) INFORMATION FOR SEQ ID NO:1445:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1445:  
TGTGGCCCCG CTCG 14
- (2) INFORMATION FOR SEQ ID NO:1446:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1446:  
TGTCGCCCTC CGTCGCC 17
- (2) INFORMATION FOR SEQ ID NO:1447:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1447:  
CGTCGCCGGC CTCGTCC 17
- (2) INFORMATION FOR SEQ ID NO:1448:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1448:  
CCTCCTGGGT GCGC 14
- (2) INFORMATION FOR SEQ ID NO:1449:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1449:  
GGCGGGCTGG TCCT 14
- (2) INFORMATION FOR SEQ ID NO:1450:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1450:  
GGCGTTTGC TCCTTCCTG 20
- (2) INFORMATION FOR SEQ ID NO:1451:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 15 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1451:  
CTGCCTCCCC GGGGT 15
- (2) INFORMATION FOR SEQ ID NO:1452:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 15 base pairs

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1452:  
TTCTGCTGCT TGCTG 15
- (2) INFORMATION FOR SEQ ID NO:1453:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1453:  
CTTCTTTCCC GTCTCC 16
- (2) INFORMATION FOR SEQ ID NO:1454:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1454:  
CTTCTTTCCC GTCTCC 16
- (2) INFORMATION FOR SEQ ID NO:1455:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1455:  
TTTTTGCCCTC TTG 14
- (2) INFORMATION FOR SEQ ID NO:1456:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1456:  
GGTTCCTGTT GTTCT 16
- (2) INFORMATION FOR SEQ ID NO:1457:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1457:  
GGCCTGCTTG GTGGCG 16
- (2) INFORMATION FOR SEQ ID NO:1458:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1458:  
GCTTGTCGT TTCC 14
- (2) INFORMATION FOR SEQ ID NO:1459:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1459:  
TCTCTCTTCT CTTGGGTCTC CGCTTCTCGT CCTGCC 36
- (2) INFORMATION FOR SEQ ID NO:1460:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1460:  
TTTTCCTGTC TCTGTCGC

18

(2) INFORMATION FOR SEQ ID NO:1461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1461:  
GCCGTTCTCTC CTCC

14

(2) INFORMATION FOR SEQ ID NO:1462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1462:  
GGCGTCCTCC TGCCC

15

(2) INFORMATION FOR SEQ ID NO:1463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1463:  
TGTGCTGTTT GCCTCGG

17

(2) INFORMATION FOR SEQ ID NO:1464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1464:  
GTGGTGCGGG TCCC

14

(2) INFORMATION FOR SEQ ID NO:1465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1465:  
GGTGCTCCCC CGGC

14

(2) INFORMATION FOR SEQ ID NO:1466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1466:  
GGGCCGGGTG GTTGCTGGG C

21

(2) INFORMATION FOR SEQ ID NO:1467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1467:  
CTGTCTGGTG GGGTGTGGG CC

22

(2) INFORMATION FOR SEQ ID NO:1468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468:  
GCTGGGTGG GGGTGTGGT

20

- (2) INFORMATION FOR SEQ ID NO:1469:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1469:  
GGCTCTTCTG TGGCC 15
- (2) INFORMATION FOR SEQ ID NO:1470:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1470:  
TGTGGGGCTG TTGGTG 16
- (2) INFORMATION FOR SEQ ID NO:1471:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1471:  
TCTCTGTGGG CGTGTG 16
- (2) INFORMATION FOR SEQ ID NO:1472:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1472:  
CTGGGTCTTG GGGCTTC 17
- (2) INFORMATION FOR SEQ ID NO:1473:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1473:  
CTCCCTTGTG CTGGG 15
- (2) INFORMATION FOR SEQ ID NO:1474:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1474:  
TGCGGCCTCC CCGC 14
- (2) INFORMATION FOR SEQ ID NO:1475:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1475:  
CCCCCTTCTG GGCC 14
- (2) INFORMATION FOR SEQ ID NO:1476:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1476:  
GGTGGCCTGG CTCCTTGTGG 20
- (2) INFORMATION FOR SEQ ID NO:1477:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1477:  
GCGCTTCTGG CTCTTG

16

(2) INFORMATION FOR SEQ ID NO:1478:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1478:  
CCCTGTCCTT CTCGCCTCG T

21

(2) INFORMATION FOR SEQ ID NO:1479:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1479:  
GGCTGCTGGG CTGC

14

(2) INFORMATION FOR SEQ ID NO:1480:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1480:  
GTTGGGCTTG GCCGGGG

17

(2) INFORMATION FOR SEQ ID NO:1481:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1481:  
CTGCCCGGTG CCTCC

15

(2) INFORMATION FOR SEQ ID NO:1482:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1482:  
TCTTGGCTGG TCCCTCGT

18

(2) INFORMATION FOR SEQ ID NO:1483:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1483:  
TGTCTTGGG CCCC

14

(2) INFORMATION FOR SEQ ID NO:1484:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1484:  
GCTCCCCTG CTCGGCCTCC GT

22

(2) INFORMATION FOR SEQ ID NO:1485:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1485:  
GTTCTTTGGC CTCTTGCTCC 20
- (2) INFORMATION FOR SEQ ID NO:1486:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1486:  
GCCTGCTGTC TTGTCC 16
- (2) INFORMATION FOR SEQ ID NO:1487:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1487:  
CGTCCCCTCC TCGCTTGCCT TTC 23
- (2) INFORMATION FOR SEQ ID NO:1488:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1488:  
CCTCTTCCTT GTCTTCCA 18
- (2) INFORMATION FOR SEQ ID NO:1489:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1489:  
GGCCTTCCTC CGCTTCCGCT GC 22
- (2) INFORMATION FOR SEQ ID NO:1490:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1490:  
TGGGGCCCCG GCCGG 15
- (2) INFORMATION FOR SEQ ID NO:1491:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1491:  
GGGGGCGCTC GGCTCCGCGG CTTCTCCCC GG 32
- (2) INFORMATION FOR SEQ ID NO:1492:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1492:  
CTGGGGGGTC CTGG 14
- (2) INFORMATION FOR SEQ ID NO:1493:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1493:  
TCTCCGGGGC CTGCGGCTCG C

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(2) INFORMATION FOR SEQ ID NO:1494:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1494:  
GGGCTCGGGG CTGCGTGCGC C

21

(2) INFORMATION FOR SEQ ID NO:1495:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1495:  
GCGCGCGGCG TCCGCGGTG

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(2) INFORMATION FOR SEQ ID NO:1496:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1496:  
GGTGGCGCTG TCCCGCC

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(2) INFORMATION FOR SEQ ID NO:1497:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1497:  
GTGGTGTGTC TCCGTTCTCG TCCTGCGCCG TC

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(2) INFORMATION FOR SEQ ID NO:1498:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1498:  
CTGGTCTGCC CGTGG

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(2) INFORMATION FOR SEQ ID NO:1499:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1499:  
GGTCCTGGGC GTGGTGG

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(2) INFORMATION FOR SEQ ID NO:1500:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1500:  
GGGGCGTCTG GTGC

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- (2) INFORMATION FOR SEQ ID NO:1501:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 15 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1501:  
CTCGTCTGCC CCGTG 15
- (2) INFORMATION FOR SEQ ID NO:1502:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 15 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1502:  
GGGCTTCGGG CTCGG 15
- (2) INFORMATION FOR SEQ ID NO:1503:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 34 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1503:  
GGCTGTTTCGT CCCCCCTGCC GCTCTGTGGC CTCG 34
- (2) INFORMATION FOR SEQ ID NO:1504:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 16 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1504:  
GGGGCTCCTC GTTTTC 16
- (2) INFORMATION FOR SEQ ID NO:1505:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 21 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1505:  
GCTGCTTCGG GTGTCCTTCT C 21
- (2) INFORMATION FOR SEQ ID NO:1506:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 15 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1506:  
GGCGTGTGGC CCCGG 15
- (2) INFORMATION FOR SEQ ID NO:1507:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 29 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1507:  
GTCCCGGCC TGCTGGGCTG GCGGGGTC 29
- (2) INFORMATION FOR SEQ ID NO:1508:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 25 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1508:  
GCTGCCCTGG GCTTCTGGCC CGTCT 25

- (2) INFORMATION FOR SEQ ID NO:1509:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1509:  
GGTGTCTGT CGGT
- (2) INFORMATION FOR SEQ ID NO:1510:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 19 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1510:  
GCTTGTCTCG GGTTCCTGG
- (2) INFORMATION FOR SEQ ID NO:1511:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1511:  
CCTCTGTGCT GGGC
- (2) INFORMATION FOR SEQ ID NO:1512:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1512:  
GCTTCTCTGC CTCCTGCTCC
- (2) INFORMATION FOR SEQ ID NO:1513:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 16 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1513:  
GCCCTCCTGG TGGCTC
- (2) INFORMATION FOR SEQ ID NO:1514:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 19 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1514:  
GGCTGGGGGT GCGGCTGCG
- (2) INFORMATION FOR SEQ ID NO:1515:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 19 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1515:  
GGGGTGGGTG TGGGTGTT
- (2) INFORMATION FOR SEQ ID NO:1516:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1516:  
TTCGGGTCC TCCCCTTCCC
- (2) INFORMATION FOR SEQ ID NO:1517:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1517:  
GTTTCATCTT GGCTTTATCC 20

(2) INFORMATION FOR SEQ ID NO:1518:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1518:  
TCTCCCCCTTG TTCCTCCCC 19

(2) INFORMATION FOR SEQ ID NO:1519:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1519:  
TCTCCTGCTC TGGRGTCTCC TC 22

(2) INFORMATION FOR SEQ ID NO:1520:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1520:  
TTCCCTCCCT CCCCTGCC 18

(2) INFORMATION FOR SEQ ID NO:1521:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1521:  
GTGTTGTCTG TGGGTGTCC 19

(2) INFORMATION FOR SEQ ID NO:1522:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1522:  
GTTTCGCTCT TGTGCCC 18

(2) INFORMATION FOR SEQ ID NO:1523:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1523:  
TGGGCCCTTC CTGCTGG 18

(2) INFORMATION FOR SEQ ID NO:1524:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1524:  
GGGGGAGTTT CATCTTGG 18

(2) INFORMATION FOR SEQ ID NO:1525:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear



- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1525:  
GGGGGBGTTT CBTCTTGGCT TT 22
- (2) INFORMATION FOR SEQ ID NO:1526:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1526:  
GGGGGBGTTT CBTCTTGGCT T 21
- (2) INFORMATION FOR SEQ ID NO:1527:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1527:  
GGGGGBGTTT CBTCTTGGCT 20
- (2) INFORMATION FOR SEQ ID NO:1528:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1528:  
GGGGGBGTTT CBTCTTGGC 19
- (2) INFORMATION FOR SEQ ID NO:1529:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1529:  
GGGGGBGTTT CBTCTTGG 18
- (2) INFORMATION FOR SEQ ID NO:1530:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1530:  
GGGGGBGTTT CBTCTTG 17
- (2) INFORMATION FOR SEQ ID NO:1531:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1531:  
GGGGGBGTTT CBTCTT 16
- (2) INFORMATION FOR SEQ ID NO:1532:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1532:  
GGGGGBGTTT CBTCT 15
- (2) INFORMATION FOR SEQ ID NO:1533:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1533:  
GGGGGBGTTT CBTCT 14

- (2) INFORMATION FOR SEQ ID NO:1534:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1534:  
GGGGGBGTTT CBT 13
- (2) INFORMATION FOR SEQ ID NO:1535:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1535:  
GGGGGBGTTT CB 12
- (2) INFORMATION FOR SEQ ID NO:1536:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1536:  
GGGGBGTTTC BTCTGGCTT T 21
- (2) INFORMATION FOR SEQ ID NO:1537:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1537:  
GGGGBGTTTC BTCTGGCTT 20
- (2) INFORMATION FOR SEQ ID NO:1538:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1538:  
GGGGBGTTTC BTCTGGCT 19
- (2) INFORMATION FOR SEQ ID NO:1539:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1539:  
GGGGBGTTTC BTCTGGC 18
- (2) INFORMATION FOR SEQ ID NO:1540:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1540:  
GGGGBGTTTC BTCTGG 17
- (2) INFORMATION FOR SEQ ID NO:1541:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1541:  
GGGGBGTTTC BTCTG 16
- (2) INFORMATION FOR SEQ ID NO:1542:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1542:  
GGGGBGTTTC BTCTT

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(2) INFORMATION FOR SEQ ID NO:1543:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1543:  
GGGGBGTTTC BTCT

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(2) INFORMATION FOR SEQ ID NO:1544:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1544:  
GGGGBGTTTC BTC

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(2) INFORMATION FOR SEQ ID NO:1545:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1545:  
GGGGBGTTTC BT

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(2) INFORMATION FOR SEQ ID NO:1546:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1546:  
GGGBGTTTCB TCTTGGCTTT

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(2) INFORMATION FOR SEQ ID NO:1547:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1547:  
GGGBGTTTCB TCTTGGCTT

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(2) INFORMATION FOR SEQ ID NO:1548:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1548:  
GGGBGTTTCB TCTTGGCT

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(2) INFORMATION FOR SEQ ID NO:1549:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1549:  
GGGBGTTTCB TCTTGGC

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(2) INFORMATION FOR SEQ ID NO:1550:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1550:  
GGGBGTTTCB TCTTG

(2) INFORMATION FOR SEQ ID NO:1551:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1551:  
GGGBGTTTCB TCTTG

(2) INFORMATION FOR SEQ ID NO:1552:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1552:  
GGGBGTTTCB TCTT

(2) INFORMATION FOR SEQ ID NO:1553:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1553:  
GGGBGTTTCB TCT

(2) INFORMATION FOR SEQ ID NO:1554:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1554:  
GGGBGTTTCB TC

(2) INFORMATION FOR SEQ ID NO:1555:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1555:  
GGBGTTTCBT CTTGGCTTT

(2) INFORMATION FOR SEQ ID NO:1556:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1556:  
GGBGTTTCBT CTTGGCTT

(2) INFORMATION FOR SEQ ID NO:1557:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1557:  
GGBGTTTCBT CTTGGCT

(2) INFORMATION FOR SEQ ID NO:1558:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1558:  
GGBGTTTCBT CTTGGC

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- (2) INFORMATION FOR SEQ ID NO:1559:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1559:  
GGBGTTTCBT CTTGG 15
- (2) INFORMATION FOR SEQ ID NO:1560:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1560:  
GGBGTTTCBT CTTG 14
- (2) INFORMATION FOR SEQ ID NO:1561:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1561:  
GGBGTTTCBT CTT 13
- (2) INFORMATION FOR SEQ ID NO:1562:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1562:  
GGBGTTTCBT CT 12
- (2) INFORMATION FOR SEQ ID NO:1563:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1563:  
GBGTTTCBTC TTGGCTT 18
- (2) INFORMATION FOR SEQ ID NO:1564:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1564:  
GBGTTTCBTC TTGGCTT 17
- (2) INFORMATION FOR SEQ ID NO:1565:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1565:  
GBGTTTCBTC TTGGCT 16
- (2) INFORMATION FOR SEQ ID NO:1566:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1566:  
GBGTTTCBTC TTGGC 15
- (2) INFORMATION FOR SEQ ID NO:1567:  
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1567:  
GBGTTTCBTC TTGG 14
- (2) INFORMATION FOR SEQ ID NO:1568:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1568:  
GBGTTTCBTC TTG 13
- (2) INFORMATION FOR SEQ ID NO:1569:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1569:  
GBGTTTCBTC TT 12
- (2) INFORMATION FOR SEQ ID NO:1570:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1570:  
BGTTTCBTCT TGGCTT 17
- (2) INFORMATION FOR SEQ ID NO:1571:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1571:  
BGTTTCBTCT TGGCTT 16
- (2) INFORMATION FOR SEQ ID NO:1572:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1572:  
BGTTTCBTCT TGGCTT 16
- (2) INFORMATION FOR SEQ ID NO:1573:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1573:  
BGTTTCBTCT TGGCT 15
- (2) INFORMATION FOR SEQ ID NO:1574:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1574:  
BGTTTCBTCT TGGC 14
- (2) INFORMATION FOR SEQ ID NO:1575:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1575:  
BGTTTCBTCT TGG

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(2) INFORMATION FOR SEQ ID NO:1576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1576:  
BGTTTCBTCT TG

12

(2) INFORMATION FOR SEQ ID NO:1577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1577:  
GTTTCBTCTT GGCTT

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(2) INFORMATION FOR SEQ ID NO:1578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1578:  
GTTTCBTCTT GGCTT

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(2) INFORMATION FOR SEQ ID NO:1579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1579:  
GTTTCBTCTT GGCT

14

(2) INFORMATION FOR SEQ ID NO:1580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1580:  
GTTTCBTCTT GGC

13

(2) INFORMATION FOR SEQ ID NO:1581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1581:  
GTTTCBTCTT GG

12

(2) INFORMATION FOR SEQ ID NO:1582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1582:  
TTTCBTCTTG GCTTT

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(2) INFORMATION FOR SEQ ID NO:1583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1583:  
TTTCBTCTTG GCTT

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- (2) INFORMATION FOR SEQ ID NO:1584:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 13 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1584:  
TTCBTCTTG GCT 13
- (2) INFORMATION FOR SEQ ID NO:1585:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 12 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1585:  
TTCBTCTTG GC 12
- (2) INFORMATION FOR SEQ ID NO:1586:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1586:  
TTCBTCTTGG CTTT 14
- (2) INFORMATION FOR SEQ ID NO:1587:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 13 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1587:  
TTCBTCTTGG CTT 13
- (2) INFORMATION FOR SEQ ID NO:1588:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 12 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1588:  
TTCBTCTTGG CT 12
- (2) INFORMATION FOR SEQ ID NO:1589:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 13 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1589:  
TCBTCTTGGC TTT 13
- (2) INFORMATION FOR SEQ ID NO:1590:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 12 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1590:  
TCBTCTTGGC TT 12
- (2) INFORMATION FOR SEQ ID NO:1591:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1591:  
GGGGGBGTTT CBTCTTGGCT TT 22
- (2) INFORMATION FOR SEQ ID NO:1592:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 21 base pairs



- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1592:  
GGGGBGTTTC BTCTTGCTT T 21
- (2) INFORMATION FOR SEQ ID NO:1593:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1593:  
GGGGBGTTTCB TCTTGGCTTT 20
- (2) INFORMATION FOR SEQ ID NO:1594:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1594:  
GGBGTTTCBT CTTGGCTTT 19
- (2) INFORMATION FOR SEQ ID NO:1595:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1595:  
GBGTTTCBTC TTGGCTTT 18
- (2) INFORMATION FOR SEQ ID NO:1596:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1596:  
BGTTTCBTCT TGGCTTT 17
- (2) INFORMATION FOR SEQ ID NO:1597:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1597:  
GTTTCBTCTT GGCTTT 16
- (2) INFORMATION FOR SEQ ID NO:1598:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1598:  
TTCBTCTTG GCTTT 15
- (2) INFORMATION FOR SEQ ID NO:1599:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1599:  
TTCBTCTTGG CTTT 14
- (2) INFORMATION FOR SEQ ID NO:1600:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1600:  
TCBTCTTGGC TTT 13
- (2) INFORMATION FOR SEQ ID NO:1601:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1601:  
CBTCTTGGCT TT 12
- (2) INFORMATION FOR SEQ ID NO:1602:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1602:  
GGGGGBGTTT CBTCTTGGCT T 21
- (2) INFORMATION FOR SEQ ID NO:1603:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1603:  
GGGGBGTTTC BTCTTGGCTT 20
- (2) INFORMATION FOR SEQ ID NO:1604:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1604:  
GGGBGTTTCB TCTTGGCTT 19
- (2) INFORMATION FOR SEQ ID NO:1605:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1605:  
GGBGTTTCBT CTTGGCTT 18
- (2) INFORMATION FOR SEQ ID NO:1606:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1606:  
GBGTTTCBTC TTGGCTT 17
- (2) INFORMATION FOR SEQ ID NO:1607:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1607:  
BGTTTCBTCT TGGCTT 16
- (2) INFORMATION FOR SEQ ID NO:1608:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1608:  
GTTTCBTCTT GGCTT 15

- (2) INFORMATION FOR SEQ ID NO:1609:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1609:  
TTTCBTCTTG GCTT 14
- (2) INFORMATION FOR SEQ ID NO:1610:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 13 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1610:  
TTCBTCTTGG CTT 13
- (2) INFORMATION FOR SEQ ID NO:1611:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 12 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1611:  
TCBTCTTGGC TT 12
- (2) INFORMATION FOR SEQ ID NO:1612:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1612:  
GGGGGBGTTT CBTCTTGGCT 20
- (2) INFORMATION FOR SEQ ID NO:1613:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 19 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1613:  
GGGGBGTTTC BTCTTGGCT 19
- (2) INFORMATION FOR SEQ ID NO:1614:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 18 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1614:  
GGGBGTTTCB TCTTGGCT 18
- (2) INFORMATION FOR SEQ ID NO:1615:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1615:  
GGBGTTTCBT CTTGGCT 17
- (2) INFORMATION FOR SEQ ID NO:1616:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 16 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1616:  
GBGTTTCBTC TTGGCT 16
- (2) INFORMATION FOR SEQ ID NO:1617:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1617:  
BGTTTCBTCT TGGCT 15

(2) INFORMATION FOR SEQ ID NO:1618:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1618:  
GTTTCBTCTT GGCT 14

(2) INFORMATION FOR SEQ ID NO:1619:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1619:  
TTTCBTCTTG GCT 13

(2) INFORMATION FOR SEQ ID NO:1620:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1620:  
TTCBTCTTGG CT 12

(2) INFORMATION FOR SEQ ID NO:1621:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1621:  
GGGGGBGTTT CBTCTTGGC 19

(2) INFORMATION FOR SEQ ID NO:1622:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1622:  
GGGGBGTTTC BTCTTGGC 18

(2) INFORMATION FOR SEQ ID NO:1623:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1623:  
GGGBGTTTCB TCTTGGC 17

(2) INFORMATION FOR SEQ ID NO:1624:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1624:  
GGBGTTTCBT CTTGGC 16

(2) INFORMATION FOR SEQ ID NO:1625:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1625:  
GBGTTTCBTC TTGGC

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(2) INFORMATION FOR SEQ ID NO:1626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1626:  
BGTTTCBTCT TGGC

14

(2) INFORMATION FOR SEQ ID NO:1627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1627:  
GTTTCBTCTT GGC

13

(2) INFORMATION FOR SEQ ID NO:1628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1628:  
TTTCBTCTTG GC

12

(2) INFORMATION FOR SEQ ID NO:1629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1629:  
GGGGGBGTTT CBTCTTGG

18

(2) INFORMATION FOR SEQ ID NO:1630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1630:  
GGGGBGTTTC BTCTTGG

17

(2) INFORMATION FOR SEQ ID NO:1631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1631:  
GGGBGTTTCB TCTTGG

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(2) INFORMATION FOR SEQ ID NO:1632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1632:  
GGBGTTTCBT CTTGG

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(2) INFORMATION FOR SEQ ID NO:1633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1633:  
GBGTTTCBTC TTGG

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- (2) INFORMATION FOR SEQ ID NO:1634:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 13 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1634:  
BGTTCBTCT TGG 13
- (2) INFORMATION FOR SEQ ID NO:1635:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 12 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1635:  
GTTTCBTCTT GG 12
- (2) INFORMATION FOR SEQ ID NO:1636:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1636:  
GGGGGBGTTT CBTCTTG 17
- (2) INFORMATION FOR SEQ ID NO:1637:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 16 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1637:  
GGGGBGTTTC BTCTTG 16
- (2) INFORMATION FOR SEQ ID NO:1638:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 15 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1638:  
GGGBGTTTCB TCTTG 15
- (2) INFORMATION FOR SEQ ID NO:1639:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1639:  
GGBGTTTCBT CTTG 14
- (2) INFORMATION FOR SEQ ID NO:1640:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 13 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1640:  
BGTTTCBTC TTG 13
- (2) INFORMATION FOR SEQ ID NO:1641:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 12 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1641:  
BGTTCBTCT TG 12
- (2) INFORMATION FOR SEQ ID NO:1642:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 16 base pairs

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1642:  
GGGGGBGTTT CBTCTT 16
- (2) INFORMATION FOR SEQ ID NO:1643:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1643:  
GGGGBGTTTC BTCTT 15
- (2) INFORMATION FOR SEQ ID NO:1644:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1644:  
GGGBGTTTCB TCTT 14
- (2) INFORMATION FOR SEQ ID NO:1645:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1645:  
GGGBGTTTCB TCTT 14
- (2) INFORMATION FOR SEQ ID NO:1646:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1646:  
GGBGTTTCBT CTT 13
- (2) INFORMATION FOR SEQ ID NO:1647:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1647:  
GBGTTTCBTC TT 12
- (2) INFORMATION FOR SEQ ID NO:1648:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1648:  
GGGGGBGTTT CBTCT 15
- (2) INFORMATION FOR SEQ ID NO:1649:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1649:  
GGGGBGTTTC BTCT 14
- (2) INFORMATION FOR SEQ ID NO:1650:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1650:  
GGGBGTTTCB TCT

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- (2) INFORMATION FOR SEQ ID NO:1651:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1651:  
GGBGTTTCBT CT

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- (2) INFORMATION FOR SEQ ID NO:1652:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1652:  
GGGGGBGTTT CBTC

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- (2) INFORMATION FOR SEQ ID NO:1653:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1653:  
GGGGBGTTTC BTC

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- (2) INFORMATION FOR SEQ ID NO:1654:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1654:  
GGGBGTTTCB TC

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- (2) INFORMATION FOR SEQ ID NO:1655:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1655:  
GGGGGBGTTT CBT

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- (2) INFORMATION FOR SEQ ID NO:1656:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1656:  
GGGGBGTTTC BT

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- (2) INFORMATION FOR SEQ ID NO:1657:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1657:  
GGGGGBGTTT CB

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- (2) INFORMATION FOR SEQ ID NO:1658:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1658:  
TCTCCCCTTG TTCCTCCCC

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- (2) INFORMATION FOR SEQ ID NO:1659:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1659:  
TCTCCTGCTC TGGTGTCTCC TC 22
- (2) INFORMATION FOR SEQ ID NO:1660:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 18 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1660:  
TTCCCTCCCT CCCCTGCC 18
- (2) INFORMATION FOR SEQ ID NO:1661:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 19 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1661:  
GTGTTGTCTG TGGGTGTCC 19
- (2) INFORMATION FOR SEQ ID NO:1662:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 18 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1662:  
GTTTCGCTCT TGTGCCC 18
- (2) INFORMATION FOR SEQ ID NO:1663:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 18 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1663:  
TGGGCCCTTC CCTGCTGG 18
- (2) INFORMATION FOR SEQ ID NO:1664:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 24 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1664:  
GCTGGTCCTC TGCTGTCCTT GCTG 24
- (2) INFORMATION FOR SEQ ID NO:1665:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1665:  
GTGCTCBTGG TGTCTTTCC 20
- (2) INFORMATION FOR SEQ ID NO:1666:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 28 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1666:  
GCCCTGGGGC CCCCTGTCT TCTTGGGG 28
- (2) INFORMATION FOR SEQ ID NO:1667:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1667:  
CCTCTTCCCT CTGGGGGCCG 20
- (2) INFORMATION FOR SEQ ID NO:1668:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1668:  
TCTCTCTCCC TCTTTGCGT CTCTC 25
- (2) INFORMATION FOR SEQ ID NO:1669:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1669:  
TCTTTCTCTC TCTCTCTTCC CC 22
- (2) INFORMATION FOR SEQ ID NO:1670:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1670:  
TTTCCCGCTC TTTCTGTCTC 20
- (2) INFORMATION FOR SEQ ID NO:1671:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1671:  
GGTGTCTGGT TTTCTCTCTC C 21
- (2) INFORMATION FOR SEQ ID NO:1672:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1672:  
GCTGGCTGCC TGTCTGGCCT GCGCTCTT 28
- (2) INFORMATION FOR SEQ ID NO:1673:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1673:  
GGCCTGTGCT GTTCTTCC 18
- (2) INFORMATION FOR SEQ ID NO:1674:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1674:  
TCCGGTTCCT GTCTCTCTG TCTGTC 26
- (2) INFORMATION FOR SEQ ID NO:1675:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1675:  
GCCCCCTCTG GGGTCTCCCT CTGGC 25
- (2) INFORMATION FOR SEQ ID NO:1676:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1676:  
GTGGTGGTCT TGTGCTT 18
- (2) INFORMATION FOR SEQ ID NO:1677:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1677:  
GGGCTGGGCT CCGTGTCTC 19
- (2) INFORMATION FOR SEQ ID NO:1678:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1678:  
CBGTGCTCBT GGTGTCC 17
- (2) INFORMATION FOR SEQ ID NO:1679:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1679:  
GCTGBGGGBG CGTCTGCTGG C 21
- (2) INFORMATION FOR SEQ ID NO:1680:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 329 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1680:  
TGCTTTTCTT TTCTGGGCCT CTGTGGTCTG TTTTTTCTG GCCCTGCTGG GCGCTCTCC 60  
GCCGCCCGCC TGGCTCCCGG BGCCBTGBT GGGCBTGGCG TGGTTCTTGC CCTCCTTTGG 120  
CTGCCGTGCC CGCTCCCGG CCTCTGGCG GGTGGCCGTT GGGCCCGTGT TCCCCTGGGG 180  
CCTGGGGCTC CCTTCTCTCG CCCTTCTTGC TGGGCCTCTG CTGCTGCTGG TGCTGTGGCC 240  
CCCGTACACC GAGGAGCCCA TGATGGGCAT GCCACAGACG ACAGGCGTBC BCCGBGGBGC 300  
CCBTGBTGGG CBTGCCBCBG BCGBCBGGC 329
- (2) INFORMATION FOR SEQ ID NO:1681:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1681:  
CTGGGCCTC 9
- (2) INFORMATION FOR SEQ ID NO:1682:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1682:  
GCCGCCCGCC TG 12
- (2) INFORMATION FOR SEQ ID NO:1683:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1683:  
GCCCCGCTCCC CGGC

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(2) INFORMATION FOR SEQ ID NO:1684:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1684:  
CBCCGGBGBG CCC

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(2) INFORMATION FOR SEQ ID NO:1685:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 304 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1685:  
GGCGCCGTGC CGCGTCTTGG TGGCGGCGGG TTCGCGCCCG CGCGGGGCCCC CTCCGGTCCG 60  
TTCGCGCCCG CGCGGGGCCC CTCCGGTCCC GGGTCGGGGC CCCCCGCGGC CGCCTCGGGG 120  
CTGGGGCGCT GGTGGCCGGG CCGCGCCTCC GCCTGCCGCT TCTGGCTGGG CCCC GGCGCG 180  
CCCCTCCCTT CTTGCTCGGG TCCCCGTGAC AGCGCGTCCT GTGTCTCCAG CAGCATGGCC 240  
GGGCCAGCTG GGCCCCBCBG CGCGTCCTGT GTCTCCBGB GCBTGGCCGG GCCBGCTGGG 300  
CCCC 304

(2) INFORMATION FOR SEQ ID NO:1686:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1686:  
GCGCGTCCTG

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(2) INFORMATION FOR SEQ ID NO:1687:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1687:  
GCTGGGCCCC GG

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(2) INFORMATION FOR SEQ ID NO:1688:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1688:  
CGGGTCGGGG CCCCC

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(2) INFORMATION FOR SEQ ID NO:1689:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1689:  
CGCGCCCGCG

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(2) INFORMATION FOR SEQ ID NO:1690:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 213 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1690:  
ACAGAGCAGT GCTGTTGTTG GGCATCTTGC CTTCCAGGG BCBGBGCBTG CTGTTGTTGG 60  
GCBTCTTGCC TTCCCBGGGC CCTTTTCTGG TGGGGTGGTG CTGTTGTTGG GCTTTCTTCT 120  
GTTCCCBGBG BCBGTGCTG TTGTTGGGCB TCTTGCCTTC CCBGGGCCCT TTTCTGGTGG 180  
GGTGGTGCTG TTGTTGGGCT TTCTTCTGTT CCC 213

(2) INFORMATION FOR SEQ ID NO:1691:  
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1691:  
GBGCBTGC

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(2) INFORMATION FOR SEQ ID NO:1692:  
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1692:  
TTGTTGGGC

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(2) INFORMATION FOR SEQ ID NO:1693:  
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1693:  
TGCCTTCCCB GGG

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(2) INFORMATION FOR SEQ ID NO:1694:  
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1694:  
TTTCCCTGG GTCTTCCCTC CTGCTCTTTT TTCATTGCT CTCCTATTAC TTTCTGTGTC  
CATTTTTTC TTAACCGAGC TGTBTTGCT CTCCTBTTC TTTCTGTGTC CBTTTTTTTCB  
TTBCCGBGC TGT

60  
120  
133

(2) INFORMATION FOR SEQ ID NO:1695:  
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1695:  
CCCCTGGG

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(2) INFORMATION FOR SEQ ID NO:1696:  
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1696:  
GCTCTCCTBT T

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(2) INFORMATION FOR SEQ ID NO:1697:  
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1697:  
CBTTBCCGB GCTG

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(2) INFORMATION FOR SEQ ID NO:1698:  
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1698:  
GCCTGTGTCT GTCTCCTGC TTCGTTCTC TCGTTCCTGC TTGGTGCCCT TGCCGGTCCT  
GCTCCTCCGG GCTGTGGGTC GTGGCCCTGG CTCCGGCTGG TGGGCTCCCC TGGCCTTCGC

60  
120

TGGCTGGCGG	CGTGCGGGTC	TTGCTCTGGG	CCTGGCTGTG	GCCGTGGTTG	GGGGCTTCG	180
CTGCCCTCGT	TTGGGTGGCT	CTCTGAATAT	TGACCTTCCT	CCATGGCGGT	CCTGCTTGGG	240
TTCTCCCGAT	CTCTGBBTB	TGBCCTTCCT	CCBTGGCGGT	CCTGCTTGGG	TTCTCCCGB	299

## (2) INFORMATION FOR SEQ ID NO:1699:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1699:

GTCCTCCT

8

## (2) INFORMATION FOR SEQ ID NO:1700:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1700:

TGTGTCTGTC CTCC

14

## (2) INFORMATION FOR SEQ ID NO:1701:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1701:

GTGGCCCTGG C

11

## (2) INFORMATION FOR SEQ ID NO:1702:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1702:

CGTGGTTGGG G

11

## (2) INFORMATION FOR SEQ ID NO:1703:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1703:

TCTCTGBBTB TTGCC

16

## (2) INFORMATION FOR SEQ ID NO:1704:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1704:

GCCTTTCCTG	GTTCTCTTGT	TGTTTTTGGG	GTTTGGCTTA	CAGTAGAGTA	GGGGATTCCA	60
TGGCAGGAGC	CATCTTCTTC	ATGGACTCCT	TCAAGGAGAC	CTTAGGTTTC	TGAGGGACTG	120
CTAACACGCC	ATCTGGAGCB	CBGTBGBGTB	GGGGBTTCB	TGGCBGBGBC	CBTCTTCTTC	180
BTGGBCTCCT	TCBBGGBGBC	CTTBGGTTTC	TGBGGGBCTG	CTBBCBCGCC	BTCTGGBGCG	240
TTGTTTTTGG	GGTTTGGCTT	GCCTTTCCTG	GTTCTCTTBC	BGTBGBGTBG	GGGBTTCCBT	300
GGCBGGBGCC	BTCTTCTTCB	TGGBCTCCTT	CBGGBGBGCC	TTBGGTTTCT	GBGGGBCTGC	360
TBBCBCGCCB	TCTGGBGC					378

## (2) INFORMATION FOR SEQ ID NO:1705:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1705:

TGGBCTCC

8

## (2) INFORMATION FOR SEQ ID NO:1706:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1706:  
CCBTCCTGGB

9

(2) INFORMATION FOR SEQ ID NO:1707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1707:  
CTGCTBBCBC G

11

(2) INFORMATION FOR SEQ ID NO:1708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1708:  
GTTTTTGGGG TTG

14

(2) INFORMATION FOR SEQ ID NO:1709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1709:

GCCTGTGTCT	GTCCTCCTGC	TTCGTTCTCTC	TCGTTCTCTGC	TTGGTGCCCT	TGCCGGTCTCT	60
GCTCCTCCGG	GCTGTGGGTC	CTCGCCCTGG	CTCCGGCTGG	TGGGCTCCCC	TGGCCTTCGC	120
TGGCTGGCGG	CGTGCCCCBG	BBCGBGBCCC	GBBCCGBCBG	GCCGTGGTTG	GGGGTCTTCG	180
CTGCCTCCGT	TTGGGTGGCG	ATCTCTGAAT	ATTGACCTTC	CATGGCGGTC	CTGCTTGGAG	240
BTCTCTGGBT	BTTGBCCTTC	CBTGGCGGTC	CTGCTTGGB			279

(2) INFORMATION FOR SEQ ID NO:1710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1710:

GCCTGTGTCT	GTCCTCCTGC	TTCGTTCTCTC	TCGTTCTCTGC	TTGGTGCCCT	TGCCGGTCTCT	60
GCTCCTCCGG	GCTGTGGGTC	CTCGCCCTGG	CTCCGGCTGG	TGGGCTCCCC	TGGCCTTCGC	120
TGGCTGGCGG	CGTGCCCCBG	BBCGBGBCCC	GBBCCGBCBG	GCCGTGGTTG	GGGGTCTTCG	180
CTGCCTCCGT	TTGGGTGGCG	ATCTCTGAAT	ATTGACCTTC	CATGGCGGTC	CTGCTTGGAG	240
BTCTCTGGBT	BTTGBCCTTC	CBTGGCGGTC	CTGCTTGGT	CGTTCCTCTC	G	291

(2) INFORMATION FOR SEQ ID NO:1711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1711:  
BGBBCGBGBC

10

(2) INFORMATION FOR SEQ ID NO:1712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1712:  
TGBBTBTG

10

(2) INFORMATION FOR SEQ ID NO:1713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1713:  
TCTCCCTTGG GCTCTGGCTC CTTCTCTCTC TCTCCCTCTC TCTCTGTGCG CTCCGCCCTG 60  
GCTGCTGGGG TGGTGGTGCT TTTGTTCTTC CTTGCTGCCG CCCCGCTGCT TGTCTTCCTC 120  
GCTCTGTCCC TCTCTCTCTG TBCTCCTCBG GCTCCBTCBT CTCCTTGGG C 171

(2) INFORMATION FOR SEQ ID NO:1714:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1714:  
GGCTCTGGC 9

(2) INFORMATION FOR SEQ ID NO:1715:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1715:  
CCCTTGG 7

(2) INFORMATION FOR SEQ ID NO:1716:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1716:  
TTGTTCTTC C 11

(2) INFORMATION FOR SEQ ID NO:1717:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 123 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1717:  
CTTGCTCCTG GGGCCTCCT GGTCCCTCCG GGTGTTCCCG GCGGGCCTGG CCTGGGGCBG 60  
GGGCCGCGTB GCGCGGGCTC GCCBGGBCGG GCBGCGCCBG CBGCBGCBGB TTCBGCBTCC 120  
TGG 123

(2) INFORMATION FOR SEQ ID NO:1718:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1718:  
GCTCCTGGGG GCCT 14

(2) INFORMATION FOR SEQ ID NO:1719:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1719:  
CGTBGGCGC 9

(2) INFORMATION FOR SEQ ID NO:1720:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1720:  
TGGCCTGGGG 10

(2) INFORMATION FOR SEQ ID NO:1721:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 132 base pairs  
(B) TYPE: nucleic acid



(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1721:  
 CTTGCTCCTG GGGGCCTCT GGTCCCTCTG GCTGTCCCCG GCCCTGGBCT GGGGCBGGGG 60  
 CCGCGTBGGC GCGGCTCGCC BGGBCGGGCB GCGCCBGCGB CBGCBGGCTC BGCBTCCTGG 120  
 CCBGGBBTT CC 132

(2) INFORMATION FOR SEQ ID NO:1722:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1722:  
 CTCCTGGGGG CTCCTG 17

(2) INFORMATION FOR SEQ ID NO:1723:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1723:  
 BTCCTGGCCB CGGBTTCC 19

(2) INFORMATION FOR SEQ ID NO:1724:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 7 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1724:  
 GTCCCTC 7

(2) INFORMATION FOR SEQ ID NO:1725:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 180 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1725:  
 GGTGTGCGGG GCCTGGTGCC CTGGGCCTC GGTGCTGCC TGTGCGCTGC CTTCTTCTCC 60  
 TGGGTCCTCG CCGGGGCCCT TGCTGCCCTG GCTGTGCCCT GGGGGTCTGG GTTCGGCTGT 120  
 CCCCBCGBGG BCCBGTCCEB TCCBCGCGT GTGBTGBGTB GCCBTTCTCC TGCBGCCGBG 180

(2) INFORMATION FOR SEQ ID NO:1726:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 16 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1726:  
 TTCTCCTGCB GCCGBG 16

(2) INFORMATION FOR SEQ ID NO:1727:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1727:  
 CTTGCTGCCC TGGCTGT 17

(2) INFORMATION FOR SEQ ID NO:1728:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1728:  
 TCTTCTCCTG G 11

(2) INFORMATION FOR SEQ ID NO:1729:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 101 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1729:  
GGGCGCGGGC GBGCBTCGCT TTGGGCTTTT CTCCTTTGGT TTGBGCGCCB GGBCCGCGCB 60  
CBGCBGCBGG GCGCGGGCGB GCBTCGCBGC GCGGGGCBGG G 101

(2) INFORMATION FOR SEQ ID NO:1730:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1730:  
GGCBGGG 7

(2) INFORMATION FOR SEQ ID NO:1731:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1731:  
TCCTTTGGTT 10

(2) INFORMATION FOR SEQ ID NO:1732:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 81 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1732:  
CCTCCTTCCT GGTCTGTCTG CCBGBCBBT TTGGGBBGTG BCBGTTTGT GBBCCBTGTT 60  
TCCCBGTCTC TGBGCTGTGG C 81

(2) INFORMATION FOR SEQ ID NO:1733:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1733:  
TTCTCCTTG GTT 13

(2) INFORMATION FOR SEQ ID NO:1734:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1734:  
TTTCTCCTTT GGTT 14

(2) INFORMATION FOR SEQ ID NO:1735:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 156 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1735:  
GCCCTGCTGC TCTTTCTGCT TCCCTTGGTG GGTTGGGCGG CTGGTTGTTC TGGGGTTCTT 60  
GCTGCCCCCTT CTGTCCCTGT TTGCTGGTGT CTGCGCCCCC BBCBGBBGBB GCBGBCBBBT 120  
TTGGGBBGTG BBCBGTTTTG GBBCCBTGTT TCCTGT 156

(2) INFORMATION FOR SEQ ID NO:1736:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1736:  
TTCCTGT 7

(2) INFORMATION FOR SEQ ID NO:1737:  
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1737:  
CTCTTTCTGC T

11

(2) INFORMATION FOR SEQ ID NO:1738:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1738:  
CCCCTTCTGT CCC

13

(2) INFORMATION FOR SEQ ID NO:1739:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 272 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1739:  
GCGCTCGGCC TGGTCCCGGG GGTCTCCTCT TGTGTTGCT TCGCCTCCT GCTGGGGGTC  
CCTCTGTTCT TGTTTGGGG GCGGGCCCG CCGTTGCTT GGTTCGGGG TTCCGTTGG  
GGTCTCCTG GCCCGGGCCT TGCCCGGCC TGGTCCCGC TTCGTTCTG TCTCCGTCTC  
GGCTCTCTG GGGCCTTGC CTGTCTTGG TGGCBCCGC CBGTGTTGGT GCGGTBCTG  
TCGCTGCBGC GCTCGGCTG GTCCGGBG GC

60  
120  
180  
240  
272

(2) INFORMATION FOR SEQ ID NO:1740:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1740:  
TCGGCCTGGT CCCGG

15

(2) INFORMATION FOR SEQ ID NO:1741:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1741:  
TGGGGGTTTC CGTTG

15

(2) INFORMATION FOR SEQ ID NO:1742:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1742:  
TGGTCCCGGB GBGC

14

(2) INFORMATION FOR SEQ ID NO:1743:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 360 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1743:  
GCGCGGGCCG GGGGCTGCTG GGGGTTGGCC CGGGGTGCCC CGCCGCTGGG TGCCCTCGTC  
CTCTGCGGTC GTGTCTCCTG GCTCTGGTTC CCCGCTGCGC CCGTTGCTCT CTGGGGTGGC  
CTTCGCTCCC GGGTCTGGTT CTTGTGTTGG GGGTCCCTTT TTGGGCTGTT TGTGGCGTGG  
CTGTGTGTT CCGTTTCTGC CTGTCTCTCC GGCCTCCCC GBGCTCCCC GGGGCBGGBT  
GBCTTTTGBG GGGGBCBCBG BTGTCTGGGC BTTGCCBGGT CCTGGGBBCB GBGCCCCGBG  
CBGGBCCBGG BGTGCGGGCB GCGCGGGCCG GGGGCTGCTG GGBGCCBTBG CGBGGCTGBG

60  
120  
180  
240  
300  
360

(2) INFORMATION FOR SEQ ID NO:1744:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1744:  
GGGGGCTGCT GGG 13

(2) INFORMATION FOR SEQ ID NO:1745:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1745:  
TGTCCTCCGG CGTCCC 16

(2) INFORMATION FOR SEQ ID NO:1746:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1746:  
GCCBTBGCGB GGCTGBG 17

(2) INFORMATION FOR SEQ ID NO:1747:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1747:  
CTCTGGGGTG GCCTTC 16

(2) INFORMATION FOR SEQ ID NO:1748:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 242 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1748:  
CCTCTTTTCT GTTTTTCCCC TCTGCCTTTG TTTGGGTTTC GTTCTTTCT GCTTCTTCCC 60  
TGTGTCTCCT GTCTCCGCTT TTTTCTTCGT CTTTGTGTGT TTCTCTTCCT TGCTGBGCBB 120  
GBTBTCTBGB TTCTGGGGTG GTCTCGBTTC TBBBGGCTTG BGBBGCTGCB BCBTTBTCC 180  
BBBGTBTBTT TGBGGCTCCB BGGBTCBCGB CCBTCTTCCC BGGCBTTTTB BGTGCTGTG 240  
GT 242

(2) INFORMATION FOR SEQ ID NO:1749:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1749:  
CTGTCGT 7

(2) INFORMATION FOR SEQ ID NO:1750:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1750:  
TGCTTCTTCC 10

(2) INFORMATION FOR SEQ ID NO:1751:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 249 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1751:  
BBGTGBGBGC TGBGBGBBC TGTGBGCBB TCBTGBCTTC BBGBGTTCTT TTCBCCCGTT 60  
CTTGGCTTCT TCTGTCCGTT GGCTTCTCGT TGTCCCTGTG GGCTTCTCGT TGTCCCCCCT 120  
TCGGGGGGCTG GTGGGGCCGT CCTTGCCTGC TGGGTTCTTG GCTTCTCTG TCCGTTGGCT 180  
TCTCGTTGTC CCTGTGGGCT TCTCGTTGTC CCCCCTTCGG GGGCTGGTGG GGCCGTCCTT 240  
GCCTGCTGC 249

- (2) INFORMATION FOR SEQ ID NO:1752:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1752:  
CCTTGCCTGC TGG 13
- (2) INFORMATION FOR SEQ ID NO:1753:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1753:  
GTTGTCCC 8
- (2) INFORMATION FOR SEQ ID NO:1754:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 77 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1754:  
TTTTCTCTTT CGCTTTCTTT TCGTCTCCTG TTCCTCCTTT TTTGCTGTTT TTTCTCCTTC 60  
TTCTCTCCTT TCTTTTC 77
- (2) INFORMATION FOR SEQ ID NO:1755:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1755:  
TCCTTTCTTT TC 12
- (2) INFORMATION FOR SEQ ID NO:1756:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1756:  
CTCCTTTT 8
- (2) INFORMATION FOR SEQ ID NO:1757:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 77 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1757:  
TTTTCTCTTT CGCTTTCTTT TCGTCTCCTG TTCCTCCTTT TTTGCTGTTT TTTCTCCTTC 60  
TTCTCTCCTT TCTTTTC 77
- (2) INFORMATION FOR SEQ ID NO:1758:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1758:  
CCTTTCTTTT C 11
- (2) INFORMATION FOR SEQ ID NO:1759:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1759:  
CTGTTCTCTC TTTT 14
- (2) INFORMATION FOR SEQ ID NO:1760:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1760:

CTCTGTCTTG TTCTGGTCCT TCGTGGGGCT CTGTGTCGCG TGGGTGCGGC CGTGCCCGGC 60  
GGBCCBGGBG TTGBGBCBGG BGCBBGBCGG GCBGGCGGCT CBTGTTTGGT TCGGCBGGBG 120  
GCBCTC 126

## (2) INFORMATION FOR SEQ ID NO:1761:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1761:

GGBGGCBCTC 10

## (2) INFORMATION FOR SEQ ID NO:1762:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1762:

GTGGGGCTCT G 11

## (2) INFORMATION FOR SEQ ID NO:1763:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1763:

TCTGGGGTGT CCTGGCCTTC GTGGTTCCTC TTCCTTCGTT TGCCGTCCGC GGGGGCCCCC 60  
GGGCCTGGCT GCGCTCCTGC CCCGCCCTTT TCCCGGGCTC TTGCGCTGGG GGGTGCTCCC 120  
GTGTGTTTGC GCCCTCTCC TGGTCGCGCT TGTCGTTTGG GGGCCGGCTT TGCCCGCCTC 180  
CCGGCGCCTG GCCCGGCCTT CCTGGGCTGC GTGCGCGTTC TGTCTTCTT CCTGGCTCTG 240  
GGGTGTCCTG GCCTTCGTGG TTCCTCTTCC TTCGTTTGCC GTCCGCGGGG GCCCCCGGGC 300  
CTGGCTGCGC TCCTGCCCCG CCTCTTTCCC GGGCTCTTGC GCTGGGGGGT GCTCCCGTGT 360  
GTTTGCGCCC TCCTCCTGGT CGCGCTTGTC GCTTGGGGC CGGCTTTGCC CGCCTCCCGG 420  
CGCCTGGCCC GGCTTCCTG GGCTGCGTGC GCGTCTGTT CTTCTTCTG GCGCAGGAGA 480  
CAGGGCAGGG CGATCAGGAG CAGCGTGAGC CAAAGGAGGA CCATCGGGAA CGCAGCTCCG 540  
GAACGCAGGA CAGAGGTGCC GCBGBGBCB GGGCBGGGCG BTCBGBGCB GCGTGBGCCB 600  
BBGGBGBCC BTCGGGBCG CBGCTCCGG BCGBGGBCB GBGGTGCC 648

## (2) INFORMATION FOR SEQ ID NO:1764:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1764:

GBGGTGCC 8

## (2) INFORMATION FOR SEQ ID NO:1765:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1765:

GCCCCGC 7

## (2) INFORMATION FOR SEQ ID NO:1766:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1766:

CTCTGGTTGG CTTCTTCGC CGGCBCBTGC TBGCBGGBBG BCBGBGGGG GBBGCBGTTG 60  
GGBGGTGBB CCCBTTBBTB GGTGTCGB 88

(2) INFORMATION FOR SEQ ID NO:1767:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1767:  
GCCGGCBCEB

9

(2) INFORMATION FOR SEQ ID NO:1768:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1768:  
TTCCTTC

7

(2) INFORMATION FOR SEQ ID NO:1769:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 562 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1769:

TCTGCCCTGT	CCGCCGGCTC	TTCGGTGGCT	CGGCCCGGCT	CCTTGCTCTG	CCGCGGGTTG	60
GTTCTCTGGC	CTGGTTCTTG	CGGGCGTTTC	GGTCTGCTGG	CTGGTCTGGG	CCCGCGGTGC	120
GGCGGGTGGC	TTGCTGTTCT	GCCTGGGCTC	TCCCTCTCTC	TCCTTTTCTC	CCTTCCTCTG	180
TCTTGCCCTC	TTCTCTGGG	TCCTCTTGGC	CTGGGCGCTC	TTCCCTCTCG	GCGGCTGCGG	240
GCGCTCGTGC	TGCCTGGTCC	GCTCCCTGGG	GGTCTCCTT	CCCTTTCCCC	GCTCGTGGGG	300
TTTGCGGGGC	TGGGCTGCCC	TGGGGGGTCT	GGGCCTTTTG	GGGTCTGGCTG	GCTGCTGCTT	360
CGGGCCGCCT	GGGCTTCCCT	GTGCCCTTTT	CCTCTGCTGG	GTCCCCCTCC	CGTTCCAAGC	420
TGCACCGCAC	AGACCGGCGC	TACAGGACAG	AGCCAGGCAA	GCACCCATGG	GGATCCAGGC	480
CCAGCTGTTC	CBGCTGCBBC	CGCBGCBCC	GGCGCTBCBG	GBCBGBGCCB	GGCBBGCBC	540
CBTGGGGBTC	CBGGCCCBGC	TG				562

(2) INFORMATION FOR SEQ ID NO:1770:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1770:  
TCTGCGC

7

(2) INFORMATION FOR SEQ ID NO:1771:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1771:  
CCTGCTCCTG GGG

13

(2) INFORMATION FOR SEQ ID NO:1772:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1772:

TCCCTGTTTC	CCCCTTTCG	TTCTGCGTTT	GCCTTGCGCG	TTTTTTGTTT	GTTTTCTCTC	60
TCCGTCTTTC	TTCTCCCTG	TGGGBBTTTC	TGTGGGGBTG	GCBTBCBCGT	BGGCBGCTCC	120
BBGBGCTBGC	BBBCTCBBT	GCBGBBGBCT	CCTCBTGGCT	CTGBBBCCGT	GGGAATTTCT	180
GTGGGGBTGG	CATACACGTA	GGCAGCTCCA	AGAGCTAGCA	AACTCAAATG	CAGAAGCATC	240
CTCATGGCTC	TGAAACG					257

(2) INFORMATION FOR SEQ ID NO:1773:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1773:  
GCCCCGGG

8

## (2) INFORMATION FOR SEQ ID NO:1774:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1774:

GGGTTTCT

8

## (2) INFORMATION FOR SEQ ID NO:1775:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1775:

GTGGGGBTGG C

11

## (2) INFORMATION FOR SEQ ID NO:1776:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1776:

CCBBGBGCTB GC

12

## (2) INFORMATION FOR SEQ ID NO:1777:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1777:

GTGGGAATTT CTGTGGGGBT GGCATACACG TAGGCAGCTC CAAGAGCTAG CAAACTCAAA  
TGCAGAAGCA TCCTCATGC TCTGAAACG

60

89

## (2) INFORMATION FOR SEQ ID NO:1778:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1778:

CTCAGTGGCC CCCAAAAGGA TGAGTAATAC ATGCGCCACG ATGATCATAT CCTTTTTACT  
ATGAGGCCGT GTCTGTCGTG TCTTTCCTTT GCTCTTGGTG TGTCTTTGCT GTGCCCTGCC  
TCTCTGCCCG TGTCTGTCGT GTCTTTCCTT TGCTCTGGT GTGTCTTTGC TGTGCCCTGC  
CTCTCTGCC GTGTCTGTCG TGTCTTTCCT TTGCTCTTG TGTGTCTTTG CTGTGCCCTG  
CCTCTCTGC

60

120

180

240

249

## (2) INFORMATION FOR SEQ ID NO:1779:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1779:

CCGTGTC

7

## (2) INFORMATION FOR SEQ ID NO:1780:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1780:

GCCCTGCC

8

## (2) INFORMATION FOR SEQ ID NO:1781:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1781:  
CTCBGTGGCC CCCBBBBGGG TGBGTBBTBC BTGCGCCBCG BTGBCBTBT CCTTTTTBCT  
BTGBGG

60  
66

(2) INFORMATION FOR SEQ ID NO:1782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 869 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1782:

GGGGGTGGCT	TCCTGCCGCG	TCTCTGGGCC	GTCCCGTCCC	TCGGCCCCCG	GCCGCGCTCG	60
GCTCCTCTCC	CTCTGGCCCG	GCTCGGGGCG	GGGCGGGGCG	GTGGGCGGGC	GGCGCTGCCC	120
TGCGCGCGGC	GCTGGCCCT	GCTGGCCGTC	GGCTGCGCGC	TGCTGGCTGC	CCTGTGGGCC	180
GCGCCGGGGC	CTGTCCGCCT	CTGCGGGCGC	TGTCTCTGG	CTGTCTTCC	GGCTCTTCTG	240
CTGGGGTGGG	GCTGGGCGGC	CGGCCCGGTG	CTGGGGCTCC	TCGGGGGGGG	GGGCTCTTCC	300
GGGCTGTCTC	CCTCCGGGGC	GGGGGTTTCT	GGCCGTGGGG	GTCTTGCCTG	GCCTCCGGGC	360
TCCTGCTTGT	CTTGCCCTTC	TTCTCTGGTC	GGTTGTGGCT	CGGGGCTCCG	TGGGTCCCTG	420
GCGCCCGTTT	GTGTTTTGTC	TTTCCCTG	GCCTCCCTGT	GCCCCTCTCC	TCTCCTTCTT	480
CTGCTTCTCG	CTCTCCTTTG	TGGGGCCCTC	CCTGCTGCTC	TTGGTTTTGG	GCTTTTTTTC	540
TCTTCTCCT	TTTTCTGCG	TGGGCCTCCG	CACGCTCTT	GCCACCTCCT	GCGCAGGGCA	600
GCGCCTTGGG	GCCAGCGCG	CTCCCGGCGC	GGCCAGCAGG	GCAGCCAGCA	GCGCGCAGCC	660
GACGGCCAGC	ATGCTTCCTC	CTCGGCTACC	ACTCCATGGT	CCCGCAGAGG	CGGACAGGCG	720
CBCGCCTCTT	GCCBCCTCCT	GCGCBGGGCB	GCGCCTTGGG	GCCBGCGCCG	CTCCCGGCGC	780
GGCCBGCBBG	GCBGCCBGC	GCGCGCBGCC	GBCGGCCBGC	BTGCTTCCTC	CTCGGCTBCC	840
BCTCCBTGGT	CCCGCBGBGG	CGGBCBGGC				869

(2) INFORMATION FOR SEQ ID NO:1783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1783:

GCBGCCBGC

13

(2) INFORMATION FOR SEQ ID NO:1784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1784:

CGCBGCCBGC

14

(2) INFORMATION FOR SEQ ID NO:1785:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 869 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1785:

GGGGGTGGCT	TCCTGCCGCG	TCTCTGGGCC	GTCCCGTCCC	TCGGCCCCCG	GCCGCGCTCG	60
GCTCCTCTCC	CTCTGGCCCG	GCTCGGGGCG	GGGCGGGGCG	GTGGGCGGGC	GGCGCTGCCC	120
TGCGCGCGGC	GCTGGCCCT	GCTGGCCGTC	GGCTGCGCGC	TGCTGGCTGC	CCTGTGGGCC	180
GCGCCGGGGC	CTGTCCGCCT	CTGCGGGCGC	TGTCTCTGG	CTGTCTTCC	GGCTCTTCTG	240
CTGGGGTGGG	GCTGGGCGGC	CGGCCCGGTG	CTGGGGCTCC	TCGGGGGGGG	GGGCTCTTCC	300
GGGCTGTCTC	CCTCCGGGGC	GGGGGTTTCT	GGCCGTGGGG	GTCTTGCCTG	GCCTCCGGGC	360
TCCTGCTTGT	CTTGCCCTTC	TTCTCTGGTC	GGTTGTGGCT	CGGGGCTCCG	TGGGTCCCTG	420
GCGCCCGTTT	GTGTTTTGTC	TTTTCCCTG	GCGTCCCTGT	GCCCCTCTCC	TCTCCTTCTT	480
CTGCTTCTCG	CTCTCCTTTG	TGGGGCCCTC	CCTGCTGCTC	TTGGTTTTGG	GCTTTTTTTC	540
TCTTCTCCT	TTTTCTGTCG	TGGGCCTCCG	CACGCTCTT	GCCACCTCCT	GCGCAGGGCA	600
GCGCCTTGGG	GCCAGCGCG	CTCCCGGCGC	GGCCAGCAGG	GCAGCCAGCA	GCGCGCAGCC	660
GACGGCCAGC	ATGCTTCCTC	CTCGGCTACC	ACTCCATGGT	CCCGCAGAGG	CGGACAGGCG	720
CBCGCCTCTT	GCCBCCTCCT	GCGCBGGGCB	GCGCCTTGGG	GCCBGCGCCG	CTCCCGGCGC	780
GGCCBGCBBG	GCBGCCBGC	GCGCGCBGCC	GBCGGCCBGC	BTGCTTCCTC	CTCGGCTBCC	840
BCTCCBTGGT	CCCGCBGBGG	CGGBCBGGC				869

(2) INFORMATION FOR SEQ ID NO:1786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1786:

488

GGGGCBGG

8

(2) INFORMATION FOR SEQ ID NO:1787:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1787:

GBBGGCBGCB GGC

13

(2) INFORMATION FOR SEQ ID NO:1788:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1788:

CCBGGBGCBCG CCCC

14

(2) INFORMATION FOR SEQ ID NO:1789:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1789:

BGGGBGBBGG CBBC

14

(2) INFORMATION FOR SEQ ID NO:1790:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1790:

CTCCTGGGGG TBCTGGGGCB GGGGBGGCBG CBGGCBBCBC CBGGBGCBCG CCCBGGGBGB  
BGGCBBCCTG BCCGBBGGCG CTTGTGGBGB BGGBTTCBT BGCTGGGCTC CTGGBGGGGB  
GBTBGBGC

60

120

128

(2) INFORMATION FOR SEQ ID NO:1791:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 244 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1791:

GGGGTGGBBB GGTGTGGBT BTGTCTTTBT GCBCTGBCBT CTBBGTTCTT TBGCBCTCCT  
TGGCBBBBCT GCBCTTCBC BCBGBGCTGC BGGBTBCBG BBGGCTGCCB BGBGBGCCBC  
GGCCBGCTTG GBBGTCBTGT TTBCBCBCBG TGBGTGGTT CCTCCGGGC TTGTGTGCTC  
TGCTGTCTCT TGGTTCCTTC CGGTGGTTTC TTCCTGGCTC TTGTCCTTC TCTTGGCCCT  
TGGC

60

120

180

240

244

(2) INFORMATION FOR SEQ ID NO:1792:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1792:

GGBGTBTG

8

(2) INFORMATION FOR SEQ ID NO:1793:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1793:

GCBCTGBCBT CT

12

(2) INFORMATION FOR SEQ ID NO:1794:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1794:  
CCGGTGG

7

(2) INFORMATION FOR SEQ ID NO:1795:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1795:  
GGCCCTTGGC

10

(2) INFORMATION FOR SEQ ID NO:1796:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 87 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1796:  
GGGGTGGBBB GGTTTGGBT BTGTCTTBT GCBCTGBCBT CTBBGTTCTT TBGCBCTCCT  
TGGCBBBCT GCBCTTCBC BCBGGC

60  
87

(2) INFORMATION FOR SEQ ID NO:1797:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 489 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1797:  
GGGCTCCCGC CGGBGBGGT TBTGGGCTCC CBGGBCCBCC CGCBCCGCGC GGBCGTTTBC  
BTTCCGCCBG CBGTGCGCGG CCGBCBTGBC GBBGTGGGC GCBTCBGGG TGGCGCCGCB  
GBBGTGGCCT CCGCGCBGCT GCBGGGBCBC CBTGBBGGGC CBCGCGTGGG GCCGCGCTCG  
CCGGCCCCC BCBTCTCCG BGGCCBGGC GGTGCCCCC BGCBCBBGG CCGGCBGGBC  
BCBGGCGBGG BGCBCGCGB GTCGGCGGCC GBGGTCTBT GTGGGGCTGG GGCTCCGGGG  
TCTCTGCCCC TCCGTGCTGG TGGGGCTGGG GCTCCGGGGT CTCTGCCCT CCGTGCCGCG  
TGGGGCCGCG CTCGCCGCC CCCCCCTGCC GGGTGGGCTC CCGCCGCGCG CCGGCCTGCC  
GGCCCCCTCGT GGGTCTGT GGGCGGGTCC GGGTCCCGGG GTGGGGCGC GBGTCGGCGG  
CCGBGGGTC

60  
120  
180  
240  
300  
360  
420  
480  
489

(2) INFORMATION FOR SEQ ID NO:1798:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1798:  
GGTGGGGC

8

(2) INFORMATION FOR SEQ ID NO:1799:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1799:  
GGGGCCG

7

(2) INFORMATION FOR SEQ ID NO:1800:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1800:  
GGCCGGGTCC GGG

13

(2) INFORMATION FOR SEQ ID NO:1801:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 317 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1801:  
GGGCTCCC GC CGGBGGGT TBTGGGCTCC CBGGBCCBCC CGCBCCGCGC GGBCGTTTBC 60  
BTTGCGCCBCG CBGTGCGCGG CCGBCBTGBC GBBGTTGGGC GCBTCBGGG TGGCGCCGCB 120  
GBBGTGGCCT CCGCGCBGCT GCBGGGBCBC CBTGBBGGGC CBGCGGTGGG GCCGCGCTCG 180  
CCGGCCCCCC BCBTCTCCG BGGCCBGGC GGTGCCCCC BGCBCBGG CCGGCBGGBC 240  
BCBGGCGBGG BGCBCGCGB GTCGGCGGCC GBGGGTCTG GTGGGGCTGG GGCTCCGGGG 300  
TCTCTGCCCC TCCGTGC 317

(2) INFORMATION FOR SEQ ID NO:1802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1802:

CGGGBGTGGG GGTCTGGBC GGCBCBTGBG GCBTCCBGGG CTCCTTCCB GTCCTTCTTG 60  
TCCGCTGCCB GCBCCCTTC BTTCBGBGG CTGBTGGCCT CCBCBGGGB CBTGBTTBGG 120  
TBGBBBCTBG GBGGCCGGCC TCCBCBGGG BCBTGGTCT TCTGTCCGC TGCCTCTCTG 180  
GGGTTTTCGG TCTGGGTGGG CTTTCTCTCT GGGGCTGCTG CTGGGCTCTT CTTTTTGTG 240  
CTGGCCTGGT GCTCTCTGT GCCCTTTCCC TTGGGTGTCT TGTTTTGTG GCCTCCBCCB 300  
GGGBCBTG 308

(2) INFORMATION FOR SEQ ID NO:1803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1803:

CGGGBGTGGG GG

12

(2) INFORMATION FOR SEQ ID NO:1804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1804:

GCCBGCBCCC C

11

(2) INFORMATION FOR SEQ ID NO:1805:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1805:

CCBCCBG

7

(2) INFORMATION FOR SEQ ID NO:1806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1806:

CGGGBGTGGG GGTCTGGBC GGCBCBTGBG GCBTCCBGGG CTCCTTCCB GTCCTTCTTG 60  
TCCGCTGCCB GCBCCCTTC BTTCBGBGG CTGBTGGCCT CCBCBGGGB CBTGBTTBGG 120  
TBGBBBCTBG GBGGCC 136

(2) INFORMATION FOR SEQ ID NO:1807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1807:

CCCTCCCBT CTGCTCTGBC CTGCTGGBT CTGGBTCTGB BGTBCCGCCB TGTBGGGGCG 60  
GGBGTGGGGC CTGCTCTCCC GGCCTCCGT GBTCTCCCCT GCCTCBGCCC CBGTGGGTBG 120  
GBGBBBGGCC BGCBBBGGCB GGBGTGGCTG CBTCTTTCCT GGTGGGGCCT GCTCTCCCGG 180  
CCTCCGTGTG TTGCTGGGTG TTTTCCCGTC TCTGGTCTGC CTTGGGGGT CGT 233

(2) INFORMATION FOR SEQ ID NO:1808:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1808:  
 GBBGBTBCGC C

11

(2) INFORMATION FOR SEQ ID NO:1809:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 9 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1809:  
 CBGCCCCBG

9

(2) INFORMATION FOR SEQ ID NO:1810:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 12 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1810:  
 TCCCGTCTCT GG

12

(2) INFORMATION FOR SEQ ID NO:1811:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 150 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1811:  
 CCCTCCBCBT CTGCTCTGBC CTGCTGGBCT CTGGBTCTGB BGBTBCGCCB TGTBGGGGCG 60  
 GGBGTGGGGC CTGCTCTCCC GGCCTCCGBT GBTCTCCCT GCCTCBGCCC CBGTGGGTBG 120  
 GBGBBBGGCC BGCBBBGC BGGTGGCTG 150

(2) INFORMATION FOR SEQ ID NO:1812:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 222 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1812:  
 CCGGGGCTGC BGCBBCTCB TCBGCTCTTG CCTGGBGTGG CTCBGCCTGG GCCTGCBGGG 60  
 CCBCCBGGBG BBTGGCBGCB BGGBTGGCB GGGTCCTCBT GGCTGGGGTC BCBGTCCTC 120  
 TBGCTBGGCB GGTGBCCBG BGGGGCGGG TCCTCBTGGC TGGGGGCCTG GGCCTGCBGG 180  
 GCGCTCTTG CCTGGBGTGG CTCGCCCBG GTCTTCCCTG GT 222

(2) INFORMATION FOR SEQ ID NO:1813:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 7 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1813:  
 CCGGGGC

7

(2) INFORMATION FOR SEQ ID NO:1814:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 14 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1814:  
 GGGCCTGCBG GGCC

14

(2) INFORMATION FOR SEQ ID NO:1815:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 10 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1815:  
 GGCBGCBGG

10

## (2) INFORMATION FOR SEQ ID NO:1816:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1816:

CCGGGGCTGC BGCBBCTCB TCBGCTCTTG CCTGGBGTGG CTCBGCCTGG GCCTGCBGGG 60  
 CCBCCBGGBG BBTGGCBGCB BGGBTGGCGB GGGTCCTCBT GGCTGGGGTC BCBGCTCCTC 120  
 TBGCTBGGCB GGGTGBCCBG BGBGGGC 147

## (2) INFORMATION FOR SEQ ID NO:1817:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1817:

CGCTGCBBTC TGCTCCGGGG CTGCBGCBBC CTCBTCBGCT CTTGCCTGGB GTGGCTCBGC 60  
 CTGGGCCTGC BGGGCCBCCB GGBGBBTGGC BGCBBGGBTG GCGBGGGTCC TCBTGGCTGG 120  
 GGTBCBCTGG BGGBGGGBGB GCBGGGGGTC CTCBTGGCTG GGGTCCCTCT CTCCCGTCCT 180

## (2) INFORMATION FOR SEQ ID NO:1818:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1818:

GGCBGCBGGG 10

## (2) INFORMATION FOR SEQ ID NO:1819:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1819:

GGCTGGGG 8

## (2) INFORMATION FOR SEQ ID NO:1820:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1820:

GGGGTCBCC 9

## (2) INFORMATION FOR SEQ ID NO:1821:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1821:

CGCTGCBBTC TGCTCCGGGG CTGCBGCBBC CTCBTCBGCT CTTGCCTGGB GTGGCTCBGC 60  
 CTGGGCCTGC BGGGCCBCCB GGBGBBTGGC BGCBBGGBTG GCGBGGGTCC TCBTGGCTGG 120  
 GGTBCBCTGG BGGBGGGBGB GCBGG 145

## (2) INFORMATION FOR SEQ ID NO:1822:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1822:

GTCTTTGTTT CTGGGCTCGT GCCCCBTCCC GGCTTCTCTC TGGTCCGTC CTCTGTGGTG 60  
 TTTGGCCCTG CTTCTTTTG CTGTGTAGG GGGCAGCAGT TGGGCCCCAA AGGCCCTCTC 120  
 GTTCACCTTC TGGCAGGAG TTGCATCCCC ATAGTCAAAC TCTGTGGTCG TGTCATAGTC 180  
 CTCTGTGGTG TTTGGAGTTT CCATCCCGGC TTCTCTCTGG TTCCAAGGGA GBGGGGGCBG 240  
 CBGTTGGGCC CCBGGGCC TCTCGTTCBC CTTCTGGCBC GGBGTTGCBT CCCCBTBGTG 300  
 BBBCTCTGTG GTCGTGTCBT BGTCTCTGT GGTGTTTGGB GTTCCBTCC CGGCTTCTCT 360  
 CTGTTCCBB GGG 374

(2) INFORMATION FOR SEQ ID NO:1823:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1823:

GGGCCCC

7

(2) INFORMATION FOR SEQ ID NO:1824:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1824:

GGGGGCBGC

9

(2) INFORMATION FOR SEQ ID NO:1825:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1825:

CCCGGCTTC

9

(2) INFORMATION FOR SEQ ID NO:1826:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1826:

GGGCBGCGGG	CBGTGGGCGG	GCBTGTBGG	CBBGCBGCB	GGGTGTGGTG	TCCGBGGBBT	60
BTGGGGBGGC	BGBTGCBGGB	GCGCBGBGGG	CBGTBGCBBT	GBGGBTGBCB	GCGBGGCGTG	120
CCGCGGBGBC	CTTCBTGGTB	CCTGTGGBGB	GGCTGTCCGB	GGGGGTGTGG	TGTCCGCTTG	180
GCGTTCTTT	CGGGTGTTC	TTCTCTGGGT	TGGCCTGCTG	CTCGTCGTGG	TCGCTCCGCT	240
CCCGGGTTCG	TCTCGTCTG	TCGCCCTTC	CTTCCTTGTC	GTGTTCTTCC	CTTCCTTGCC	300
TCT						303

(2) INFORMATION FOR SEQ ID NO:1827:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1827:

GGGTTGGC

8

(2) INFORMATION FOR SEQ ID NO:1828:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1828:

CGGGGCBG

8

(2) INFORMATION FOR SEQ ID NO:1829:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1829:

CCCGGGTTCG

10

(2) INFORMATION FOR SEQ ID NO:1830:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1830:

GGGTGTGGTG

10

## (2) INFORMATION FOR SEQ ID NO:1831:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1831:

GGGCBCGGGG CBGTGGGCGG GCBTGTBGG CBBGCBGCB GGGTGTGGTG TCCGBGGBBT 60  
 BTGGGGBGGC BGBTGCBGGB GCGCBGBGG CBGTBGCBBT GBGGBTGBCB GCGBGGCGTG 120  
 CCGCGGBGBC CTTCBTGGTB CCTGTGGBB GGCTGTCCGB GG 162

## (2) INFORMATION FOR SEQ ID NO:1832:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1832:

GCTGCCCCGG GGGGTGTGCG CTTGGCGCTC CCGTGCTCGG TTCTCTGTCT CCCGGTCCCC 60  
 CTTGCCTGGC GTCTCGGGCC TTCGTCCTCT TCCTCTTCTT CCTTCCGCTC CGTGGGGGGCT 120  
 GCTTGGTGGG GGCCTGTGCC TCGGGGTCCC GGGGCTTCTG GCCCTTGCCG TTCATGGTGG 180  
 CTAGGTGGGG CGTTCBTGGT GGCTBGGTGG GGC 213

## (2) INFORMATION FOR SEQ ID NO:1833:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1833:

GGTGGGGC

8

## (2) INFORMATION FOR SEQ ID NO:1834:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1834:

GCCCCGCGGG G

11

## (2) INFORMATION FOR SEQ ID NO:1835:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1835:

CGGGGCTTCT GGCCC

15

## (2) INFORMATION FOR SEQ ID NO:1836:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1836:

GGGGTGGGTB GGCCGTGTCT GGGGTTGGC CBGTGTGGT GCCTCTTGGT GGTGCGCCGG 60  
 GCGCGTCTTG GCTTTCTTCT CTTCCGGGCC CTCGGGCCG TGCTTGTGGG CTCCTCCCGG 120  
 GCGGCCTCCC CGGGCGGGG CTTCTGGCG CTGGCGGGG GGCCTCTGC TCTGTGGCTG 180  
 GGCGTTTCCT GGTGTTCTGG GTGGTGGCG GCGTGTGGC CTCTGTGGG GCCCGCGGCT 240  
 GCBGGGGTTG CCTGTCTGCT TCGTCCTTTG CGTCCCGGG CCGCCGGGGT GGGTAGGCCG 300  
 TGTCTGGGGG TTGGCCATGT TGGTGGCCG GCCCGCGGCT GCAGGGG 347

## (2) INFORMATION FOR SEQ ID NO:1837:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1837:

CCCCGGCGG

9



## (2) INFORMATION FOR SEQ ID NO:1838:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1838:

GGCGGGGGG CC

12

## (2) INFORMATION FOR SEQ ID NO:1839:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1839:

CCCCGGCCGC C

11

## (2) INFORMATION FOR SEQ ID NO:1840:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1840:

GGCCGTGT

8

## (2) INFORMATION FOR SEQ ID NO:1841:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 664 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1841:

CGGTTTCCTT	TGCGGTCTTG	GCCCGGGCTC	CGGGTGCCCG	CCCGCCCGCC	GGCCGCCGCC	60
CCGCCGGGCT	GTCCCCGCC	CGCCCCGCC	CGGGGCGCGG	GGCGGGCCCT	CCCCCCCCTC	120
TGGGCCGGCG	CGGGCGTCGG	CCGCTCGCGC	CTGGGGTTCC	CTCTCCTCCC	CCTGTGCGCC	180
TGCCTCTTGC	TCTTCTGCGT	CCGCTGCCTT	CTCCCCTCTC	CTCGGCCGTT	GCCTGTGCTG	240
TCCGTCCTGT	CGCCCTCCG	TGGTGCTGTT	GTCTCTTCTG	CCCTCGGTGT	GCTGGTGCTG	300
GTGGTGGTGC	CTCTGCCCCG	GCTCGCCCTG	CCTGGGCTGG	CCTCTTCGGG	TGTGGCTTTG	360
GGGCTCTCTT	GGTTGCCCTT	TCTTCTCGTG	GTGCCTCTCC	TCCCTGGCTT	GGTCGTTGTC	420
TGGGGTGGTG	CTCCTCTCCC	TTCCCTGCT	GGCCGTTTGT	CCTGTTTCT	GTCTTCCTCT	480
TTCTCCTGT	TTCTCCGTTT	GGCTTGCTGC	TTGCGGGGCT	GTCTCCCTTG	CCCCTGTGGG	540
CTTCCCTGG	TCCGTCTTC	TCCTTGGGG	TCGCCCTTCT	TGGTGGGCTG	GCTCGTCTGT	600
CTTTTCTCTT	CCTGGGGGTG	GCCGTTGTGG	GCCTGTGGT	CCGCCTTGCC	TCTGCTGGTC	660
TTTC						664

## (2) INFORMATION FOR SEQ ID NO:1842:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1842:

GGCCCCGGG

9

## (2) INFORMATION FOR SEQ ID NO:1843:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1843:

GCCGGCGCGG GCG

13

## (2) INFORMATION FOR SEQ ID NO:1844:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1844:

GCCTGGGCTG GCC

13

## (2) INFORMATION FOR SEQ ID NO:1845:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1845:  
 GGGGGTGGCC G 11

(2) INFORMATION FOR SEQ ID NO:1846:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1846:  
 GGGGGTGGCC GTTGTGGCG G 21

(2) INFORMATION FOR SEQ ID NO:1847:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 266 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1847:  
 GBTGTTTGT BCCBBGCBT CBBGBBTBGC TTTGCTBTCT BBGGBTCBCB TTBGBCBTB 60  
 GGBBBBCGCT GTBGGTCBGB BBGBTGTGCT TBCCTTCBCB CBGBGCTGCB GBBBTBGGGB 120  
 BGGCTGCCBB GBGBGCCBCG GCCBGCTTGG BGTCTGTGTT BCBCBCBGTG BGGTGCTCCG 180  
 GTGGCTTTT GCTTGTGTGC TCTGCTGTCT CTGTTCCTTC CGGTGTTTC TTCCTGGCTC 240  
 TTGTCCTTC TCTTGCCCT TGGCCC 266

(2) INFORMATION FOR SEQ ID NO:1848:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 7 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1848:  
 GCTCCG 7

(2) INFORMATION FOR SEQ ID NO:1849:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 10 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1849:  
 CBBGBBTBGC 10

(2) INFORMATION FOR SEQ ID NO:1850:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1850:  
 CBCBCBGTGB GGTGC 15

(2) INFORMATION FOR SEQ ID NO:1851:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1851:  
 BCCBBBGCBT CBBGBBTBGC 20

(2) INFORMATION FOR SEQ ID NO:1852:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1852:  
 GCCBBGBGBG CCBCGGCCBG C 21

## (2) INFORMATION FOR SEQ ID NO:1853:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1853:

GBTGTTTGT	BCCBBGCBT	CBBGBBTBGC	TTTGCTBTCT	BBGGBTCBCB	TTTBGBCBTB	60
GGBBBBCGCT	GTBGGTCBGB	BBGBTGTGCT	TBCCTTCBCB	CBGBGCTGCB	GBBBTCBGGB	120
BGGCTGCCBB	GBGBGCCBCG	GCCBGCTTGG	BGTCBTGTTT	BCBCBCBG TG	BGGTGCTCCG	180
GTGGCTTTTT	GCTTGT					196

## (2) INFORMATION FOR SEQ ID NO:1854:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1854:

ACAGGGGCTG	TAATCTTCAT	CTGCAGGTGG	CATGCCAGTG	AAATTTAGAT	CATCAAAATC	60
CCACATCTGT	GGATCTGTAA	TATTTGACAT	GTCCTCTTCA	GTTTCAGCAA	TGGTTTGATC	120
TAACGAAGC	ACCGGCCAGG	BCBGGGGCTG	TBBTCTTCBT	CTGCBGGTGG	CBTGCCBG TG	180
BBBTTTGBT	CBTCBBB BT	CCBCBTCTGT	GGBTCTGTBB	TBTTTGBCBT	GTCCTCTTCB	240
GTTTCBGCBB	TGGTTTGBTC	TBBCTGBBGC	BCCGGCCBGG	TGGCTCGGTG	CTTCTGCCCC	300
TGTTGTTGCG	GCGCTCGGTT	GGTGTGGCCC	CTGTGGTGCT	TCGTTTCCCC	CTCTTTCTCT	360
TTGTTCGGGG	GTTCTTG TGG	CGGGCTGCTT	GTCTCGTTCC			400

## (2) INFORMATION FOR SEQ ID NO:1855:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1855:

CBGGGGC

7

## (2) INFORMATION FOR SEQ ID NO:1856:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1856:

GCBGGTGCC

9

## (2) INFORMATION FOR SEQ ID NO:1857:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1857:

GCGGCGCTC

9

## (2) INFORMATION FOR SEQ ID NO:1858:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1858:

ACAGGGGCTG	TAATCTTCAT	CTGCAGGTGG	CATGCCAGTG	AAATTTAGAT	CATCAAAATC	60
CCACATCTGT	GGATCTGTAA	TATTTGACAT	GTCCTCTTCA	GTTTCAGCAA	TGGTTTGATC	120
TAACGAAGC	ACCGGCCAGG					140

## (2) INFORMATION FOR SEQ ID NO:1859:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1859:

BCBGGGGCTG	TBBTCTTCBT	CTGCBGGTGG	CBTGCCBG TG	BBBTTTGBT	CBTCBBB BT	60
CCBCBTCTGT	GGBTCTGTBB	TBTTTGBCBT	GTCCTCTTCB	GTTTCBGCBB	TGGTTTGBTC	120

TBBCTGBBGC BCCGGCCBGG

140

## (2) INFORMATION FOR SEQ ID NO:1860:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1860:

CTTGBGCBGG	BGGCTCTGGG	GCBGGGBGCT	GGCBGGGGCC	BGGGGGGTGG	CTTCCTGCBC	60
TGTCCBGBGT	GCBCTGTGCC	BCBGCBCBGC	CTGCBGGGCC	BTBGCCTTCB	TGGGGCTCTG	120
GGTGGCBGGT	CCBGCCBTGG	GTCTGGGTGG	GGCTGGGCTG	CBGGCTCCGG	GCGSTCCBGC	180
CBTGGGTCTG	GGGGCTGGGC	TGCBGGCTCC	GGGCGGGCGG	GTGCGGGCTG	CGTGCTGGGG	240
GCTGCCCCGC	AGGCCCTGCG	GTCCBGCBBT	GGGTCTGGGG	GCTGGGCTGC	BGGCTCCGGG	300
CGGGCGGGTG	CGGGCTGCCT	GCTGGGGGCT	GCCCCGAGG	CCCTGC		346

## (2) INFORMATION FOR SEQ ID NO:1861:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1861:

GBGCBGGBBG

10

## (2) INFORMATION FOR SEQ ID NO:1862:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1862:

GCCBCBGCBCB CBGC

14

## (2) INFORMATION FOR SEQ ID NO:1863:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1863:

GGGTGCGGGC

10

## (2) INFORMATION FOR SEQ ID NO:1864:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1864:

CTTGBGCBGG	BGGCTCTGGG	GCBGGGBGCT	GGCBGGGGCC	BGGGGGGTGG	CTTCCTGCBC	60
TGTCCBGBGT	GCBCTGTGCC	BCBGCBCBGC	CTGCBGGGCC	BTBGCCTTCB	TGGGGCTCTG	120
GGTGGCBGGT	CCBGCCBTGG	GTCTGGGTGG	GGCTGGGCTG	CBGGCTCCGG	GC	172

## (2) INFORMATION FOR SEQ ID NO:1865:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1865:

GCBCCGCCTG	GBGCCCTGGG	GCCCCCTGT	CTTCTTGGGG	BGCGCCTCCT	CGGCCBGTCT	60
CBGCTCCCGG	BTBGTGCTTT	CBGTGCTCBT	GGTGTCTTTT	CCBGGGGGBG	GBGGGGCTGG	120
TCCTCTGCTG	TCCTTGCTGG	TGCTCBTGGT	GTCTTTTCCG	CCCTGGGGCC	CCCCTGTCTT	180
CTTGGGGCCT	CTTCCCTCTG	GGGGCCGTCT	CTCTCCCTCT	CTTGCGTCTC	TCTCTTTCTC	240
TCTCTCTCTT	CCCCTTTCCC	GCTCTTTCTG	TCTCGGTGTC	TGGTTTCTC	TCTCCGCTGG	300
CTGCCTGTCT	GGCCTGCGCT	CTTGGCCTGT	GCTGTTCCTC	CTCCGGTTCC	TGTCCTCTCT	360
GTCTGTGCGC	CCCTCTGGGG	TCTCCCTCTG	GGTGGTGGTC	TTGTTGCTTG	GGCTGGGGCTC	420
CGTGTCTCCB	GTGCTCBTGG	TGTCCGCTGB	GGGBGCGTCT	GCTGGCGCTG	GTCTCTGTCT	480
GTCTGTGCTG	GTGCTCBTGG	TGTCTTTTCC	GCCCTGGGGC	CCCCCTGTCT	TCTTGGGGGCC	540
TCTTCCCTCT	GGGGGCCGTC	TCTCTCCCTC	TCTTGGCTCT	CTCTCTTTCT	CTCTCTCTCT	600
TCCCTTTTCC	CGCTCTTTCT	GTCTCGGTGT	CTGGTTTCT	CTCTCCGCTG	GCTGCCTGTC	660
TGGCCTGCGC	TCTTGGCCTG	TGCTGTTCCT	CCTCCGGTTC	CTGTCTCTCT	TGTCTGTCTG	720
CCCCTCTGGG	GTCTCCCTCT	GGCGTGGTGG	TCTTGTGTCT	TGGGCTGGGC	TCCGTGTCTC	780
CBGTGCTCBT	GGTGTCCGCT	GBGGGBGCGT	CTGCTGGC			818

- (2) INFORMATION FOR SEQ ID NO:1866:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1866:
- GGGGCCCCC
- 10
- (2) INFORMATION FOR SEQ ID NO:1867:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1867:
- GGGGCCCGTC T
- 11
- (2) INFORMATION FOR SEQ ID NO:1868:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1868:
- CCBGGGGBGB GBGGGGCTGG
- 20
- (2) INFORMATION FOR SEQ ID NO:1869:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1869:
- |            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| CTCGGTBGB  | CGGCTCGBBC | TCGGGTGGGC | CGGTGGTGBG | CGGCGGCGBC | BCGCGGBBGG | 60  |
| CCCTGCGCGC | CGBGBTCBCC | TGCBGGGBGB | BGTBGGCTTG | CBGCBGGBCT | CCCBGGBGGG | 120 |
| TGBCBGCBCG | CBGTBGBGCT | BCCTCGTCTC | TCBTGGTBCC | GTGCGTGTGG | TGGCBGCGGC | 180 |
| TGTGTGTGBB | GGCGBGCTGG | GCCCCGTCTG | CTGCTCCTCG | TGCCGCCTCG | TCCTTCATGG | 240 |
| TACCGTCGGT | GTGGTGGCCT | CGGGTGGGCC | GGTGGTGGGG | CGCGCGCGCT | CGCGTGGCTC | 300 |
| CGGCTCTTCT | TTCCCGGCTC | CGTGGGCCCG | GGGGCCTTGG | TCTCCCTCGT | CCTTCBTGGT | 360 |
| BCCG       |            |            |            |            |            | 364 |
- (2) INFORMATION FOR SEQ ID NO:1870:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1870:
- GCBGCBGGBC
- 10
- (2) INFORMATION FOR SEQ ID NO:1871:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1871:
- CCCGGCTCCG
- 10
- (2) INFORMATION FOR SEQ ID NO:1872:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1872:
- CGGCCCCGGG GCC
- 13
- (2) INFORMATION FOR SEQ ID NO:1873:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1873:

CBCGCGG

7

(2) INFORMATION FOR SEQ ID NO:1874:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1874:

CTCGGTBGB	C	G	C	T	C	G	B	B	C	T	C	G	G	G	T	G	G	G	C	C	G	T	G	B	G	C	B	C	G	G	C	G	C	G	B	C	B	C	G	G	B	B	G		60
CCCTGCGCG	C	G	B	B	T	C	B	C	C	T	G	C	B	G	G	B	B	G	B	G	T	G	G	C	T	T	G	C	B	G	C	B	G	B	C	T	C	C	B	G	B	G	G		120
TGBCBGC	B	G	C	B	G	C	B	G	C	T	B	C	T	C	T	G	C	T	B	C	C	T	G	T	B	C	C	G	T	G	G	T	G	G	T	G	G	T	G	G	T	G		180	
TGTGTGT	G	B	B	G	G	C	B	G	C	T	G	G																																200	

(2) INFORMATION FOR SEQ ID NO:1875:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 530 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1875:

BCCGGCGGB	G	C	C	C	B	G	G	G	T	G	G	B	G	T	G	G	G	T	T	C	C	C	G	C	G	T	T	C	T	C	B	C	C	C	B	C	C	G		60			
CGCTGBGCT	C	B	G	C	C	T	B	B	G	B	C	T	G	T	T	C	T	G	G	B	G	C	T	C	C	T	T	G	B	C	B	B	B	B	B	B	B	B	B	B	B		120
GBGBGBBB	B	T	C	B	G	C	B	B	B	T	B	B	T	C	C	B	T	T	C	T	G	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B		180	
CCCGTTGCG	C	T	G	G	C	G	C	G	C	G	C	T	G	C	G	G	T	T	C	C	T	G	G	G	T	T	C	C	T	C	C	C	C	C	C	C	C	C	C	C	C		240
TGTTGCCTT	T	G	T	T	G	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T		300	
TTTCTTTGT	G	T	C	G	G	T	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G		360	
TGCCTGCG	C	G	C	G	T	G	C	G	G	T	T	C	T	C	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T		420	
CCTTTGTGG	C	T	T	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T		480	
TTGTGCTCG	T	T	G	T	G	G	T	C	C	T	T	G	C	C	T	T	G	C	C	T	T	G	C	C	T	T	G	C	C	T	T	G	C	C	T	T	G	C	C	T		530	

(2) INFORMATION FOR SEQ ID NO:1876:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1876:

CCGGCGGBGC CGCCBGGGTG GBC

23

(2) INFORMATION FOR SEQ ID NO:1877:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1877:

CCGCCBGGG

9

(2) INFORMATION FOR SEQ ID NO:1878:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1878:

GGCGCGCGC

9

(2) INFORMATION FOR SEQ ID NO:1879:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1879:

GTGGGTCCGC

10

(2) INFORMATION FOR SEQ ID NO:1880:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1880:  
GCCCTGTCGG GCGGGAAGCC TCTCTCTCT CCCCAGATCC GCGACAGGCC GCAGGCAAGA 60  
ACCAGCGCAA CCAGGGCGCG TCCGCACAGA CTTGGAGGCG GCTGCATGCT GCTACCTGCT 120  
CCAGAAGCGT CCGGTGGCCG CCGCGCCCTG TCGGGCGGGB BGCCTCTCTC CTCTCCCCBG 180  
BTCCGCBBCB GGCCGCBGCG BBGBCCBGC GCBCCBGGG CGCGTCCGCB CBGBCTTGG 240  
GGCGGCTGCB TGCTGCTBCC TGCTCGGCG GGBGCCTCC GGTGGCCGCC GCGCGTCCGG 300  
TGGCGCCCGC GCCTCTCTCC TCTCCCGTG GCCTGTCCG GCGGGTCCTG CCGTCTGTCT 360  
TCCTTTTCTT TTGCTGTCTT GTCTCCCGT CTCTGCTTT 399

(2) INFORMATION FOR SEQ ID NO:1881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1881:  
CGGGCGGGBB GCC

13

(2) INFORMATION FOR SEQ ID NO:1882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1882:  
CGGGCGGG

8

(2) INFORMATION FOR SEQ ID NO:1883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1883:  
CCGCBBCBGC

10

(2) INFORMATION FOR SEQ ID NO:1884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1884:  
GCCCTGTCGG GCGGGAAGCC TCTCTCTCT CCCCAGATCC GCGACAGGCC GCAGGCAAGA 60  
ACCAGCGCAA CCAGGGCGCG TCCGCACAGA CTTGGAGGCG GCTGCATGCT GCTACCTGCT 120  
CCAGAAGCGT CCGGTGGCCG CCGC 144

(2) INFORMATION FOR SEQ ID NO:1885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1885:  
GCCCTGTCGG GCGGGBBGGC TCTCTCTCT CCCCAGATCC GCGACAGGCC GCBGGCBGBB 60  
BCCBGCGBB CCBGGGCGCG TCCGCBGBB CTTGGBGGCG GCTGCBTCT GCTBCCTGCT 120  
CCBGBBGGT CCGGTGGCCG CCGC 144

(2) INFORMATION FOR SEQ ID NO:1886:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 784 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1886:  
GTCTGTCTC CCGTCTCCT CCACTGCTT CTCCCGGGG CTCCCCGGG TTCGGGTGGC 60  
CGGTGTCCG GGCTCCGGG CGGCGGCGG TTCGGGTGGG GGTGGGTGGC GCGGGCTGCC 120  
GGGTCCGCG CCGGCTGGG CCTTGTGCT GCTTTTGTG TGTTCCTTC TGGCTGTCTC 180  
GGTCTGTGT GTGGTTGTTT TGTCTCTCT TGGGTGTGG CCTGCGGTT TTGGCTGTGG 240  
GCCCTTTGG GCCTTGCTT CTGGCTCGT TGTCTCTCC GTCTCTCTC ACTGCTTCTC 300  
CCGGGGGCTT CCGGCTTC GGTGGCCGG TGTCCGGGC TCCGGCGCG CGGCGGCTTC 360  
GGCTGCGGGT GGTGCGCGG GGCTGCCGG TCCGCGCGG GCCTGGGCCC TTGTGCTGCT 420  
TTTTGCTGT TCCGTTCTG CTGCTCCGT CTGTGTTGT GTTGTGTTT TTCTTCTTGG 480  
GTGTGGGCT TGCGTTTTG GCTGTGGGC CTTGGGGCC TTGGCTTCT GCTCCATCCA 540  
CATGATTGCT TAGATTGTG CTGTATCTT CAGGATTATC ACTGATTACA CATCCAACCA 600

GTGCCAGCCA AAAGGATGCC CTGAGGCAAA GGGTTTCCAT CTTGAGGCAA ATTTGAGGAC 660  
 BTCCBCBTGB TTGCTTBGBT TTGTGCTGB TCTCTCBGGB TTBTCBCTGB TTBCBCBTCC 720  
 BBCCBGTGCC BGCCBBBGG BTGCCCTGBG GCBGBGGTT TCCBTCTTGB GGCBBBTTTG 780  
 BGGG 784

## (2) INFORMATION FOR SEQ ID NO:1887:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1887:

GBGGCBBBGG G

11

## (2) INFORMATION FOR SEQ ID NO:1888:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1888:

GCCBGCBBB BGGG

14

## (2) INFORMATION FOR SEQ ID NO:1889:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1889:

CGCCTGGGCC C

11

## (2) INFORMATION FOR SEQ ID NO:1890:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1890:

CTGCTGBGGG TTGGGTCTCC GGGCGBTTCT CTGCBGBBGG TGCTCBBBGG GCTCCGGCBG 60  
 TTCCTCCTTG BTCTGGTCGC TGTCGTBCCB GTCGGBCCBG TBBTTCBGBT CBTCTTTGGC 120  
 TCCTBTCTTCT TCTGCBBCB GCTGBGTGGB GBCBBGBBBB BBGBCTGCCB BGGCCBCGBG 180  
 GBTTTTCBTG TTGBTTTTG CGBCGGBCBG TCCCGCGGGG TGCTGAGTTT CTCTGGTTCC 240  
 TCCGBGCGCB CGTGGTCGCT CCGCGTTTCT CTGGTTCCTC CGGTCCCGCG GGTGCTGTG 300  
 TGTCGCTGT CGTGGCTTGG GTCTCCGGGC GGTTCCTTC CTTTTCCGC 349

## (2) INFORMATION FOR SEQ ID NO:1891:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1891:

CTCCGGGCGB

10

## (2) INFORMATION FOR SEQ ID NO:1892:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1892:

GGCCBCBGGG

10

## (2) INFORMATION FOR SEQ ID NO:1893:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1893:

GGGTCTCCGG GCG

13

## (2) INFORMATION FOR SEQ ID NO:1894:

## (i) SEQUENCE CHARACTERISTICS:



(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1894:  
GGGTCTCCGG GCGG

14

(2) INFORMATION FOR SEQ ID NO:1895:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 250 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1895:  
CTGCTGBGGC TTGGGTCTCC GGGCGBTCTCT CTGCBGBBGB TGCTCBBBGG GCTCCGGCBG 60  
TTCTCTCTTG BTCTGGTCGC TGTCGTCCCB GTCCGBCCBG TBBTTCBGBT CBTCBTTGGC 120  
TCCTBTTTCT TCTGCBBCB GCTGBGTGGB GBCBBGBBBB BBGBCTGCCB BGGCCBCBGB 180  
GBTTTTCTG TTGGBTTTG CGBCGGBCBG TCCC GCGGGG TGCTGAGTTT CTCTGGTTCC 240  
TCCGBGCGCB 250

(2) INFORMATION FOR SEQ ID NO:1896:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 662 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1896:  
GGGCTBBGBT GTCCBCBTC BCTBCCBCGT TGCCCBCCBC BGBGGTCBCC BCBBTGBCCG 60  
TGTBGGCBGC TGCCBBBGG BCBTTTGCC BGGCTGGTTG CBCGBECTGB TTGGTTCCG 120  
BGGTGTBGT GGBGBTGTTT GGGGBGBGGT CTGBGTCCBC CGGGBGBGCG TTBTCCBTIT 180  
CGBBGCTBGG CGGTBBBGGC CTBCTBTCTG TBCBCBCCCC CCCTCTGCBG CBGBGTCTCTG 240  
TCGTGGCGCC TGGGGCTCBG GGTCCGGGCT AAGATGATCC ACATCACTAC CACGTTGCC 300  
ACCACAGAGG TCACCACAAT GACCGTGTAG GCAGCTGCCC AAAGGACAAT TTGCCAGGCT 360  
GGTTCACGA ACTGATTGGG TTCCGAGGTG TTAGTGGAGA TGTTGGGGA GAGGTCTGAG 420  
TCCACCGGGA GGACGTTATC CATTTGGAAG CTAGGCGGTA AAGCCCTACT ATCTGTACAC 480  
AACCCCTCTG TGCAGCAGAG TCCTGTCTGT GCGCCTGGGG CTCAGGGTCC GTCCTGTCGT 540  
GGCGCCTGGG GCTCTTCTTT TGTGGGCTCT TTGGTGGCTG TGGCTGTGGT CTCTGTGGTT 600  
GCTGCCCTGG GTCTGGGGGT GTGGCCTTGG GGCCGTCCTC TGGCTCCTCC TCGTGGGCCC 660  
CC 662

(2) INFORMATION FOR SEQ ID NO:1897:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1897:  
GGGBGGBCG

9

(2) INFORMATION FOR SEQ ID NO:1898:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1898:  
GGGTCCG

7

(2) INFORMATION FOR SEQ ID NO:1899:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1899:  
GGGCCCCC

8

(2) INFORMATION FOR SEQ ID NO:1900:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 567 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1900:  
GGBGCTGBTB CTGCBGATTT CBGBGGGBBG BBCCCTGBTB CTCBCCBGT TCBGCTCTGG 60

60

BGCBCBBGBG	BBBGBGCBGC	BGGGGGBGBG	GBBGBBGBGC	CBTCTTCCCB	GBGBGGCTGC	120
CTGBGCBBBT	GCTGGTTTTT	CTTTCCBGTC	TTGGGTTTTB	TBBCTCCCBG	BBGGCBBGBG	180
BGGGGCBBGG	CGTTTTCTTC	TCTCGCTGGT	TTTCCTTTCC	TGGCAGTGGG	TGGGGGTGGG	240
GGTGGGGTGG	CTTCCTTGTT	CCTGGGGGTG	TCCTCTTGCT	CTGGGCTTTT	CTCCCCTTTT	300
CCTTCTGTG	TGTTTTCTCG	GGGCTCTCCT	CTGTCTCTGT	GTCTTGCCCC	TGGCCCTCTT	360
CCCTCTCCTG	TCTCCTGTCC	CTGTGTTCCG	CCCGTCTTCC	CTCTCCTGAC	CTCCTTTTCC	420
TCCGCTGGGT	GGGGCCCTGC	CTGTTCTCTG	CTCCCTGGCT	TGGGGTTTCT	TCTGTGTGTC	480
TTCTTCTCT	GTTGGCTGGC	TTTCTCCTTC	TTTGTCTTTC	CTGGGTGCCC	CTTCTCCTT	540
TCTTGGGTCC	TTGGTGCTTG	GGCTGGG				567

## (2) INFORMATION FOR SEQ ID NO:1901:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1901:

GGBGCBCBBG

10

## (2) INFORMATION FOR SEQ ID NO:1902:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1902:

GBBGCBCG

8

## (2) INFORMATION FOR SEQ ID NO:1903:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1903:

GGGGCBBGGC G

11

## (2) INFORMATION FOR SEQ ID NO:1904:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1904:

GGBGCTGBTB	CTGCBGATT	CBGBGGGBBG	BBCCCTGBTB	CTCBCCBGCT	TCBGCTCTGG	60
BGCBCBBGBG	BBBGBGCBGC	BGGGGGBGBG	GBBGBBGBGC	CBTCTTCCCB	GBGBGGCTGC	120
CTGBGCBBBT	GCTGGTTTTT	CTTTCCBGTC	TTGGGTTTTB	TBBCTCCCBG	BBGGCBBGBG	180
BGGGGCBBGG						190

## (2) INFORMATION FOR SEQ ID NO:1905:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2028 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1905:

GCGTCTTGGG	GTGCBGGGCC	CBTCCTGCTG	CGCCTGGGCG	CTGCTGTGCG	TCCGTCTGCT	60
GGGGGGCCGG	GGTGGCTGGG	CCCTGCTTGC	CGCACGACCC	CGGGCCGACC	CGAGGCTCGG	120
GGGGCTGTGT	TCTGGCGCTG	GTGGGCTTGG	GCCCCCTCTG	GGGCTGGGTT	TCCTGCTGCG	180
CCTGGGGCGCT	GGCGTCTTGG	GGTGCGGGGC	CGGGGGGCCG	GGGGGCCGCT	GTTCTGTGGC	240
CTGGGGGTGC	CTGTGGCTGC	CGGTTGCCCC	GGTTGGTGCC	GCCGTCCTGC	TGCCGGTCTG	300
TGGCTGGGTC	CCCCCGCCCC	TTTCTGGGGG	TCCGCGTGGG	GTGCTCCGGT	TCCTCGTGCC	360
GCTGCTGCCT	TGCTTTTCCG	GCCGTGGCGG	CGTGGTGGTC	CGCCCCCCTT	GGCCTTCTGC	420
TCCGGGTCTG	GCTGGTTGCC	GGTGCCCTTG	GCGGCGGTCT	TCTTCCTGGT	GGCTCTGGGC	480
CCGGCCGGTC	TCCGGCGTCT	CGTGTTCCGT	CTTGTGCTGT	TCCGGCCGCT	CCTTCTCTTT	540
CCGCCGCCGC	CGCTCCCCGC	CCGCTCGTGC	CCCTGGCCCC	GCCTCCTCCT	GGCCGCTGTC	600
TCCGGCGGCG	GCCTTGGCGC	TCCGTTTGGG	GCTGCCTCTG	GCGCTTCCGG	CCCTCGGCCT	660
GGGCGCTCTC	TTCGCGCTGT	GCTGGTGGCC	CTCGTGGGCC	CCTCCTGGCC	TCCGGTGTCC	720
TGTGTTCCCC	CGGCTGGTGG	CCGGGCCGGT	TGGGCGGGCG	TGGGCGCCGG	CGGGTCTCTC	780
GGGCTGCCCT	TCTCCGCCGG	GGGTCCCGCG	CTCCTGCTGT	TCCCTGGGCT	CTTCTGCCTC	840
TCTCCTGGGT	GGGTGCTGGG	TGCCGGGGTC	TCCGGGCTTG	CCCCGCGCTG	CTGGGCGTTC	900
TGCGGTCTTG	GGGTTGTCTG	TGGCCCCGCT	CGTGTGCGCC	TCCGTCGCCC	GTCGCCGGCC	960
TCGTCCCCCT	CTGGGTGCGC	GGCGGGCTGG	TCCTGGCGTT	TTGCTCCTTC	CTGGGCGTCT	1020
TGGGGTGCBG	GGCCCBTCCT	GCTGCGCCTG	GGCGCTGCTG	TGCGTCCGTC	TGCTGGGGGG	1080
CCGGGGTGGC	TGGGCCCTGC	TTGCCGCACG	ACCCCGGGCC	GACCCGAGGC	TCCGGGGGGT	1140

GTGTTCTGGC	GCTGGTGGG	TTGGGCCCC	CTGGGGGCTG	GGTTTCCTGC	TGCGGCTGGG	1200
CGCTGGCGTC	TTGGGGTGG	GGGCCGGGG	GCCGGGGGG	CGCTGTTCGT	GGGCCTGGGG	1260
GTGCCTGTGG	CTGCCGTTG	CCCCGGTTG	TGGCGCCGTC	CTGCTGCCGG	TCGTTGGCTG	1320
GGTCCCCCG	CCCGTTTCT	GGGTCCGCG	TGGGGTGCTC	CGGTTCTCTG	TGCCGCTGCT	1380
GCCTTGTCTT	TCCGGCCGTG	GCGGCGTGGT	GGTCCGCCCC	CCCTGGCCTT	CTGCTCGGGG	1440
TCTGGCTGGT	TGCCGGTGCC	CTTGGCGGCG	GTCTTCTTCC	TGGTGGCTCT	GGGCCCGGCC	1500
GGTCTCGGGC	GTCTCGTGT	CGCTCTTGTG	CTGTTCCGGC	CGCTCCTTCC	TCTTCCGCCG	1560
CCGCCGCTCC	CCGCCGCTC	GTCCGCTGG	CCCGGCCTCC	TCCTGGCCCG	TGTCTCGGGC	1620
GGCGGCCTTG	GCGCTCCGTT	TGGGGCTGCC	TCTGGCGCTT	CCGGCCCTCG	GCCTGGGCGC	1680
TCTCTTCCGC	CTGTGCTGGT	GGCCCTCGTG	GGCCCTCCT	GGCCTCCGGT	GTCTGTGGT	1740
CCCCCGGCTG	GTGGCCGGGC	CGGTTGGGCG	GGCGTGGGCG	CCGGCGGGTC	CTCCGGGCTG	1800
CCCTTCTCCG	CCGGGGGTCC	CGCGCTCCTG	CTGTTCCCTG	GGCTCTTCTG	CCTCTCTCCT	1860
GGGTGGGTGC	TGGGTGCCGG	GGTCTCCGGG	CTTGCCCGCG	GCTGCTGGGC	GTTCTGCGGT	1920
CTTGGGGTTG	TCTGTGGCCC	CGCTCGTGTC	GCCCTCCGTC	GCCCGTCGCC	GGCCTCGTCC	1980
CCTCCTGGGT	GCGCGGCGGG	CTGGTCCTGG	CGTTTTGCTC	CTTCTGG		2028

## (2) INFORMATION FOR SEQ ID NO:1906:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1906:

GCGGGGCCG

9

## (2) INFORMATION FOR SEQ ID NO:1907:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1907:

CGGGGGGC

8

## (2) INFORMATION FOR SEQ ID NO:1908:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1908:

GCGCGGCGGG C

11

## (2) INFORMATION FOR SEQ ID NO:1909:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1909:

CGGTCTTGGG GTGCBGGGCC CBTCTGCTG CGCTGGGCG CTG

43

## (2) INFORMATION FOR SEQ ID NO:1910:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1910:

CTGCCCCBGT	TTTTGTCCT	CBCBTGCCGT	GGGGBGGBCB	BTGGCTGCCT	CCCCGGGGTT	60
TCTGCTGCTT	GCTGCTTCTT	TCCCGTCTCC	CTTCTTCC	GTCTCCTTTT	TGCCTCTTTG	120
GGTTCCTGTT	GTTTCTGGCC	TGCTTGGTGG	CGGCTGTGCG	GTTTCCTCTC	TCTTCTCTTG	180
GGTCTCCGCT	TCTCGTCCTG	CCTTTTCTCG	TCTCTGTGCG	GCCGTTCCCTC	CTCCGGCGTC	240
CTCCTGCCCT	GTGCTGTTTG	CCTCGGGTGG	TGCGGGTCCC	GGTGCTCCCC	CGGCGGGCCG	300
GCTGGTTGCC	TGGGCTGTG	TGGTGGGGTG	TGGGGCCGCT	GGGTGGGGGG	TGTGGTGGGC	360
TCTTCTGTGG	CCTGTGGGGG	TGTTGGTGTG	TCTGTGGGCG	TGTGCTGGGT	CTTGGGGCTT	420
CCTCCCTTGT	GCTGGGTGCG	GCCTCCCCGC	CCCCCTTCTG	GGCCGGTGGC	CTGCTCCTT	480
GTGGGCGCTT	CTGGCTCTTG	CCCTGTCTT	CTTCGCCTCG	TGGCTGCTGG	GCTGC	535

## (2) INFORMATION FOR SEQ ID NO:1911:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1911:  
CCCCGGGG

8

(2) INFORMATION FOR SEQ ID NO:1912:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1912:  
GGGGCCGCTG GG

12

(2) INFORMATION FOR SEQ ID NO:1913:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1913:  
GGGGGTGTGG

10

(2) INFORMATION FOR SEQ ID NO:1914:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1914:  
CTGCCCCBGT TTTTGTCTT CBCBTGCCGT GGGGBGGBCB BTGG

44

(2) INFORMATION FOR SEQ ID NO:1915:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1915:  
CGGCCCTTCT CACTGGAGGC ACCGGGACGT CCTCCATGGG AGGGTTGGGC TTGGCCGGGG 60  
CTGCCCCGTG CCTCCTCTTG GCTGGTCCCT CGTTGTCTT GGGCCCCGCT CCCGCTGCTC 120  
GGCCTCCGTG TTCTTTGGCC TCTTGCTCCG CCGTCTGTCT TGTCCTGCTC CCTCCTCGCT 180  
TGCGTTTCCC TCTTCTTGT CTTCAGGCC TTCCTCCGCT TCCGCTGCTG GGGCCCCGCG 240  
CGGGGGGGCG CTCGGCTCCG CGGCTTCCTC CCCGGCTGGG GGGTCTGTGT CTCCGGGGCC 300  
TGCGGCTCGC GGGCTCGGGG CTGCGTGC GC CGCGCGCGG GTCCGCGGTG GGTGGCGCTG 360  
TCCCGCCGTG GTGTGTCTCC GTTCTCGTCC TGCGCCGTCC TGGTCTGCCC GTGGGGTCTC 420  
GGGCGTGGTG GGGGGCGTCT GGTGCCTCGT CTGCCCCGTG GGGCTTCGGG CTCGGGGCTG 480  
TTCGTCCCCC CTGCGCTCT GTGGCTCCG GGGCTCCTCG TTTTCGCTGC TTCGGGTGTC 540  
CTTCTCGGCG TGTGGCCCCG GGTCCCGGCC CTGCTGGGCT GGGCGGGGTC GCTGCCCTGG 600  
GCTTCTGGCC CGTCTGGTTG TCTGTGCGTG CTGTCTCGG GTTCTGGCC TCTGTGCTGG 660  
GCGCTTCTCT GCCTCCTGCT CCGCCCTCCT GGTGGCTCGG CTGGGGGTGC CCGTGCGGGG 720  
GTGGGTGTGG GGTGTTTTCG GGTCTCTCCC CTTCCTC 756

(2) INFORMATION FOR SEQ ID NO:1916:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1916:  
GGGCGGGGTC GC

12

(2) INFORMATION FOR SEQ ID NO:1917:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1917:  
GCGCCGTCC

9

(2) INFORMATION FOR SEQ ID NO:1918:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1918:  
GGGCGTGGTG G

11

(2) INFORMATION FOR SEQ ID NO:1919:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1919:  
CGGCCCTTCT CACTGGAGGC ACCGGGCAGT CCTCCATGGG AGG

43

(2) INFORMATION FOR SEQ ID NO:1920:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1920:  
GTTTCATCTT GGCTTTATCC TCTCCCCTTG TTCCTCCCCT CTCCTGCTCT GGRGTCTCCT 60  
CTTCCCTCCC TCCCCTGCCG TGTGTCTGT GGGTGTCTGT TCGCTCTTGT TGCCCTGGGC 120  
CCTTCCCTGC TGGGGGGGAG TTTCATCTTG GGTTCBTCT TGGCTTTBTC CTCTCCCCTT 180  
GTTCTCCCC TCTCTGCTC TGGGTCTCC TCTTCCCTCC CTCCCCTGCC GTGTTGTCTG 240  
TGGGTGTCGT TTCGTCTTG TTGCCCTGGG CCCTTCCCTG CTGGGGGGGB GTTTCBTCTT 300  
GG 302

(2) INFORMATION FOR SEQ ID NO:1921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1921:  
GGGGGAGTT

9

(2) INFORMATION FOR SEQ ID NO:1922:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1922:  
GCCCTGGGCC C

11

(2) INFORMATION FOR SEQ ID NO:1923:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1923:  
GTTTCATCTT GGCTTTATCC TCTCCCCTTG TTCCTCCCCT CTCCTGCTCT GGRGTCTCCT 60  
CTTCCCTCCC TCCCCTGCCG TGTGTCTGT GGGTGTCTGT TCGCTCTTGT TGCCCTGGGC 120  
CCTTCCCTGC TGGGGGGGAG TTTCATCTTG G 151

(2) INFORMATION FOR SEQ ID NO:1924:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1924:  
GTTTCBTCTT GGCTTTBTCC TCTCCCCTTG TTCCTCCCCT CTCCTGCTCT GGRGTCTCCT 60  
CTTCCCTCCC TCCCCTGCCG TGTGTCTGT GGGTGTCTGT TCGCTCTTGT TGCCCTGGGC 120  
CCTTCCCTGC TGGGGGGGBG TTTCBTCTTG G 151

(2) INFORMATION FOR SEQ ID NO:1925:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1925:  
GGGGGBG

7

508

(2) INFORMATION FOR SEQ ID NO:1926:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1926:  
GTGGGTGTCC

10

(2) INFORMATION FOR SEQ ID NO:1927:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 91 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1927:  
CCGTGTTGTC BGTGGTGCTG CCGTTTGBG GTBTGGCGCT CCBCCBBTTC CCTTTTCTCC  
TTGTTTCCG TTTCTCTTGC CGTCTGTGGT T

60  
91

(2) INFORMATION FOR SEQ ID NO:1928:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1928:  
CCCGTTTGBG GTBTGGC

17

(2) INFORMATION FOR SEQ ID NO:1929:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1929:  
GCTCCBCCBB TTCCCTTTTC TCC

23

(2) INFORMATION FOR SEQ ID NO:1930:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1930:  
TTGTTTCCG TTTCTCTTG

19

(2) INFORMATION FOR SEQ ID NO:1931:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1931:  
CCGTCTGTGG TT

12

(2) INFORMATION FOR SEQ ID NO:1932:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1932:  
CCCGTTTGAG GTATGGC

17

(2) INFORMATION FOR SEQ ID NO:1933:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1933:  
GCTCCBCCAA TTCCCTTTTC TCC

23

(2) INFORMATION FOR SEQ ID NO:1934:  
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1934:  
GGGCCCCBGCC CCGCCGCCTT TTCTBGCCCC GGCC 34
- (2) INFORMATION FOR SEQ ID NO:1935:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1935:  
GGGCCCCBGCC CCGCCGCCTT TTCTBGCCCC GGC 33
- (2) INFORMATION FOR SEQ ID NO:1936:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1936:  
GGGCCCCBGCC CCGCCGCCTT TTCTBGCCCC GG 32
- (2) INFORMATION FOR SEQ ID NO:1937:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1937:  
GGGCCCCBGCC CCGCCGCCTT TTCTBGCCCC G 31
- (2) INFORMATION FOR SEQ ID NO:1938:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1938:  
GGGCCCCBGCC CCGCCGCCTT TTCTBGCCCC 30
- (2) INFORMATION FOR SEQ ID NO:1939:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1939:  
GGGCCCCBGCC CCGCCGCCTT TTCTBGCCCC 29
- (2) INFORMATION FOR SEQ ID NO:1940:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1940:  
GGGCCCCBGCC CCGCCGCCTT TTCTBGCC 28
- (2) INFORMATION FOR SEQ ID NO:1941:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1941:  
GGGCCCCBGCC CCGCCGCCTT TTCTBGC 27
- (2) INFORMATION FOR SEQ ID NO:1942:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1942:  
GGGCCCBGCC CCGCCGCCTT TTCTBG 26
- (2) INFORMATION FOR SEQ ID NO:1943:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1943:  
GGGCCCBGCC CCGCCGCCTT TTCTB 25
- (2) INFORMATION FOR SEQ ID NO:1944:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1944:  
GGGCCCBGCC CCGCCGCCTT TTCT 24
- (2) INFORMATION FOR SEQ ID NO:1945:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1945:  
GGGCCCBGCC CCGCCGCCTT TTC 23
- (2) INFORMATION FOR SEQ ID NO:1946:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1946:  
GGGCCCBGCC CCGCCGCCTT TT 22
- (2) INFORMATION FOR SEQ ID NO:1947:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1947:  
GGGCCCBGCC CCGCCGCCTT T 21
- (2) INFORMATION FOR SEQ ID NO:1948:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1948:  
GGGCCCBGCC CCGCCGCCTT 20
- (2) INFORMATION FOR SEQ ID NO:1949:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1949:  
GGGCCCBGCC CCGCCGCCT 19
- (2) INFORMATION FOR SEQ ID NO:1950:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1950:  
GGGCCCBGCC CCGCCGCC 18



- (2) INFORMATION FOR SEQ ID NO:1951:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1951:  
GGGCCCCBGCC CCGCCGC 17
- (2) INFORMATION FOR SEQ ID NO:1952:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1952:  
GGGCCCCBGCC CCGCCG 16
- (2) INFORMATION FOR SEQ ID NO:1953:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1953:  
GGGCCCCBGCC CCGCC 15
- (2) INFORMATION FOR SEQ ID NO:1954:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1954:  
GGGCCCCBGCC CCGC 14
- (2) INFORMATION FOR SEQ ID NO:1955:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1955:  
GGGCCCCBGCC CCG 13
- (2) INFORMATION FOR SEQ ID NO:1956:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1956:  
GGGCCCCBGCC CC 12
- (2) INFORMATION FOR SEQ ID NO:1957:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1957:  
GGGCCCCBGCC C 11
- (2) INFORMATION FOR SEQ ID NO:1958:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1958:  
GGCCCCBGCCC CGCCGCCTTT TCTBGCCCCG GC 32
- (2) INFORMATION FOR SEQ ID NO:1959:  
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1959:  
GCCCGCCCCC GCCGCCTTTT CTBGCCCCGG C 31
- (2) INFORMATION FOR SEQ ID NO:1960:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1960:  
CCCBGCCCCG CCGCCTTTTC TBGCCCCGGC 30
- (2) INFORMATION FOR SEQ ID NO:1961:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1961:  
CCBGCCCCGC CGCCTTTTCT BGCCCCGGC 29
- (2) INFORMATION FOR SEQ ID NO:1962:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1962:  
CBGCCCCGCC GCCTTTTCTB GCCCGGC 28
- (2) INFORMATION FOR SEQ ID NO:1963:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1963:  
BGCCCCGCCG CCTTTTCTBG CCCCCGC 27
- (2) INFORMATION FOR SEQ ID NO:1964:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1964:  
GCCCCGCCG CTTTTCTBGC CCGGC 26
- (2) INFORMATION FOR SEQ ID NO:1965:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1965:  
CCCCGCCGC TTTTCTBGCC CCGC 25
- (2) INFORMATION FOR SEQ ID NO:1966:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1966:  
CCCGCCGCT TTTCTBGCC CCGC 24
- (2) INFORMATION FOR SEQ ID NO:1967:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1967:  
CCGCCGCCTT TTCTBGCCCC GGC 23
- (2) INFORMATION FOR SEQ ID NO:1968:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1968:  
CGCCGCCTTT TCTBGCCCCG GC 22
- (2) INFORMATION FOR SEQ ID NO:1969:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1969:  
GCCGCCTTTT CTBGCCCCG C 21
- (2) INFORMATION FOR SEQ ID NO:1970:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1970:  
CCGCCTTTTC TBGCCCCGGC 20
- (2) INFORMATION FOR SEQ ID NO:1971:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1971:  
CGCCTTTTCT BGCCCCGGC 19
- (2) INFORMATION FOR SEQ ID NO:1972:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1972:  
GCCTTTTCTB GCCCCGGC 18
- (2) INFORMATION FOR SEQ ID NO:1973:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1973:  
CCTTTTCTBG CCCC GG C 17
- (2) INFORMATION FOR SEQ ID NO:1974:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1974:  
CTTTTCTBGC CCCGGC 16
- (2) INFORMATION FOR SEQ ID NO:1975:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1975:  
TTTTTCTBGC CCGGC 15

- (2) INFORMATION FOR SEQ ID NO:1976:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1976:  
TTTCTBGCCC CGGC 14
- (2) INFORMATION FOR SEQ ID NO:1977:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 13 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1977:  
TTCTBGCCCC GGC 13
- (2) INFORMATION FOR SEQ ID NO:1978:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 12 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1978:  
TCTBGCCCC GC 12
- (2) INFORMATION FOR SEQ ID NO:1979:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 11 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1979:  
CTBGCCCCG C 11
- (2) INFORMATION FOR SEQ ID NO:1980:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 25 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1980:  
GCGBGGCTGT CBCCTCGCTG GGCCC 25
- (2) INFORMATION FOR SEQ ID NO:1981:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 24 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1981:  
GCGBGGCTGT CBCCTCGCTG GGCC 24
- (2) INFORMATION FOR SEQ ID NO:1982:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 23 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1982:  
GCGBGGCTGT CBCCTCGCTG GGC 23
- (2) INFORMATION FOR SEQ ID NO:1983:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1983:  
GCGBGGCTGT CBCCTCGCTG GG 22
- (2) INFORMATION FOR SEQ ID NO:1984:  
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1984:  
GCGBGGCTGT CBCCTCGCTG G 21
- (2) INFORMATION FOR SEQ ID NO:1985:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1985:  
GCGBGGCTGT CBCCTCGCTG 20
- (2) INFORMATION FOR SEQ ID NO:1986:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1986:  
GCGBGGCTGT CBCCTCGCT 19
- (2) INFORMATION FOR SEQ ID NO:1987:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1987:  
GCGBGGCTGT CBCCTCGC 18
- (2) INFORMATION FOR SEQ ID NO:1988:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1988:  
GCGBGGCTGT CBCCTCG 17
- (2) INFORMATION FOR SEQ ID NO:1989:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1989:  
GCGBGGCTGT CBCCTC 16
- (2) INFORMATION FOR SEQ ID NO:1990:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1990:  
GCGBGGCTGT CBCCT 15
- (2) INFORMATION FOR SEQ ID NO:1991:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1991:  
GCGBGGCTGT CBCC 14
- (2) INFORMATION FOR SEQ ID NO:1992:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1992:  
GCGBGGCTGT CBC 13
- (2) INFORMATION FOR SEQ ID NO:1993:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1993:  
GCGBGGCTGT CB 12
- (2) INFORMATION FOR SEQ ID NO:1994:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1994:  
GCGBGGCTGT C 11
- (2) INFORMATION FOR SEQ ID NO:1995:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1995:  
GCGBGGCTGT 10
- (2) INFORMATION FOR SEQ ID NO:1996:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1996:  
CGBGGCTGTC BCCTCGCTGG GCCC 24
- (2) INFORMATION FOR SEQ ID NO:1997:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1997:  
BGGGCTGTCB CCTCGCTGGG CCC 23
- (2) INFORMATION FOR SEQ ID NO:1998:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1998:  
BGGCTGTCBC CTGCTGGGC CC 22
- (2) INFORMATION FOR SEQ ID NO:1999:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1999:  
GGCTGTCBCC TCGCTGGGCC C 21
- (2) INFORMATION FOR SEQ ID NO:2000:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2000:  
GCTGTCBCT CGCTGGGCC 20

- (2) INFORMATION FOR SEQ ID NO:2001:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2001:  
CTGTCBCCTC GCTGGGCCC 19
- (2) INFORMATION FOR SEQ ID NO:2002:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2002:  
TGTBCCTCG CTGGGCCC 18
- (2) INFORMATION FOR SEQ ID NO:2003:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2003:  
GTCBCCTCGC TGGGCCC 17
- (2) INFORMATION FOR SEQ ID NO:2004:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2004:  
TCBCCTCGCT GGGCCC 16
- (2) INFORMATION FOR SEQ ID NO:2005:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2005:  
CBCCTCGCTG GGCCC 15
- (2) INFORMATION FOR SEQ ID NO:2006:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2006:  
BCCTCGCTGG GCCC 14
- (2) INFORMATION FOR SEQ ID NO:2007:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2007:  
CCTCGCTGGG CCC 13
- (2) INFORMATION FOR SEQ ID NO:2008:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2008:  
CTCGCTGGGC CC 12
- (2) INFORMATION FOR SEQ ID NO:2009:  
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2009:  
TCGCTGGGCC C

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(2) INFORMATION FOR SEQ ID NO:2010:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2010:  
CGCTGGGCC

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(2) INFORMATION FOR SEQ ID NO:2011:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2011:  
GCGCGGCCGT CBTGGCGGCG TCGGCCGGG C

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(2) INFORMATION FOR SEQ ID NO:2012:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2012:  
GCGCGGCCGT CBTGGCGGCG TCGGCCGGG

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(2) INFORMATION FOR SEQ ID NO:2013:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2013:  
GCGCGGCCGT CBTGGCGGCG TCGGCCGG

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(2) INFORMATION FOR SEQ ID NO:2014:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2014:  
GCGCGGCCGT CBTGGCGGCG TCGGCCG

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(2) INFORMATION FOR SEQ ID NO:2015:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2015:  
GCGCGGCCGT CBTGGCGGCG TCGGCC

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(2) INFORMATION FOR SEQ ID NO:2016:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2016:  
GCGCGGCCGT CBTGGCGGCG TCGGC

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(2) INFORMATION FOR SEQ ID NO:2017:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid



- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2017:  
GCGCGGCCGT CBTGGCGGCG TCGGG
- (2) INFORMATION FOR SEQ ID NO:2018:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2018:  
GCGCGGCCGT CBTGGCGGCG TCGG
- (2) INFORMATION FOR SEQ ID NO:2019:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2019:  
GCGCGGCCGT CBTGGCGGCG TCG
- (2) INFORMATION FOR SEQ ID NO:2020:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2020:  
GCGCGGCCGT CBTGGCGGCG TC
- (2) INFORMATION FOR SEQ ID NO:2021:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2021:  
GCGCGGCCGT CBTGGCGGCG T
- (2) INFORMATION FOR SEQ ID NO:2022:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2022:  
GCGCGGCCGT CBTGGCGGCG
- (2) INFORMATION FOR SEQ ID NO:2023:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2023:  
GCGCGGCCGT CBTGGCGGC
- (2) INFORMATION FOR SEQ ID NO:2024:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2024:  
GCGCGGCCGT CBTGGCGG
- (2) INFORMATION FOR SEQ ID NO:2025:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2025:

GCGCGGCCGT CBTGGCG

17

## (2) INFORMATION FOR SEQ ID NO:2026:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2026:

GCGCGGCCGT CBTGGC

16

## (2) INFORMATION FOR SEQ ID NO:2027:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2027:

GCGCGGCCGT CBTGG

15

## (2) INFORMATION FOR SEQ ID NO:2028:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2028:

GCGCGGCCGT CBTG

14

## (2) INFORMATION FOR SEQ ID NO:2029:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2029:

GCGCGGCCGT CBT

13

## (2) INFORMATION FOR SEQ ID NO:2030:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2030:

GCGCGGCCGT CB

12

## (2) INFORMATION FOR SEQ ID NO:2031:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2031:

GCGCGGCCGT C

11

## (2) INFORMATION FOR SEQ ID NO:2032:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2032:

GCGCGGCCGT

10

## (2) INFORMATION FOR SEQ ID NO:2033:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2033:

CGCGGCCGTC BTGGCGGCGT CGGGCCGGGC

30

## (2) INFORMATION FOR SEQ ID NO:2034:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2034:  
GGGCCGTCB TGGCGGCGTC GGGCCGGGC 29
- (2) INFORMATION FOR SEQ ID NO:2035:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2035:  
CGGCCGTCBT GGGCGGCGTCG GGCCGGGC 28
- (2) INFORMATION FOR SEQ ID NO:2036:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2036:  
GGCCGTCBTG GGGCGGTCGG GCCGGGC 27
- (2) INFORMATION FOR SEQ ID NO:2037:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2037:  
GCCGTCBTGG CGGCGTCGGG CCGGGC 26
- (2) INFORMATION FOR SEQ ID NO:2038:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2038:  
CCGTCBTGGC GGGCTCGGGC CGGGC 25
- (2) INFORMATION FOR SEQ ID NO:2039:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2039:  
CGTCBTGGCG GCGTCGGGCC GGGC 24
- (2) INFORMATION FOR SEQ ID NO:2040:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2040:  
GTCBTGGCGG CGTCGGGCCG GGC 23
- (2) INFORMATION FOR SEQ ID NO:2041:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2041:  
TCBTGGCGGC GTCGGGCCG GC 22
- (2) INFORMATION FOR SEQ ID NO:2042:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2042:  
CBTGGCGGCG TCGGGCCGGG C 21
- (2) INFORMATION FOR SEQ ID NO:2043:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2043:  
BTGGCGGCGT CGGGCCGGGC 20
- (2) INFORMATION FOR SEQ ID NO:2044:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2044:  
TGGCGGCGTC GGGCCGGGC 19
- (2) INFORMATION FOR SEQ ID NO:2045:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2045:  
GGCGGCGTCG GCGGGGC 18
- (2) INFORMATION FOR SEQ ID NO:2046:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2046:  
GCGGCGTCGG GCCGGGC 17
- (2) INFORMATION FOR SEQ ID NO:2047:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2047:  
CGGCGTCGGG CCGGGC 16
- (2) INFORMATION FOR SEQ ID NO:2048:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2048:  
GGCGTCGGGC CGGGC 15
- (2) INFORMATION FOR SEQ ID NO:2049:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2049:  
GCGTCGGGCC GGGC 14
- (2) INFORMATION FOR SEQ ID NO:2050:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2050:

CGTCGGGCCG GGC

13

(2) INFORMATION FOR SEQ ID NO:2051:  
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2051:  
GTCGGGCCGG GC

12

(2) INFORMATION FOR SEQ ID NO:2052:  
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2052:  
TCGGGCCGGG C

11

(2) INFORMATION FOR SEQ ID NO:2053:  
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2053:  
CGGGCCGGGC

10

(2) INFORMATION FOR SEQ ID NO:2054:  
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2054:  
CCGCBGGCCB GGGCGGCCG CCGGCCGGGC CG

32

(2) INFORMATION FOR SEQ ID NO:2055:  
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2055:  
CCGCBGGCCB GGGCGGCCG CCGGCCGGGC C

31

(2) INFORMATION FOR SEQ ID NO:2056:  
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2056:  
CCGCBGGCCB GGGCGGCCG CCGGCCGGGC

30

(2) INFORMATION FOR SEQ ID NO:2057:  
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2057:  
CCGCBGGCCB GGGCGGCCG CCGGCCGGGC

29

(2) INFORMATION FOR SEQ ID NO:2058:  
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2058:  
CCGCBGGCCB GGGCGGCCG CCGGCCGGGC

28

(2) INFORMATION FOR SEQ ID NO:2059:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2059:  
CCGCBGGCCB GGGCGCGCCG CCGGCCG 27
- (2) INFORMATION FOR SEQ ID NO:2060:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2060:  
CCGCBGGCCB GGGCGCGCCG CCGGCC 26
- (2) INFORMATION FOR SEQ ID NO:2061:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2061:  
CCGCBGGCCB GGGCGCGCCG CCGGC 25
- (2) INFORMATION FOR SEQ ID NO:2062:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2062:  
CCGCBGGCCB GGGCGCGCCG CCGG 24
- (2) INFORMATION FOR SEQ ID NO:2063:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2063:  
CCGCBGGCCB GGGCGCGCCG CCG 23
- (2) INFORMATION FOR SEQ ID NO:2064:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2064:  
CCGCBGGCCB GGGCGCGCCG CC 22
- (2) INFORMATION FOR SEQ ID NO:2065:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2065:  
CCGCBGGCCB GGGCGCGCCG C 21
- (2) INFORMATION FOR SEQ ID NO:2066:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2066:  
CCGCBGGCCB GGGCGCGCCG 20
- (2) INFORMATION FOR SEQ ID NO:2067:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2067:  
CCGCBGGCCB GGGCGCGC 19
- (2) INFORMATION FOR SEQ ID NO:2068:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2068:  
CCGCBGGCCB GGGCGCGC 18
- (2) INFORMATION FOR SEQ ID NO:2069:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2069:  
CCGCBGGCCB GGGCGCG 17
- (2) INFORMATION FOR SEQ ID NO:2070:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2070:  
CCGCBGGCCB GGGCGC 16
- (2) INFORMATION FOR SEQ ID NO:2071:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2071:  
CCGCBGGCCB GGGCG 15
- (2) INFORMATION FOR SEQ ID NO:2072:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2072:  
CCGCBGGCCB GGGC 14
- (2) INFORMATION FOR SEQ ID NO:2073:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2073:  
CCGCBGGCCB GGG 13
- (2) INFORMATION FOR SEQ ID NO:2074:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2074:  
CCGCBGGCCB GG 12
- (2) INFORMATION FOR SEQ ID NO:2075:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2075:

CCGCBGGCCB G

11

(2) INFORMATION FOR SEQ ID NO:2076:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2076:

CCGCBGGCCB

10

(2) INFORMATION FOR SEQ ID NO:2077:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2077:

CCGCBGGCC

9

(2) INFORMATION FOR SEQ ID NO:2078:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2078:

CGCBGGCCBG GCGCGCCGC CGGCCGGCC G

31

(2) INFORMATION FOR SEQ ID NO:2079:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2079:

GCBGGCCBG GCGCGCCGC GCGCGGCCG

30

(2) INFORMATION FOR SEQ ID NO:2080:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2080:

CBGGCCBGG GCGCGCCGC GCCGGGCCG

29

(2) INFORMATION FOR SEQ ID NO:2081:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2081:

BGGCCBGGG GCGCGCCGC CCGGGCCG

28

(2) INFORMATION FOR SEQ ID NO:2082:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2082:

GGCCBGGGCG CGCGCCGC CCGGCCG

27

(2) INFORMATION FOR SEQ ID NO:2083:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2083:

GCCBGGGCG CGCGCCGC GGGCCG

26

(2) INFORMATION FOR SEQ ID NO:2084:



- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2084:  
CCBGGGCGCG CCGCCGGCCG GGCCG 25
- (2) INFORMATION FOR SEQ ID NO:2085:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2085:  
CBGGGCGCGC CGCCGGCCGG GCCG 24
- (2) INFORMATION FOR SEQ ID NO:2086:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2086:  
BGGGCGCGCC GCCGGCCGGG CCG 23
- (2) INFORMATION FOR SEQ ID NO:2087:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2087:  
GGGCGCGCCG CCGCCGGGC CG 22
- (2) INFORMATION FOR SEQ ID NO:2088:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2088:  
GGCGCGCCGC CGGCCGGGC G 21
- (2) INFORMATION FOR SEQ ID NO:2089:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2089:  
GCGCGCCGCC GGCCGGGCCG 20
- (2) INFORMATION FOR SEQ ID NO:2090:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2090:  
CGCGCCGCCG GCCGGGCCG 19
- (2) INFORMATION FOR SEQ ID NO:2091:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2091:  
GCGCGCCCG CCGGGCCG 18
- (2) INFORMATION FOR SEQ ID NO:2092:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2092:  
CGCCGCCGGC CGGGCCG 17
- (2) INFORMATION FOR SEQ ID NO:2093:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2093:  
GCCGCCGGCC GGGCCG 16
- (2) INFORMATION FOR SEQ ID NO:2094:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2094:  
CCGCCGGCCG GGCCG 15
- (2) INFORMATION FOR SEQ ID NO:2095:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2095:  
CGCCGGCCGG GCCG 14
- (2) INFORMATION FOR SEQ ID NO:2096:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2096:  
GCCGGCCGGG CCG 13
- (2) INFORMATION FOR SEQ ID NO:2097:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2097:  
CCGGCCGGGC CG 12
- (2) INFORMATION FOR SEQ ID NO:2098:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2098:  
CGGCCGGGCC G 11
- (2) INFORMATION FOR SEQ ID NO:2099:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2099:  
GGCCGGGCGC 10
- (2) INFORMATION FOR SEQ ID NO:2100:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2100:

GGGCGCBGGC TCCG

16

## (2) INFORMATION FOR SEQ ID NO:2101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2101:

GGGCCCCCTGG CTCGGCCCCG CGGCCCGGCT TGCCCGCCCC GCCCCG

46

## (2) INFORMATION FOR SEQ ID NO:2102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2102:

GGGCCCCCTGG CTCGGCCCCG CGGCCCGGCT TGCCCGCCCC GCCCCG

45

## (2) INFORMATION FOR SEQ ID NO:2103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2103:

GGGCCCCCTGG CTCGGCCCCG CGGCCCGGCT TGCCCGCCCC GCCC

44

## (2) INFORMATION FOR SEQ ID NO:2104:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2104:

GGGCCCCCTGG CTCGGCCCCG CGGCCCGGCT TGCCCGCCCC GCC

43

## (2) INFORMATION FOR SEQ ID NO:2105:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2105:

GGGCCCCCTGG CTCGGCCCCG CGGCCCGGCT TGCCCGCCCC GC

42

## (2) INFORMATION FOR SEQ ID NO:2106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2106:

GGGCCCCCTGG CTCGGCCCCG CGGCCCGGCT TGCCCGCCCC G

41

## (2) INFORMATION FOR SEQ ID NO:2107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2107:

GGGCCCCCTGG CTCGGCCCCG CGGCCCGGCT TGCCCGCCCC

40

## (2) INFORMATION FOR SEQ ID NO:2108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2108:

GGGCCCCCTGG CTCGGCCCCG CGGCCCGGCT TGCCCGCCCC

39

## (2) INFORMATION FOR SEQ ID NO:2109:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2109:  
GGGCCCCCTGG CTCGGCCCCG CGGCCCGGCT TGCCCCGC 38
- (2) INFORMATION FOR SEQ ID NO:2110:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2110:  
GGGCCCCCTGG CTCGGCCCCG CGGCCCGGCT TGCCCCGC 37
- (2) INFORMATION FOR SEQ ID NO:2111:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2111:  
GGGCCCCCTGG CTCGGCCCCG CGGCCCGGCT TGCCCCGC 36
- (2) INFORMATION FOR SEQ ID NO:2112:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2112:  
GGGCCCCCTGG CTCGGCCCCG CGGCCCGGCT TGCCCCGC 35
- (2) INFORMATION FOR SEQ ID NO:2113:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2113:  
GGGCCCCCTGG CTCGGCCCCG CGGCCCGGCT TGCCCCGC 34
- (2) INFORMATION FOR SEQ ID NO:2114:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2114:  
GGGCCCCCTGG CTCGGCCCCG CGGCCCGGCT TGCCCCGC 33
- (2) INFORMATION FOR SEQ ID NO:2115:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2115:  
GGGCCCCCTGG CTCGGCCCCG CGGCCCGGCT TGCCCCGC 32
- (2) INFORMATION FOR SEQ ID NO:2116:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2116:  
GGGCCCCCTGG CTCGGCCCCG CGGCCCGGCT TGCCCCGC 31
- (2) INFORMATION FOR SEQ ID NO:2117:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2117:  
GGGCCCTGG CTCGGCCCCG CGGCCGGCT 30
- (2) INFORMATION FOR SEQ ID NO:2118:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2118:  
GGGCCCTGG CTCGGCCCCG CGGCCGGC 29
- (2) INFORMATION FOR SEQ ID NO:2119:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2119:  
GGGCCCTGG CTCGGCCCCG CGGCCGG 28
- (2) INFORMATION FOR SEQ ID NO:2120:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2120:  
GGGCCCTGG CTCGGCCCCG CGGCCG 27
- (2) INFORMATION FOR SEQ ID NO:2121:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2121:  
GGGCCCTGG CTCGGCCCCG CGGCC 26
- (2) INFORMATION FOR SEQ ID NO:2122:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2122:  
GGGCCCTGG CTCGGCCCCG CGGCC 25
- (2) INFORMATION FOR SEQ ID NO:2123:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2123:  
GGGCCCTGG CTCGGCCCCG CGGC 24
- (2) INFORMATION FOR SEQ ID NO:2124:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2124:  
GGGCCCTGG CTCGGCCCCG CGG 23
- (2) INFORMATION FOR SEQ ID NO:2125:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2125:

GGGCCCCTGG CTCGGCCCCG CG

22

(2) INFORMATION FOR SEQ ID NO:2126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2126:

GGGCCCCTGG CTCGGCCCCG C

21

(2) INFORMATION FOR SEQ ID NO:2127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2127:

GGGCCCCTGG CTCGGCCCCG

20

(2) INFORMATION FOR SEQ ID NO:2128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2128:

GGGCCCCTGG CTCGGCCCC

19

(2) INFORMATION FOR SEQ ID NO:2129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2129:

GGGCCCCTGG CTCGGCCC

18

(2) INFORMATION FOR SEQ ID NO:2130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2130:

GGGCCCCTGG CTCGGCC

17

(2) INFORMATION FOR SEQ ID NO:2131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2131:

GGGCCCCTGG CTCGGC

16

(2) INFORMATION FOR SEQ ID NO:2132:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2132:

GGGCCCCTGG CTCGG

15

(2) INFORMATION FOR SEQ ID NO:2133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2133:

GGGCCCCTGG CTCG

14

(2) INFORMATION FOR SEQ ID NO:2134:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2134:  
GGGCCCTGG CTC 13
- (2) INFORMATION FOR SEQ ID NO:2135:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2135:  
GGGCCCTGG CT 12
- (2) INFORMATION FOR SEQ ID NO:2136:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 45 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2136:  
GGCCCTGGC TCGCCCCGC GCGCGGCTT GCCCGCCGG CCCGG 45
- (2) INFORMATION FOR SEQ ID NO:2137:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 44 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2137:  
GGCCCTGGCT CGCCCCGCG GCGCGGCTT GCCCGCCGG CCGG 44
- (2) INFORMATION FOR SEQ ID NO:2138:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 43 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2138:  
CCCTGGCTC GCGCCGCGG CCGGCTTGC CCGCCGGCC CGG 43
- (2) INFORMATION FOR SEQ ID NO:2139:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2139:  
CCCTGGCTCG GCGCCGCGG CCGGCTTGC CCGCCGGCC GG 42
- (2) INFORMATION FOR SEQ ID NO:2140:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 41 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2140:  
CCTGGCTCG CCGCGGGCC CGGCTTGCC GCGCGGCCG G 41
- (2) INFORMATION FOR SEQ ID NO:2141:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2141:  
CTGGCTCGC CCGCGGGCC GGCTTGCCG CCGCGGCCG 40
- (2) INFORMATION FOR SEQ ID NO:2142:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2142:  
TGGCTCGGCC CCGCGGCCCG GCTTGCCCGC CCGGCCCGG 39
- (2) INFORMATION FOR SEQ ID NO:2143:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2143:  
GGCTCGGCC CCGGCCCGG CTTGCCCGC CGGCCCGG 38
- (2) INFORMATION FOR SEQ ID NO:2144:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2144:  
GCTCGGCCCG CCGGCCCGG TTGCCCGCC GGCCCGG 37
- (2) INFORMATION FOR SEQ ID NO:2145:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2145:  
CTCGGCCCG CCGGCCCGGCT TGCCCGCCG GCCCGG 36
- (2) INFORMATION FOR SEQ ID NO:2146:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2146:  
TCGGCCCCG GGCCCGGCTT GCCCGCCCG CCCGG 35
- (2) INFORMATION FOR SEQ ID NO:2147:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2147:  
CGGCCCGCG GCCCGGCTTG CCCGCCCGG CCGG 34
- (2) INFORMATION FOR SEQ ID NO:2148:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2148:  
GGCCCCCGG CCCGGCTTG CCGCCCGGCC CGG 33
- (2) INFORMATION FOR SEQ ID NO:2149:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2149:  
GCCCCCGGC CCGGCTTGCC CGCCCGGCC GG 32
- (2) INFORMATION FOR SEQ ID NO:2150:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2150:



CCCCGCGGCC CGGCTTGCCC GCGCGCCCCG G	31
(2) INFORMATION FOR SEQ ID NO:2151: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2151: CCCCGCGGCC GGCTTGCCCC CCGGCCCCG	30
(2) INFORMATION FOR SEQ ID NO:2152: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2152: CCGCGGCCCC GCTTGCCCCG CCGGCCCCG	29
(2) INFORMATION FOR SEQ ID NO:2153: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2153: CGCGGCCCCG CTTGCCCCG CCGCCCCG	28
(2) INFORMATION FOR SEQ ID NO:2154: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2154: GCGGCCCCG TTGCCCCG GCGCCCCG	27
(2) INFORMATION FOR SEQ ID NO:2155: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2155: CGGCCCCGCT TGCCCCCG GCGGCCG	26
(2) INFORMATION FOR SEQ ID NO:2156: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2156: GGCCCCGCTT GCGGCCCCG CCGG	25
(2) INFORMATION FOR SEQ ID NO:2157: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2157: GCCCCGCTTG CCGCCCCG CCGG	24
(2) INFORMATION FOR SEQ ID NO:2158: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2158: CCCCGCTTGC CCGCCCCG CCG	23
(2) INFORMATION FOR SEQ ID NO:2159:	

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2159:  
CCGGCTTGCC CGCCGGCC GG 22
- (2) INFORMATION FOR SEQ ID NO:2160:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2160:  
CGGCTTGCC GCGCGCCG G 21
- (2) INFORMATION FOR SEQ ID NO:2161:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2161:  
GGCTTGCCCG CCGGCCCG 20
- (2) INFORMATION FOR SEQ ID NO:2162:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2162:  
GCTTGCCCG CCGGCCG 19
- (2) INFORMATION FOR SEQ ID NO:2163:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2163:  
CTTGCCCG CCGGCCG 18
- (2) INFORMATION FOR SEQ ID NO:2164:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2164:  
TTGCCCGCC GCGCCG 17
- (2) INFORMATION FOR SEQ ID NO:2165:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2165:  
TGCCCGCCG GCGCCG 16
- (2) INFORMATION FOR SEQ ID NO:2166:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2166:  
GCCCGCCG CCGC 15
- (2) INFORMATION FOR SEQ ID NO:2167:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2167:  
CCCGCCCCGGC CCGG 14

(2) INFORMATION FOR SEQ ID NO:2168:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2168:  
CCGCCCCGGCC CGG 13

(2) INFORMATION FOR SEQ ID NO:2169:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2169:  
CGCCCCGGCCC GG 12

(2) INFORMATION FOR SEQ ID NO:2170:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2170:  
GCCCCGGCCCG G 11

(2) INFORMATION FOR SEQ ID NO:2171:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2171:  
GGCGGGGGGCG GCGGCGCCTG GCTCGCCTBG GGCCCC 36

(2) INFORMATION FOR SEQ ID NO:2172:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2172:  
GGCGGGGGGCG GCGGCGCCTG GCTCGCCTBG GGCCC 35

(2) INFORMATION FOR SEQ ID NO:2173:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2173:  
GGCGGGGGGCG GCGGCGCCTG GCTCGCCTBG GGCC 34

(2) INFORMATION FOR SEQ ID NO:2174:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2174:  
GGCGGGGGGCG GCGGCGCCTG GCTCGCCTBG GGC 33

(2) INFORMATION FOR SEQ ID NO:2175:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2175:

GGCGGGGGCG GCGGCGCCTG GCTCGCCTBG GG	32
(2) INFORMATION FOR SEQ ID NO:2176: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2176: GGCGGGGGCG GCGGCGCCTG GCTCGCCTBG G	31
(2) INFORMATION FOR SEQ ID NO:2177: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2177: GGCGGGGGCG GCGGCGCCTG GCTCGCCTBG	30
(2) INFORMATION FOR SEQ ID NO:2178: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2178: GGCGGGGGCG GCGGCGCCTG GCTCGCCTB	29
(2) INFORMATION FOR SEQ ID NO:2179: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2179: GGCGGGGGCG GCGGCGCCTG GCTCGCCT	28
(2) INFORMATION FOR SEQ ID NO:2180: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2180: GGCGGGGGCG GCGGCGCCTG GCTCGCC	27
(2) INFORMATION FOR SEQ ID NO:2181: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2181: GGCGGGGGCG GCGGCGCCTG GCTCGC	26
(2) INFORMATION FOR SEQ ID NO:2182: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2182: GGCGGGGGCG GCGGCGCCTG GCTCG	25
(2) INFORMATION FOR SEQ ID NO:2183: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2183: GGCGGGGGCG GCGGCGCCTG GCTC	24
(2) INFORMATION FOR SEQ ID NO:2184:	

- (1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2184:  
GGCGGGGGCG GCGGCGCCTG GCT 23
- (2) INFORMATION FOR SEQ ID NO:2185:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2185:  
GGCGGGGGCG GCGGCGCCTG GC 22
- (2) INFORMATION FOR SEQ ID NO:2186:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2186:  
GGCGGGGGCG GCGGCGCCTG G 21
- (2) INFORMATION FOR SEQ ID NO:2187:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2187:  
GGCGGGGGCG GCGGCGCCTG 20
- (2) INFORMATION FOR SEQ ID NO:2188:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2188:  
GGCGGGGGCG GCGGCGCCT 19
- (2) INFORMATION FOR SEQ ID NO:2189:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2189:  
GGCGGGGGCG GCGGCGCC 18
- (2) INFORMATION FOR SEQ ID NO:2190:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2190:  
GGCGGGGGCG GCGGCGC 17
- (2) INFORMATION FOR SEQ ID NO:2191:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2191:  
GGCGGGGGCG GCGGCG 16
- (2) INFORMATION FOR SEQ ID NO:2192:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2192:  
GGCGGGGGCG GCGGC 15
- (2) INFORMATION FOR SEQ ID NO:2193:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2193:  
GGCGGGGGCG GCGG 14
- (2) INFORMATION FOR SEQ ID NO:2194:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2194:  
GGCGGGGGCG GCG 13
- (2) INFORMATION FOR SEQ ID NO:2195:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2195:  
GGCGGGGGCG GC 12
- (2) INFORMATION FOR SEQ ID NO:2196:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2196:  
GGCGGGGGCG G 11
- (2) INFORMATION FOR SEQ ID NO:2197:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2197:  
GGCGGGGGCGG CGGCGCTGG CTCGCTBGG GCCC 35
- (2) INFORMATION FOR SEQ ID NO:2198:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2198:  
CGGGGGCGGC GCGCCTGGC TCGCCTBGGG CCCC 34
- (2) INFORMATION FOR SEQ ID NO:2199:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2199:  
GGGGGCGGCG GCGCCTGGCT CGCCTBGGGC CCC 33
- (2) INFORMATION FOR SEQ ID NO:2200:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2200:

GGGGCGGCGG CGCCTGGCTC GCCTBGGGCC CC

32

(2) INFORMATION FOR SEQ ID NO:2201:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2201:

GGGCGGCGGC GCCTGGCTCG CTBGGGCC C

31

(2) INFORMATION FOR SEQ ID NO:2202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2202:

GGCGGCGGCG CCTGGCTCGC CTBGGGCC

30

(2) INFORMATION FOR SEQ ID NO:2203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2203:

GGCGGCGGCG CTGGCTCGCC TBGGGCC

29

(2) INFORMATION FOR SEQ ID NO:2204:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2204:

CGCGGCGGCC TGGCTCGCCT BGGGCC

28

(2) INFORMATION FOR SEQ ID NO:2205:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2205:

GGCGGCGCCT GGCTCGCCTB GGGCCC

27

(2) INFORMATION FOR SEQ ID NO:2206:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2206:

GCGGCGCCTG GCTCGCCTBG GGCCCC

26

(2) INFORMATION FOR SEQ ID NO:2207:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2207:

CGGCGCCTGG CTCGCCTBGG GCCCC

25

(2) INFORMATION FOR SEQ ID NO:2208:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2208:

GGCGCCTGGC TCGCCTBGGG CCCC

24

(2) INFORMATION FOR SEQ ID NO:2209:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2209:  
CGCCTGGCT CGCCTBGGGC CCC 23
- (2) INFORMATION FOR SEQ ID NO:2210:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2210:  
CGCCTGGCTC GCCTBGGGCC CC 22
- (2) INFORMATION FOR SEQ ID NO:2211:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2211:  
GCCTGGCTCG CCTBGGGCCC C 21
- (2) INFORMATION FOR SEQ ID NO:2212:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2212:  
CCTGGCTCGC CTBGGGCCCC 20
- (2) INFORMATION FOR SEQ ID NO:2213:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2213:  
CTGGCTCGCC TBGGGCCCC 19
- (2) INFORMATION FOR SEQ ID NO:2214:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2214:  
TGGCTCGCCT BGGGCCCC 18
- (2) INFORMATION FOR SEQ ID NO:2215:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2215:  
GGCTCGCCTB GGGCCC 17
- (2) INFORMATION FOR SEQ ID NO:2216:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2216:  
GCTCGCCTBG GGCCCC 16
- (2) INFORMATION FOR SEQ ID NO:2217:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid



- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2217:  
CTCGCCTBGG GCCC 15
- (2) INFORMATION FOR SEQ ID NO:2218:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2218:  
TCGCCTBGGG CCCC 14
- (2) INFORMATION FOR SEQ ID NO:2219:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2219:  
CGCCTBGGGC CCC 13
- (2) INFORMATION FOR SEQ ID NO:2220:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2220:  
GCCTBGGGCC CC 12
- (2) INFORMATION FOR SEQ ID NO:2221:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2221:  
CCTBGGGCC C 11
- (2) INFORMATION FOR SEQ ID NO:2222:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2222:  
CTBGGGCC 10
- (2) INFORMATION FOR SEQ ID NO:2223:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2223:  
GGGTGGGCBC GCGGCC 17
- (2) INFORMATION FOR SEQ ID NO:2224:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2224:  
GGTCGGCGBB GBGCTCGTCG TGCC 24
- (2) INFORMATION FOR SEQ ID NO:2225:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2225:

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GGTCGGCGBB GBGCTCGTCG TGG	23
(2) INFORMATION FOR SEQ ID NO:2226: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2226: GGTCGGCGBB GBGCTCGTCG TG	22
(2) INFORMATION FOR SEQ ID NO:2227: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2227: GGTCGGCGBB GBGCTCGTCG T	21
(2) INFORMATION FOR SEQ ID NO:2228: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2228: GGTCGGCGBB GBGCTCGTCG	20
(2) INFORMATION FOR SEQ ID NO:2229: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2229: GGTCGGCGBB GBGCTCGTC	19
(2) INFORMATION FOR SEQ ID NO:2230: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2230: GGTCGGCGBB GBGCTCGT	18
(2) INFORMATION FOR SEQ ID NO:2231: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2231: GGTCGGCGBB GBGCTCG	17
(2) INFORMATION FOR SEQ ID NO:2232: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2232: GGTCGGCGBB GBGCTC	16
(2) INFORMATION FOR SEQ ID NO:2233: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2233: GGTCGGCGBB GBGCT	15
(2) INFORMATION FOR SEQ ID NO:2234:	

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- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2234:  
GGTCGGCGBB GBGC 14
- (2) INFORMATION FOR SEQ ID NO:2235:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2235:  
GGTCGGCGBB GBG 13
- (2) INFORMATION FOR SEQ ID NO:2236:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2236:  
GGTCGGCGBB GB 12
- (2) INFORMATION FOR SEQ ID NO:2237:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2237:  
GGTCGGCGBB G 11
- (2) INFORMATION FOR SEQ ID NO:2238:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2238:  
GTCGGCGBBG BGCTCGTCGT GGC 23
- (2) INFORMATION FOR SEQ ID NO:2239:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2239:  
TCGGCGBBBG GCTCGTCGTG GC 22
- (2) INFORMATION FOR SEQ ID NO:2240:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2240:  
CGGCGBBBG CTCGTCGTGG C 21
- (2) INFORMATION FOR SEQ ID NO:2241:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2241:  
GGCGBBBGTC TCGTCGTGGC 20
- (2) INFORMATION FOR SEQ ID NO:2242:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2242:  
GCGBBGBGCT CGTCGTGGC 19

(2) INFORMATION FOR SEQ ID NO:2243:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2243:  
CGBBGBGCTC GTCGTGGC 18

(2) INFORMATION FOR SEQ ID NO:2244:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2244:  
GBBGBGCTCG TCGTGGC 17

(2) INFORMATION FOR SEQ ID NO:2245:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2245:  
BBGBGCTCGT CGTGGC 16

(2) INFORMATION FOR SEQ ID NO:2246:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2246:  
BGBGCTCGTC GTGGC 15

(2) INFORMATION FOR SEQ ID NO:2247:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2247:  
GBGCTCGTCG TGGC 14

(2) INFORMATION FOR SEQ ID NO:2248:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2248:  
BGCTCGTCGT GGC 13

(2) INFORMATION FOR SEQ ID NO:2249:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2249:  
GCTCGTCGTG GC 12

(2) INFORMATION FOR SEQ ID NO:2250:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2250:

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CTCGTCGTGG C

11

(2) INFORMATION FOR SEQ ID NO:2251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2251:

TCGTCTGTGGC

10

(2) INFORMATION FOR SEQ ID NO:2252:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2252:

GGGGCCCCGC GCCGCCCGC

20

(2) INFORMATION FOR SEQ ID NO:2253:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2253:

GGGGCCCCGC GCCGCCCGC

19

(2) INFORMATION FOR SEQ ID NO:2254:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2254:

GGGGCCCCGC GCCGCCCG

18

(2) INFORMATION FOR SEQ ID NO:2255:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2255:

GGGGCCCCGC GCCGCC

17

(2) INFORMATION FOR SEQ ID NO:2256:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2256:

GGGGCCCCGC GCCGCC

16

(2) INFORMATION FOR SEQ ID NO:2257:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2257:

GGGGCCCCGC GCCGC

15

(2) INFORMATION FOR SEQ ID NO:2258:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2258:

GGGGCCCCGC GCCG

14

(2) INFORMATION FOR SEQ ID NO:2259:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2259:  
GGGGCCCCGC GCC 13

(2) INFORMATION FOR SEQ ID NO:2260:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2260:  
GGGGCCCCGC GC 12

(2) INFORMATION FOR SEQ ID NO:2261:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2261:  
GGGGCCCCGC CCGCCCCGC 19

(2) INFORMATION FOR SEQ ID NO:2262:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2262:  
GGCCCCGCGC CGCCCCGC 18

(2) INFORMATION FOR SEQ ID NO:2263:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2263:  
GCCCCGCGCC GCCCCGC 17

(2) INFORMATION FOR SEQ ID NO:2264:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2264:  
CCCCGCGCGC CCGCC 16

(2) INFORMATION FOR SEQ ID NO:2265:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2265:  
CCCGCGCGC CCGCC 15

(2) INFORMATION FOR SEQ ID NO:2266:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2266:  
CCGCGCGCC CGCC 14

(2) INFORMATION FOR SEQ ID NO:2267:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2267:  
CGCGCCGCC GCC 13
- (2) INFORMATION FOR SEQ ID NO:2268:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2268:  
GCGCCGCCCG CC 12
- (2) INFORMATION FOR SEQ ID NO:2269:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2269:  
GCCCGCCCG C 11
- (2) INFORMATION FOR SEQ ID NO:2270:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2270:  
GCCCGCCGCC 10
- (2) INFORMATION FOR SEQ ID NO:2271:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2271:  
GGGGCGCGCG GGGCCGCCG G 21
- (2) INFORMATION FOR SEQ ID NO:2272:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2272:  
GGCGGGGBGC GGCBBGGCCC GGGCCC 26
- (2) INFORMATION FOR SEQ ID NO:2273:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2273:  
GGCGCGTCGC CGTCGCCCCB GTCGGGCTCG CGC 33
- (2) INFORMATION FOR SEQ ID NO:2274:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2274:  
GCGCGGGCBB CBGCGBGCCG GCGCGC 26
- (2) INFORMATION FOR SEQ ID NO:2275:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2275:

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GCGCBCGGGC CCBCTGCGC GGGC

24

(2) INFORMATION FOR SEQ ID NO:2276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2276:

GGGCGGGGTG GGCTGCCCTG CGGCCGCC

28

(2) INFORMATION FOR SEQ ID NO:2277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2277:

GGGCTGCTGC GCGGCGGCTC CGGCGA

26

(2) INFORMATION FOR SEQ ID NO:2278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2278:

CTCCCGGGCG GGGCCGGGCG CGGGG

25

(2) INFORMATION FOR SEQ ID NO:2279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2279:

GGGCTGCCGC GGTCCGGGCC CCTTTGCCG GCG

33

(2) INFORMATION FOR SEQ ID NO:2280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2280:

GCGCTCGCGC CGCTGCCGG

19

(2) INFORMATION FOR SEQ ID NO:2281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2281:

GCGCCGCTTG GCCTGTGCG GGC

23

(2) INFORMATION FOR SEQ ID NO:2282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2282:

GCTGCTCCBC GCGCTGG

17

(2) INFORMATION FOR SEQ ID NO:2283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2283:

GCCGGBGGCC GGCCBGGTCC CGCG

24

(2) INFORMATION FOR SEQ ID NO:2284:



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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2284:

CCCCGCGGCC GGCBBGGBGG GCGGGCTGGG C

31

## (2) INFORMATION FOR SEQ ID NO:2285:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2285:

GTCTCTCCCG CCCC GCCG CCG

23

## (2) INFORMATION FOR SEQ ID NO:2286:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2286:

GGCGCTCCGC TCCGGGCCGT CGGG

24

## (2) INFORMATION FOR SEQ ID NO:2287:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2287:

GCGGGCACGC GCGGGCTCTG GCGTCGGC

28

## (2) INFORMATION FOR SEQ ID NO:2288:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2288:

GGTGBCBTG	BGCBGTGCG	CGCGGTCCCG	TTBBGBGTGG	GCCCGCCAGC	CCAGCCACTC	60
CACTTGGGGG	CGGGTGGCCA	GCACGAACAG	CACCCAGAGG	AAGGGGGGCG	GCCCAGAAGG	120
GCAGCCCGCA	GGCCAGGATC	AGGTCTGCTG	CGGCCGAGA	TAATGGCATT	CACCACGCGG	180
CGGCCAGCG	CACGCCGCGC	ATCCGGCCCG	GGTTCTGACC	TGCAGCCCCC	GTCTCCTTGG	240
CATTCTTGGG	CCCCAGTCAC	TCCTCTCCCT	GCCCCCCTTG	CTGGGGCAGG	GACGGGGTGB	300
CBTTGBGCBT	GTGCGCGCGG	TCCGTTBBG	BGTGGGCCCC	CCAGCCCAGC	CACTCCACTT	360
GGGGGCGGGT	GGCCAGCACG	AACAGCACCC	AGAGGAAGGG	GGGCGGCCCA	GAAGGGCAGC	420
CCGCAGGCCA	GGATCAGGTC	TGCTGCGGCC	GGAGATAATG	GCATTACCA	CGCGGCGGCC	480
CAGCGCACGC	CGGCATCCG	GCCCGGGTTC	TGACCTGCAG	CCCCCGTCTC	CTTGGCATTC	540
CTGGGCCCCA	GTACTCCTC	TCCCTGCCCC	CCTTGCTGGG	GCAGGGACGG	CCGTGTTGTC	600
BGTGGTGCTG	CCCGTTTGBG	GTBTGGCGCT	CCBCCBTTC	CCTTTTCTCC	TTGTTTTCCG	660
TTTCTCTTGC	CGTCTGTGGT	T				681

## (2) INFORMATION FOR SEQ ID NO:2289:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2289:

GGTGBCBTG BGCBGTGCG CGC

23

## (2) INFORMATION FOR SEQ ID NO:2290:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2290:

GGTCCCGTTB BGBTGGGCC C

21

## (2) INFORMATION FOR SEQ ID NO:2291:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2291:  
GCCAGCCCAG CCACTCCACT TGGGGGC

27

(2) INFORMATION FOR SEQ ID NO:2292:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2292:  
GGGTGCCAG CACGAACAGC ACCCAGAGGA AGGGGGGC

38

(2) INFORMATION FOR SEQ ID NO:2293:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2293:  
GGCCAGAAG GGCAGCCCGC AGGCCAGGAT CAGGTCTGCT GCGGCC

46

(2) INFORMATION FOR SEQ ID NO:2294:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2294:  
GGAGATAATG GCATTCACCA CGCGGC

26

(2) INFORMATION FOR SEQ ID NO:2295:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2295:  
GGCCAGCGC ACGCCGCGCA TCCGGCCC

28

(2) INFORMATION FOR SEQ ID NO:2296:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2296:  
GGTTCTGAC CTGCAGCCCC C

21

(2) INFORMATION FOR SEQ ID NO:2297:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2297:  
GTCTCCTTGG CATTCTGGG CCC

23

(2) INFORMATION FOR SEQ ID NO:2298:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2298:  
CAGTCACTCC TCTCCCTGCC CCC

23

(2) INFORMATION FOR SEQ ID NO:2299:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2299:  
CTTGCTGGGG CAGGGACGG 19

(2) INFORMATION FOR SEQ ID NO:2300:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2300:  
GGTGBCBTTG BGCBTGTCGG CGC 23

(2) INFORMATION FOR SEQ ID NO:2301:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2301:  
GGTCCCCTTB BGBTGGGCC C 21

(2) INFORMATION FOR SEQ ID NO:2302:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2302:  
GCCAGCCAG CCACTCCACT TGGGGGC 27

(2) INFORMATION FOR SEQ ID NO:2303:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2303:  
GGGTGGCCAG CACGAACAGC ACCCAGAGGA AGGGGGGC 38

(2) INFORMATION FOR SEQ ID NO:2304:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2304:  
GGCCCAGAAG GGCAGCCGC AGGCCAGGAT CAGGTCTGCT GCGGCC 46

(2) INFORMATION FOR SEQ ID NO:2305:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2305:  
GGAGATAATG GCATTCACCA CGCGGC 26

(2) INFORMATION FOR SEQ ID NO:2306:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2306:  
GGCCAGCGC ACGCCGCGCA TCCGGCCC 28

(2) INFORMATION FOR SEQ ID NO:2307:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2307:  
GGGTTCTGAC CTGCAGCCCC C 21

- (2) INFORMATION FOR SEQ ID NO:2308:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2308:  
GTCTCCTTGG CATTCTGGG CCC 23
- (2) INFORMATION FOR SEQ ID NO:2309:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2309:  
CAGTCACTCC TCTCCCTGCC CCC 23
- (2) INFORMATION FOR SEQ ID NO:2310:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2310:  
CTTGCTGGGG CAGGGACGG 19
- (2) INFORMATION FOR SEQ ID NO:2311:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2311:  
CCGTGTTGTC BGTGGTGCTG 20
- (2) INFORMATION FOR SEQ ID NO:2312:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2312:  
CCCGTTTGBG GTBTGGC 17
- (2) INFORMATION FOR SEQ ID NO:2313:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2313:  
GCTCCBCCBB TTCCCTTTTC TCC 23
- (2) INFORMATION FOR SEQ ID NO:2314:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2314:  
TTGTTTTCCG TTTCTCTG 19
- (2) INFORMATION FOR SEQ ID NO:2315:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2315:  
CCGTCTGTGG TT 12
- (2) INFORMATION FOR SEQ ID NO:2316:  
(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2316:

CCCCGCCCCG CCTCGTGCC

19

(2) INFORMATION FOR SEQ ID NO:2317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2317:

CGTCCBTGCC GCGGGCCC

18

(2) INFORMATION FOR SEQ ID NO:2318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2318:

GCCCCGCTGC TTGGGCTGCT CTGCCGGG

28

(2) INFORMATION FOR SEQ ID NO:2319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2319:

TCTGTGCTCC TCTGCCTGG G

21

(2) INFORMATION FOR SEQ ID NO:2320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2320:

TGGTGGGGTG GGTCTTGGTG G

21

(2) INFORMATION FOR SEQ ID NO:2321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2321:

CTGTCCCTGG TCCTGTG

17

(2) INFORMATION FOR SEQ ID NO:2322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2322:

GGTCCCGCTT CTTC

14

(2) INFORMATION FOR SEQ ID NO:2323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2323:

GGGGTTGTTG TTGGTCTGG

19

(2) INFORMATION FOR SEQ ID NO:2324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2324:  
TGTCCTCTTT CTGC 14

(2) INFORMATION FOR SEQ ID NO:2325:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2325:  
GCCTCGGGCC TCCC 14

(2) INFORMATION FOR SEQ ID NO:2326:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2326:  
GGCTGGGGTC TCGGT 15

(2) INFORMATION FOR SEQ ID NO:2327:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2327:  
GGCCGGGGGT CGGTGGGTCC GCTG 24

(2) INFORMATION FOR SEQ ID NO:2328:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2328:  
GGGCTGGGGT GCTGGCTGG GG 22

(2) INFORMATION FOR SEQ ID NO:2329:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2329:  
GGGGCTGGGG CCTGGGCC 18

(2) INFORMATION FOR SEQ ID NO:2330:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2330:  
GCCTGGGTGG GCTTGGGGC 20

(2) INFORMATION FOR SEQ ID NO:2331:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2331:  
GCTGGGTCTG TGCTGTGCC 20

(2) INFORMATION FOR SEQ ID NO:2332:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2332:  
GTTGTGTGGG GGGCC 15

- (2) INFORMATION FOR SEQ ID NO:2333:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 27 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2333:  
GCTGGGTCGG GGGGCCTCTG GGCTGTC 27
- (2) INFORMATION FOR SEQ ID NO:2334:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2334:  
GCCCCGGGGC CCCC 14
- (2) INFORMATION FOR SEQ ID NO:2335:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2335:  
TGGCTCCCCC CTCC 14
- (2) INFORMATION FOR SEQ ID NO:2336:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2336:  
GCTCCCCCCT TTCC 14
- (2) INFORMATION FOR SEQ ID NO:2337:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 16 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2337:  
CGGACGAAGA CAGAGA 16
- (2) INFORMATION FOR SEQ ID NO:2338:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2338:  
GGCTTTGTGG GCTC 14
- (2) INFORMATION FOR SEQ ID NO:2339:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2339:  
GCCTGCTCTC CCCC 14
- (2) INFORMATION FOR SEQ ID NO:2340:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 19 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2340:  
CCCCGGCCCCG CCBCGBBCC 19
- (2) INFORMATION FOR SEQ ID NO:2341:  
(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2341:  
CCCGGCCCCG CCBG

15

(2) INFORMATION FOR SEQ ID NO:2342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2342:  
CCCGGCCCCG CCBGGBCC

19

(2) INFORMATION FOR SEQ ID NO:2343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2343:  
CCCGGCCCCG CCBG

15

(2) INFORMATION FOR SEQ ID NO:2344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2344:  
CCGGBCCCCG CCTCBBG

17

(2) INFORMATION FOR SEQ ID NO:2345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2345:  
CCGGBCCCCG CCTC

14

(2) INFORMATION FOR SEQ ID NO:2346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2346:  
CCGGCCCCCG CTC

13

(2) INFORMATION FOR SEQ ID NO:2347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2347:  
CCCGBBCCCCG CBTBGTGCC

19

(2) INFORMATION FOR SEQ ID NO:2348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2348:  
CCCGCBTBTG GCC

13

(2) INFORMATION FOR SEQ ID NO:2349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single



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(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2349:  
CCCCGBCCCB CCBBGTGCC 19

(2) INFORMATION FOR SEQ ID NO:2350:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2350:  
CBGBBCCCCG CTCGTGCC 18

(2) INFORMATION FOR SEQ ID NO:2351:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2351:  
CCCGCCTCGT GCC 13

(2) INFORMATION FOR SEQ ID NO:2352:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2352:  
CCGGCBCCGC CTCBTGCC 18

(2) INFORMATION FOR SEQ ID NO:2353:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2353:  
CCGGCCCCGC CBCBTGCC 18

(2) INFORMATION FOR SEQ ID NO:2354:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2354:  
CCGGBCCCCG BCTCG 15

(2) INFORMATION FOR SEQ ID NO:2355:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2355:  
CCCGGCCBCG BCTCG 15

(2) INFORMATION FOR SEQ ID NO:2356:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2356:  
CCCGGCCCBG CCTBG 15

(2) INFORMATION FOR SEQ ID NO:2357:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2357:  
CCCGGCBCBG BCTCGTBCC 19

- (2) INFORMATION FOR SEQ ID NO:2358:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2358:  
CCCCGGCCCCG CCBCG 15
- (2) INFORMATION FOR SEQ ID NO:2359:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2359:  
CCCCGGCCCCG CCBCG 15
- (2) INFORMATION FOR SEQ ID NO:2360:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2360:  
TCCBTGCCGC GGGC 14
- (2) INFORMATION FOR SEQ ID NO:2361:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2361:  
TCCBTGCCBC GGGCC 15
- (2) INFORMATION FOR SEQ ID NO:2362:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2362:  
TCCBTGCCBC GGGCC 15
- (2) INFORMATION FOR SEQ ID NO:2363:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2363:  
TCCBTGCCBC BGGCC 15
- (2) INFORMATION FOR SEQ ID NO:2364:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2364:  
GTCCBTGBCG CCG 13
- (2) INFORMATION FOR SEQ ID NO:2365:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2365:  
TCCBTGBCGC GGG 13
- (2) INFORMATION FOR SEQ ID NO:2366:  
(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2366:

TCTGBGCTCC TCTBBCTGG G

21

(2) INFORMATION FOR SEQ ID NO:2367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2367:

CTGTGCBCTT BBCTCTGGG

20

(2) INFORMATION FOR SEQ ID NO:2368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2368:

TGTGTCCBC TBCTCTGGG

19

(2) INFORMATION FOR SEQ ID NO:2369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2369:

TCTGTBCTCB BCTCBCTG

19

(2) INFORMATION FOR SEQ ID NO:2370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2370:

TGCTCCTCBC BBCTGGG

17

(2) INFORMATION FOR SEQ ID NO:2371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2371:

CTCCTCTBGC CTGG

14

(2) INFORMATION FOR SEQ ID NO:2372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2372:

GTGCTCCBBT CBCTGGG

18

(2) INFORMATION FOR SEQ ID NO:2373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2373:

GTGCBCCBBT CBCTGGG

18

(2) INFORMATION FOR SEQ ID NO:2374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2374:  
TCTGTGCBCC TCTGBBCT 18

(2) INFORMATION FOR SEQ ID NO:2375:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2375:  
TBBTCCTBBC BCCTGG 16

(2) INFORMATION FOR SEQ ID NO:2376:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2376:  
TGTGCTBBTC BCBCBTGGG 19

(2) INFORMATION FOR SEQ ID NO:2377:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2377:  
GTGCBCCBCT CBCCTG 16

(2) INFORMATION FOR SEQ ID NO:2378:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2378:  
CTGTGCBCT CTC 13

(2) INFORMATION FOR SEQ ID NO:2379:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2379:  
CBGTGCBCCB CTCBCCTG 18

(2) INFORMATION FOR SEQ ID NO:2380:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2380:  
GTGCBCCBCT CBCCTG 16

(2) INFORMATION FOR SEQ ID NO:2381:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2381:  
CBCCTCTCBC CTGGG 15

(2) INFORMATION FOR SEQ ID NO:2382:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2382:  
CCTCTCBCCT GGG 13

- (2) INFORMATION FOR SEQ ID NO:2383:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2383:  
GCTCCBCTCG CCT 13
- (2) INFORMATION FOR SEQ ID NO:2384:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2384:  
TGCTCCTCBC GCC 13
- (2) INFORMATION FOR SEQ ID NO:2385:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2385:  
GTTGTTGBTC TGG 13
- (2) INFORMATION FOR SEQ ID NO:2386:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2386:  
GGTTGBBBTT GGTCTGG 18
- (2) INFORMATION FOR SEQ ID NO:2387:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2387:  
GGTTGTTGBT GBCTG 16
- (2) INFORMATION FOR SEQ ID NO:2388:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2388:  
GGGTTBBBGT TGBTCTGG 18
- (2) INFORMATION FOR SEQ ID NO:2389:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2389:  
GGGTTBBBGT TGBTCTGG 18
- (2) INFORMATION FOR SEQ ID NO:2390:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2390:  
TTGTTGTBGB TCTGG 15
- (2) INFORMATION FOR SEQ ID NO:2391:  
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2391:  
GGGTBGBBGB GTCCGCTG 18

(2) INFORMATION FOR SEQ ID NO:2392:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2392:  
GGGTCBGBGG BTCBGCTG 18

(2) INFORMATION FOR SEQ ID NO:2393:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2393:  
GGGTBGGTGG GTC 13

(2) INFORMATION FOR SEQ ID NO:2394:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2394:  
GGGTCGGBGG GTCBGC 16

(2) INFORMATION FOR SEQ ID NO:2395:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2395:  
CCTGGGTGGG CTT 13

(2) INFORMATION FOR SEQ ID NO:2396:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2396:  
GGGTGGGCTT GGG 13

(2) INFORMATION FOR SEQ ID NO:2397:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2397:  
CCTGGGTGGG BBTGGG 16

(2) INFORMATION FOR SEQ ID NO:2398:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2398:  
CCTGGBTGGG CBTGGG 16

(2) INFORMATION FOR SEQ ID NO:2399:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2399:  
GCCTGBGTGB BCTTGGG 17
- (2) INFORMATION FOR SEQ ID NO:2400:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2400:  
CCCAVGCCV CCCAGGC 17
- (2) INFORMATION FOR SEQ ID NO:2401:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2401:  
AGCCCACCCA GGC 13
- (2) INFORMATION FOR SEQ ID NO:2402:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2402:  
BCCTGGGTGG GCTB 14
- (2) INFORMATION FOR SEQ ID NO:2403:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2403:  
GGTGGGCTTG GG 12
- (2) INFORMATION FOR SEQ ID NO:2404:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2404:  
CCBBGGTGGG CTTGGG 16
- (2) INFORMATION FOR SEQ ID NO:2405:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2405:  
CTGGGTGGGB BTGGG 15
- (2) INFORMATION FOR SEQ ID NO:2406:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2406:  
CCBGGGTGGG CTTGG 15
- (2) INFORMATION FOR SEQ ID NO:2407:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2407:  
GGGTGGGCTT GG 12

## (2) INFORMATION FOR SEQ ID NO:2408:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2408:

CCTGBGTGBG CBTGGG

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## (2) INFORMATION FOR SEQ ID NO:2409:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7800 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2409:

GGCGGCGCTGG	AAAGCTGAGA	TGGAGGGCGG	CATGGCGGGC	ACAGGCTGGG	CTGCTTTTCT	60
TTTCTGGGCG	TCTGTGGTCT	GTTTTTTTCT	GGCCCTGCTG	GGGCGCTCTC	CGCCGCCCGC	120
CTGGCTCCCG	GBGCCCBTGB	TGGGCBTGCC	GTTGTTCTTG	CCCTCCTTTG	GCTGCCGTGC	180
CCGCTCCCGG	GCCTCCTGGC	GGGTGGCCGT	TGGGCCCCGT	TTCCCTGGG	GCCTGGGGCT	240
CCCTTCTCTC	GCCCTTCTTG	CTGGGCTCT	GCTGCTGCTG	GTGCTGTGGC	CCCCGTACAC	300
CGAGGAGCCC	ATGATGGGCA	TGCCACAGAC	GACAGGCGTB	CBCCGBGGBG	CCCBTGBTGG	360
GCBTGCCCBG	GBCGBCBGGC	GGCGCCGTGC	CGCGTCTTGG	TGGCGGCGGG	TTGCGGCCCC	420
CGCGGGGCCC	CTCCGGTCCG	TTCGCGCCCC	CGCGGGGCCC	CTCCGGTCCC	GGGTGCGGGC	480
CCCCCGCGGC	CGCCTCGGGG	CTGGGGCGCT	GGTGGCGGGG	CCGCGCCTCC	GCCTGCCGCT	540
TCTGGCTGGG	CCCCGGGCGC	CCCCTCCCT	CTTGCTCGGG	TCCCGGTGAC	AGCGCGTCCT	600
GTGTCTCCAG	CAGCATGGCC	GGGCCAGCTG	GGCCCCBCBG	CGCGTCTGT	GTCTCCBGB	660
GCBTGGCCCG	GCGBGCTGGG	CCCCACAGAG	CAGTGTCTGT	GTTGGGCATC	TGCTCTTCCC	720
AGGGBCBGBG	CBTGTCTTGG	TTGGGCBTCT	TGCCCTCCCB	GGGCCCTTTT	CTGGTGGGGT	780
GGTGTCTTGG	TTGGGCTTTC	TTCTGTTCCT	BCBGBGCBGT	GCTGTGTGTG	GGCBTCTTGC	840
CTTCCCBGGG	CCCTTTTCTG	GTGGGGTGGT	GCTGTGTGTG	GGCTTTCTTC	TGTTCCCTTT	900
CCCCTGGGCT	TTCCCTCCTG	CTCTTTTCTC	ATTGCTCTC	CTATTACTTT	CTGTGTCCAT	960
TTTTTCATTA	ACCGAGCTGT	BTTTGCTCTC	CTBTBCTTT	CTGTGTCCBT	TTTTTCBTTB	1020
BCCGBGCTGT	GCCTGTGTCT	GTCCTCCTGC	TTGCTTCTC	TCGTTCTGCT	TTGGTGCCCT	1080
TGCCGCTCCT	GCTCCTCCGG	GCTGTGGGTC	GTGGCCCTGG	CTCCGGCTGG	TGGGCTCCCC	1140
TGGCCTTCGG	TGGCTGGCGG	CGTGCGGGTC	TTGCTCTGGG	CCTGGCTGTG	GCCTGTGGTG	1200
GGGGTCTTCG	GTGCTCCCGT	TTGGGTGGCT	CTCTGAATAT	TGACCTTCCT	CCATGGCGGT	1260
CCTGCTTGGA	TTCTCCCGAT	CTCTGBBTBT	TGBCCTTCCT	CCBTGGCGGT	CCTGCTTGGB	1320
TTCTCCCBG	CCTTTCCTGG	TTCTCTTGT	GTTTTTGGGG	TTTGGCTTAC	AGTAGAGTAG	1380
GGGATTCCAT	GGCAGGAGCC	ATCTTCTTCA	TGGAATCCTT	CAAGGAGACC	TAGGTTTCT	1440
GAGGGAAGTC	TAACACGCCA	TCTGGAGCBC	BGTBGBGTBG	GGGBTTCBT	GGCBGBGGCC	1500
BTCTTCTTCB	TGGBCTTCTT	CBGBGBGGCC	TTBGGTTTCT	GBGGGBCTGC	TBGBGBGGCC	1560
TCTGGBGCGT	TGTTTTTGGG	GTTTGGCTTG	CCTTTCCTGG	TTCTCTTBCB	GTBGBGTBGG	1620
GGBTTCBGT	GCBGBGBGCC	TCTTCTTCBT	GBBCTCCTTC	BBGBGBBCTT	TBGGTTTCTG	1680
BGGGBCTGCT	BBCBCGCCBT	CTGGBGCGCC	TGTGTCTGTC	CTCCTGCTTC	GTTCTCTCTG	1740
TTCTGCTTCT	GTGCCCTTGC	CGGTCTGCT	CCTCCGGGCT	GTGGGTCTCT	GCCCTGGCTC	1800
CGGCTGGTGG	GTCCTCCCTG	CCTTCGCTGG	CTGGCGGCGT	GCCCBGBBCC	GBGBCCGGB	1860
CCGBCBGGCC	GTGGTTGGGG	GTCTTCGCTG	CCTCCGTTTG	GGTGGCGATC	TCTGAATATT	1920
GACCTTCCAT	GGCGGTCTCT	CTTGGAGBTC	TCTGBBTBTT	GBCTTTCBT	GGCGGTCTCT	1980
CTTGGBTCTG	GGGTGTCTCT	GCCTTCGTGG	TTCTCTTCTC	TTCTGTTGCC	GTCGCGGGGG	2040
GCCCCCGGGC	CTGGCTGCGC	TCTGCCCCC	CCTCTTTCCC	GGGCTCTTGC	GCTGGGGGGT	2100
GCTCCCGTGT	GTTTGCGCC	TCCTCCTGGT	CGCGCTTGTG	GTTTGGGGG	CGGCTTTGCC	2160
CGCTCCCGG	CGCCTGGCCC	GGCCTTCCTG	GGCTGCGTGC	GCCTTCTGTT	CTTCTTCCTG	2220
GCTCTGGGGT	GTCCTGGCCT	TGCTGGTTCC	TCTTCTTCTG	TTTGCCGTCC	GCGGGGGCCC	2280
CCGGGCTTGG	CTGCGCTCCT	GCCCCGCTC	TTTCCGGGCT	TCTTGCCTG	GGGGGTGCTC	2340
CCGTGCTTTT	GCGCCCTCCT	CCTGGTCCGG	CTTGTCTGTT	TGGGGCCGGC	TTTGCCCGCC	2400
TCCCGGCGCC	TGGCCCGGCC	TTCTTGGGCT	GCGTGGCGCT	TCTGTTCTTC	TTCTTGGCGC	2460
AGGAGACAGG	GCAGGGCGAT	CAGGAGCAGC	GTGAGCCAAA	GGAGGACCAT	CGGGAACGCA	2520
GCTCCGGAAC	GCAGGACAGA	GGTGCCGCBG	GBGBCBGGGC	BGGGCBGTCT	GGBGCBCGCT	2580
GBGCCBBBGG	BGBCCBCTCG	TCCGGBBCCG	BGGBCBGBGG	TGCCTCTGCC		2640
CTGTCCGCCG	GCTCTTCGGT	GGCTCGGCCC	CGCTCCTTGT	CTTGCCCGCG	GTTGGTTTCT	2700
GGGCTTGGTT	CTTGCGGGCG	TTTCGGTCTG	CTGGCTGGTC	TGGGCCCCGG	GTGCGGCGGG	2760
TGCTTGTCTG	TTCTGCCTGG	GCTCTCCCC	CTCCTCCTTT	TCTCCTTCTC	TCTGTCTTGC	2820
CTCCTTCTCT	TGGGTCTCT	TGGCTGGGG	GCTCTTCCCC	TGCGGCGGCT	GCGGGGCGCT	2880
GTGCTGCTCT	GTCGCTCCC	TGGGGTGGCT	CCTTCCCTTT	CCCCGCTCGT	GGGGTTTGGC	2940
GGGCTGGGCT	GCCCTGGGGG	GTCTGGGCT	TTTGGGGTCT	GCTGGGCTGT	GCTTCCGGCC	3000
GCCTGGGCTT	CCCTGTGCCC	CTTCTCTCTG	CTGGGTCCCC	CTCCCGTTCC	AAGCTGCACC	3060
GCACAGACCG	GCGCTACAGG	ACAGAGCCAG	GCAAGCACCC	ATGGGGATCC	AGGCCAGCT	3120
GTTCCBBGCT	CBCCGCBBCB	GBCCGGCGCT	BCBGBBCBGB	GCCBGGCBBG	CBCCCBTGGG	3180
GBTCCBGGCC	GBCCTGCTCA	GTGGCCCCCA	AAAGGATGAG	TAATACATGC	GCCACGATGA	3240
TCATATCCTT	TTTACTATGA	GGCCGTGTCT	GTCGTGTCTT	TCCTTTGCTC	TTGGTGTGTC	3300
TTTGTGTGTC	CCTGCCTCTC	TGCCCGTGTG	TGTCGTGTCT	TTCTTTTGCT	CTTGGTGTGT	3360
CTTGTGTGTG	CCCTGCCTCT	CTGCCCGTGT	CTGTGCTGTG	TTTCTTTTGC	TCTTGGTGTG	3420
TCTTGTGTGT	GCCCTGCCTC	TCTGCGGGGG	TGGCTTCTCT	CCGCGTCTCT	GGGCGGTCCT	3480



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GTCCCTCGGC	CCCCGCGCCG	GCTCGGCTCC	TCTCCCTCTG	GCCCGGCTCG	GGGCGGGGCG	3540
GGGCGGTGGG	CGGGCGGGCG	TGCCCTGCGC	GCGGCGCTGG	CCCCTGCTGG	CCGTCGGGCTG	3600
CGCGCTGCTG	GCTGCCCTGC	TGGCCGCGCC	GGGGCTGTGC	CGCCTCTGCG	GGGCTGTCT	3660
CCTGGCTTGT	CTTCCGGCTC	TTCTGCTGGG	GTGGGCTGGG	GCGGCCGGCC	CGGTGCTGGG	3720
GCTCCTCGGG	GGGGGGGGCT	CTTCCGGGCT	GTCTCCCTCC	GGGGCGGGGG	TTTCTGGCCG	3780
TGGGGGTCTT	GCCTGGCCTC	CGGGCTCCTG	CTTGTCTTGC	CTTCCTTCTC	TGGTCGGTTC	3840
TGGCTCGGGG	CTCCGTGGGT	CCCTGGCGCC	CGTTTGTGTT	TGTCTTTTC	CCCTGGCGTC	3900
CCTGTGCCCC	TCTCCTCTCC	TTCTCTGCT	TCTCGCTCTC	CTTTGTGGGG	CCCTCCCTGC	3960
TGCTCTTGGT	TTTGGGCTTT	TTTTCTCTTC	CTCCTTTTTC	GTGCGTGGGC	CTCCGCACGC	4020
CTCTTGCCAC	CTCCTGCGCA	GGGACAGCCG	TTGGGGCCAG	CGCCGCTCCC	GGCGCGGCCA	4080
GCAGGGCAGC	CAGCAGCGCG	CAGCCGACGG	CCAGCATGCT	TCCTCCTCGG	CTACCACTCC	4140
ATGGTCCCGC	AGAGGCGGAC	AGGCGCBGCG	CTCTTGCCBC	CTCCTGCGCB	GGGCBGCGCC	4200
TTGGGGCCBG	CGCCGCTCCC	GGCGCGGCCB	GCBGGGCBGC	CBGCBGCGCG	CBGCGCBGCG	4260
CCBGBTGCT	TCCTCCTCGG	CTBCCBCTCC	BTGGTCCCGC	BGBGGCGGBC	BGGCGCTGCC	4320
CGGCGGGGTG	TGCGCTTGGC	GCTCCCGTGC	TGCGTTCTCT	GTCTCCCGGT	CCCCCTTGCC	4380
TGGCGTCTCG	GGCCTTCGTC	CTCTTCTCT	TCTTCTTCC	GCTCCGTGGG	GGGTGCTTGG	4440
TGGGGGCTTG	TGCTCGGGG	TCCCGGGGCT	TCTGGCCCTT	GCCGTTTCATG	GTGGCTAGGT	4500
GGGGCGTTCB	TGGTGGCTBG	GTGGGGCGGG	GTGGGTBGGC	CGTGTCTGGG	GGTTGGCCBT	4560
GTTGGTTGCC	TCTTGGTGGT	GCGCCGGGCG	CGTCTTGGCT	TTCTTCTCCT	TGCGGCCCTC	4620
GGGCCGGTGC	TTGTGGGCTC	CTCCCGGGCG	GCCTCCCCGG	GCGGGGGGCT	CTTGGCGCTG	4680
GCGGGGGGGC	CTCCTGCTCT	GTGGCTGGGC	GTTCTTGGT	GTTCTGGGTG	GTGGCGGGCG	4740
TGGTGGCCTC	TGTGGGGGCC	CGCGGCTGCB	GGGGTTGCCT	GTCTGCTTCG	TCCTTTGCGC	4800
TCCCGGGCCG	CCGGGGTGGG	TAGGCGGTGT	CTGGGGGTGG	GCCATGTTGG	TTGCCGGGCC	4860
CGCGGCTGCA	GGGACAGGG	GCTGTAATCT	TCATCTGCAG	GTGGCATGCC	AGTGAATTT	4920
AGATCATCAA	AATCCACAT	CTGTGGATCT	GTAAATTTG	ACATGTCCTC	TTCAAGTTTCA	4980
GCAATGGTTT	GATCTAACTG	AAGCACCGGC	CAGGBCBGGG	GCTGTBBTCT	TCBTCTGCBG	5040
GTGGCBTGCC	BGTGBBTTT	BGBTCBTCBB	BBTCCBCBT	CTGTGGBTCT	GTBBBTBTG	5100
BCBTGTCTC	TTCBGTTTCB	GCBBTGGTTT	GBTCTBBCTG	BBGCBCCGGC	CBGGTGGCTC	5160
GGTGGCTTCT	CCCTGTGTT	TGCGGCGCTC	GGTGGTGTG	GCCCTGTGG	TGCTTCGTTT	5220
CCCCCTCTTT	CTCTTTGTT	GGGGGTCTT	GTGGCGGGCT	GCTTGTCTCG	TTCCGCCCTG	5280
TGCGGGCGGA	AGCCTCTCTC	CTCTCCCCAG	ATCCGCGACA	GGCCGACAGC	AAGAACCAGC	5340
GCAACCAGGG	CGCGTCCGCA	CAGACTTGA	GGCGGCTGCA	TGCTGCTACC	TGCTCCAGAA	5400
GCGTCCGGTG	GCCGCCGCGC	CCTGTCCGGC	GGGBBGGCTC	TCTCCTCTCC	CCBGTCCGCG	5460
GBCBGGCCGC	BGGCBGBBCC	BGGCGCGCTC	CGCBGBBCT	TGGBGGCGGC		5520
TGCBTGCTGC	TBCCTGCTCG	GGCGGGBBGC	CTCCGGTGGC	CGCCGCGCGT	CCGTGGCCGC	5580
CCGCGCCTCT	CTCCTCTCCC	CGTGGCCCTG	TGCGGCGGGT	CCTGCCGTCC	TGCTCCTTT	5640
TCTTTTGCTG	TCTTGTCTTC	CCGTCTCTGC	TTTGTCTGTC	CTCCCCGTCT	CCTCCCACTG	5700
CTTCTCCCGG	GGGCTTCCCG	GGCTTCGGGT	GGCCGGTGTG	CCGGGCTCCG	GCGCGCGCGC	5760
GGCTTCGGCT	GCGGGTGGGT	GGCGCGGGCT	GCCGGGTCCG	CGCGGCGCCT	GGGCCCTTGT	5820
GCTGCTTTTT	GCTTGTTCGG	TTCTGGCTGC	TCCGGTCTGT	GTTGTGGTTG	TTTTGTCTCT	5880
TCTTGGGTGT	GGGCTTGGCG	GTTTGGCTG	TGGGCCCTTT	GGGGCCTTGG	CTTCTGGCTC	5940
GTCTGTCTCT	CCCGTCTCCT	CCCACTGCTT	CTCCCGGGGG	CTTCCCGGGC	TTCGGGTGGC	6000
CGGTGTCCCG	GGCTCCGCGC	CGCGCGGGCG	TTCCGGCTCG	GGTGGGTGGC	GCGGGCTGCC	6060
GGGTCCGCGC	GGCGCCTGGG	CCCTTGTGCT	GCTTTTGGT	TGTTCCGTTT	TGGCTGCTCC	6120
GGTCTGTGTT	GTGGTTGTTT	TGTTTCTTCT	TGGGTGTGGG	CCTTGGCGGT	TGGCTGTGG	6180
GCCCTTTGGG	GCCTTGGCTT	CTGGCTCCAT	CCACATGATT	GCTTAGATTT	GTGCTGTATC	6240
TCTCAGGATT	ATCACTGATT	ACACATCCAA	CCAGTGCCAG	CCAAAAGGAT	GCCCTGAGGC	6300
AAAGGGTTTC	CATCTTGAGG	CAAATTTGAG	GACBTCCBCB	TGBTTGCTTB	GBTTTGTGCT	6360
GTBTCTCTCB	GGBTBTBCB	TGBTTBCBCB	TCCBCCBGT	GCCBCCBBB	BGGBTGCCCT	6420
GBGGCBBBGG	GTTTCCBTCT	TGBGGCBBBT	TTGBGGGGG	CTBBGBTGBT	CCBCBTCBCT	6480
BCCBCGTTGC	CCBCCBCBGB	GGTCBCCBCB	BTGBCCGTGT	BGGCBGCTGC	CCBBBGGBCB	6540
BTTTGCCBGG	CTGGTTGCB	GBBCTGBTG	GGTCCGBGG	TGTTBGTGGB	GBTGTTTGGG	6600
GBGBGGTCTG	BGTCCBCCGG	GBGGBCGTTB	TCCBTTTCGB	BGCTBGGCGG	TBBBGGCCTB	6660
CTBTCTGTBC	BCBBCCCCC	TCTGCBGCBG	BGTCTGTGCG	TGGCGCCTGG	GGCTCBGGGT	6720
CCGGGCTAAG	ATGATCCACA	TCACTACCAC	GTTGCCACC	ACAGAGGTCA	CCACAATGAC	6780
CGTGTAGGCA	GCTGCCCAAA	GGACAATTTG	CCAGGCTGGT	TGCACGAAT	GATTGGGTTT	6840
CGAGGTGTTA	GTGGAGATGT	TTGGGGAGAG	GTCTGAGTCC	ACCGGGAGGA	CGTTATCCAT	6900
TTCAAGCTA	GGCGGTAAG	CCCTACTATC	TGTACACAAC	CCCCCTCTGC	AGCAGAGTCC	6960
TGTCGTGGCG	CCTGGGGGCTC	AGGGTCCGTC	CTGTCTGGC	GCCTGGGGCT	CTTCTTTTGT	7020
GGGCTCTTTG	GTGGCTGTGG	CTGTGGTCTC	TGTGGTTGCT	GCCCTGGGTC	TGGGGGTGTG	7080
GCCTTGGGGC	CGTCTCTGCG	CTCTCCTCG	TGGGCCCCCG	GTGCBTGTG	GCBTGTGCGC	7140
GCGGTCCCGT	TBBBGTGGG	CCCGCCAGCC	CAGCCACTCC	ACTTGGGGGC	GGGTGGCCAG	7200
CACGAACAGC	ACCCAGAGGA	AGGGGGGCGG	CCCAGAAGGG	CAGCCCCGAG	GCCAGGATCA	7260
GGTCTGCTGC	GGCCGAGAT	AATGGCATT	ACCACGCGGC	GGCCAGCGC	ACGCCGCGCA	7320
TCCGGGCCGG	GTTCTGACCT	GCAGCCCCG	TCTCCTTGGC	ATTCTTGGG	CCAGTCACT	7380
CCTCTCCCTG	CCCCCTTGC	TGGGGCAGGG	ACGGGTGBC	BTTGBGCBTG	TCCGGCGGGT	7440
CCCGTTBBGB	GTGGGCCGCG	CAGCCAGCC	ACTCCACTTG	GGGGCGGGTG	GCCAGCACGA	7500
ACAGCACCCA	GAGGAAGGGG	GGCGGCCAG	AAGGGCAGCC	CGCAGGCCAG	GATCAGGTCT	7560
GTCGCGGCCG	GAGATAATGG	CATTACACAC	GCGGCGGCC	AGCGCACGCC	GCGCATCCGG	7620
CCCGGGTTCT	GACCTGCAGC	CCCGTCTCC	TTGGCATTCC	TGGGCCCCAG	TCACTCTCT	7680
CCCTGCCCCC	CTTGCTGGGG	CAGGGACGGC	CGTGTGTCB	GTGGTGTGCT	CCGTTTGBGG	7740
TBTGGCGCTC	CBCCBTTCC	CTTTTCTCCT	TGTTTTCCGT	TTCTCTTGCC	GTCTGTGGTT	7800

- (A) LENGTH: 6225 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2410:

CTTGCTCCTG	GGGGCCTCCT	GGTCCCTCTG	GCTGTTCCCG	GCCCTGGBC	GGGGCBGGGG	60
CCGCGTBGGC	GCGGCTCGCC	BGBBCGGGCB	GCGCCBGC	CBGCBGGCTC	BGCBTCCTGG	120
CCBCGGBBTT	CCGGTGTGCG	GGGCTGTG	CCCCTGGGCC	TCGGGTGCTG	CCTGTGCGCT	180
GCCTTCTTCT	CTGGGTCTCT	CGCCGGGGCC	CTTGCTGCCC	TGGCTGTGCC	CTGGGGGTCT	240
GGGTTCCGGCT	GTCCCBGCB	GGBCCBGTCC	CBTCCBCBGC	GTGTGBTBG	TBGGCBTTCT	300
CCTGCBGCCG	BGGGGCGCGG	GCBGCBTCG	CTTTGGGCTT	TTCTCCTTTG	GTTTGBGCGC	360
CBGGBCCGCG	CBCBGCBCB	GGGCGCGGGC	GBGCBTCGB	GCGGCGGGCB	GGGGGGCTCC	420
CGCCGCBGB	GGTTBTGGGC	TCCCBGGGCC	BCCCGBCCG	CGCGGBCGTT	TBCBTTCGCC	480
BCGCBGTGCG	CGGCCGCBCT	GBGCBGGTTG	GGCGCBTCB	GGGTGGCGCC	GCBGBBGTGG	540
CCTCCGCGCB	GCTGCBGGGB	CBCCBTGBBG	GGCCBCGCGT	GGGGCCGCGC	TCGCGCGCCC	600
CCCBCTTCT	CCBGGGCCB	CGCGGTGCCC	CCCBGCBGCB	BGGCCGGCBG	GBCBCBGGCG	660
BGGBGBCBG	CGBTGCGCG	GCCGBGGGTC	BTGGTGGGGC	TGGGGCTCCG	GGGTCTCTGC	720
CCCTCCGTGC	TGGTGGGGCT	GGGGCTCCGG	GGTCTCTGCC	CCTCCGTGCC	GCCTGGGGCC	780
GCGCTCGCG	GCCCGCTCGG	GCCCGGTGGG	TCCCGCGCG	GCGCGGCTCC	CGGCGGCGG	840
CGTGGGTCT	GCTGGCGGG	TCCGGGTCCC	GGGGGTGGGG	CGCGGTGCGG	CGGCGGCGG	900
TCCCTCCBC	BTCTGCTCTG	BCCTGCTGGB	CTCTGGBTCT	GBBGBTBGCG	CBTGTBGGGG	960
CGGBGTGGG	GCCTGCTCTC	CCGGCCTCCG	BTGCTCTCCC	CTGCCTCBGC	CCCBGTGGGT	1020
BGBGBBBGG	CCBGCBBGG	CBGBGTGGG	TGCBTCTTTC	CTGGTGGGGC	CTGCTCTCCC	1080
GGCCTCCGTG	TGTTGCTGGG	TGTTTTCCCG	TCTCTGGTCT	GCCTTCGGGG	GTCTGCTGGG	1140
GCTGCBGCB	CCTCBTCBGC	TCTTGCTGG	BGTGGCTCBG	CCTGGGCTTG	CBGGGCCBCC	1200
BGBGBBBTGG	CBGCBGGBT	GGCGBGGGTC	CTCBTGGCTG	GGGTCTCBGB	TCCTCTBGCT	1260
BGGCBGGGTG	BCCBGBBGG	GCGGGTCTC	BTGGCTGGGG	GCCTGGGCTT	GCBGGGCCGC	1320
TCTTGCTGG	BGTGGCTCGC	CCBGBGTCTT	CCCTGGTCCG	TGCBTCTGCT	TCCGGGGCTG	1380
CBGCBCCCTC	BTGCBGCTCT	CCCTGGGCTG	GCTCBGCTTG	GGCTGCBGG	GCCBCCBGG	1440
GBBTGGCBGC	BGBGBTGGCG	BGGGTCTCTB	TGGCTGGGGT	CBCTGGBGG	BGGGBGBGCB	1500
GGGGGTCTCT	BTGGCTGGGG	TCCCTCTCTC	CCGTCTCTCG	TTTCTCTTGC	GGTCTTGGCC	1560
CGGGCTCCGG	GTGCCCCGCC	GCCCGCGCGG	CGCCGCCCGG	CCGGGTGCTC	CCCGCCCCGC	1620
CGCCGCGCG	GGCGCGGGG	GCCCGCTCTG	GCCCGCGCGG	GCGGCGCGG	GCGTGGCGCG	1680
CTCGGCTCTG	GGGTCTCTCT	TCTCTCTCTC	GTGCGCTCTG	CTCTTGTCTT	TCTGCTCTCG	1740
CTGCTTCTCT	CCCTCTCTCT	GGCGGTGCTC	TGTGCTGTCC	GTCTGTCTGC	CCTTCCGTGG	1800
TGCTGTTGTC	TCTTCTGCCC	TGCGTGTGCT	GGTGTGCTG	GTGGTGCCTC	TGCGCGTGCT	1860
CGCCCTGCTT	GGGTGGGCTT	CTTCCGGGTG	GGCTTTGGGG	CTCTCTTGGT	TGCCCTTTCT	1920
TCTGCTGGTG	CCCTCTCTCT	CTGGCTTGGT	GGTGTCTG	GGTGGTGCTC	CTCTCCCTTT	1980
CCCTGCTGGC	CGTTTGTCTT	GTTTTCTGTC	TTCCTCTTTC	CTCTGTTTC	TCCGTTTGGC	2040
TTGCTGCTTG	CGGGGCTGTC	TCCCTTGCCC	CTGTGGGCTT	TCCCTGGTCC	GGTCTTCTCC	2100
TTGGGGGTG	CCCTTCTTGG	TGGGCTGGCT	CGTCTGTCTT	TTTCTTCTCT	GGGGGTGGCC	2160
GTTGTGGGCG	GTGTGGTCCG	CCTTGCTCTT	GCTGGTCTTT	CCTCGGTBGB	CGCGCTCGBB	2220
CTCGGCTGGG	CCGGTGGTGB	GCGCGGGBG	CBGCGGGBG	GCCCTGCGCG	CCGBGCTCBC	2280
CTGCBGGGBG	BGBTBGGCTT	GCBGCBGGBC	TCCCBGGBGG	GTGCBGCBG	CCBGTBGBGC	2340
TBCTCTGCTC	TTCBTGGTBC	CGTCGGTGTG	GTGCBGCGGG	CTGTGTGTGB	BGGCBGCTG	2400
GGCCCCGTCT	GCTGCTCTCT	GTGCGGCTCT	GTCCTTCATG	GTACCGTCCG	TGTGGTGGCC	2460
TCGGGTGGGG	CGGTGGTGGG	GCGCGCGCGC	TCCGTGGGCT	CCGGCTCTTC	TTTCCCGGCT	2520
CCGTGCGGCC	GGGGGCTTGG	GTCTCCCTCG	CTCTTCTTGG	TBCCGBCCGG	CGGBGCGCGC	2580
BGGGTGGBCT	GGGBGTGGGT	TTCTCCCCGC	CGTTCTCBCC	CBCCGCGCTG	BGCTCBGCGC	2640
CTBBGCTGCT	TGTTTCTGGB	GCTCCTTGGC	BGGCCBCCBB	CBGCBGGBG	BBBCTCBTGB	2700
CGBBBTBCTC	CBTTCTGBBB	BBBGGGBBCT	BBBBCCTCC	CGTCCCCCGT	TCGCTGGGCG	2760
CGCGCTGCGG	GTCTCTGCTG	GGTTCTCTCC	CGCGTCTCTC	CGGTCTGTTG	CCTTGTGGGG	2820
CTTCTGTGCT	TTTTGGGCTG	TCTTTTCTCT	CTTGGGCTCT	TTTCTTTTCT	TGTGCTCGG	2880
TTGTGGGTCC	GCTGGTCTTT	TGCCCTGTGT	GTTTCTGCTG	CCCGTTCGCC	TGGCGCGCGC	2940
TGCGGGTTCC	TCGTGGGTTT	CTCCCCGCGG	TTCTCCGGTC	TGTTGCCCTT	GTGGGCTTCT	3000
TGCTTTTTTG	GCTGTTTCTT	TCCTGCTTGG	CGTCTTTTCC	TTTCTTGTG	CTCGGTTGTG	3060
GGTCCGCTGG	TCCTTTGCCC	TGTGTGTTTC	TGCTGGGBCG	TGCTBCTGCB	GATTTCBGBG	3120
GGBBGBBCCC	TGCTBCTCBC	CBGCTTCBGC	TCTGGGBCBC	BBGBGBBBG	GCBGCBGGGG	3180
GBGBGBBBG	BGCBGCBTCT	TCCCBGBBGB	GCTGCCTGBG	CBBBTGTCTG	TTTTCTTTCT	3240
CBGTCTTGGG	TTTTBTBBCT	CCCBGBBGGC	BGBGBBGGGG	CBGGGCGTTT	TCTTCTCTCG	3300
TGGGTTTTTC	TTTTCTGGCA	GTGGGTGGGG	GTTGGGTTGG	GGTGGCTTCC	TTGTTCTCTG	3360
GGGTGCTCTC	TTGCTCTGGG	CTTTTCTCCC	CTTTTCTTTC	CTGTCTGTTT	TCTGGGGCTC	3420
CTCTCTGTC	TCTGTGCTCT	TGCCCTGGCC	CTCTTCCCTC	TCCTGTCTCC	TGTCCCTGTG	3480
TTCCGCCCCG	CTTCCCTCTC	CTGACCTCCT	TTTCTCTCCG	TGGGTGGGGC	CCTGCCTGTT	3540
CTCTGCTCCC	TGGCTTGGGG	TTTCTTCTGT	GTGTCTTCTT	CCTCTGTTGG	CTGGCTTTCT	3600
CCTTCTTTTG	TCTTCTGCGG	TGCCCTTCTT	TCCTTTCTTG	GGTCTTGGT	GCTTGGGCTG	3660
GGGCGTCTTG	GGGTGCBGGG	CCCBTCTCTG	TGCGCTGGG	CGCTGCTGTG	CGTCCGCTCG	3720
CTGGGGGGCC	GGGGTGGCTG	GGCCTGCTT	GCCGACGAC	CCCGGGCCGA	CCCGAGGCTC	3780
GGGGGGCTGT	GTTCTGGCGC	TGGTGGGCTT	GGGCCCCCTC	GGGGGCTGGG	TTTCTGCTG	3840
CGCTGGGGCT	CTGGCGTCTT	GGGGTGGCGG	GCCGGGGGGG	CGGGGGGGCG	CTGTTCTGTG	3900
GCCTGGGGGT	GCCTGTGGCT	GCCGTTTGGC	CCGCTTGGTG	GCGCGCTCCT	GCTGCGGCTC	3960
GTTGGCTGGG	TCCCCCGGCC	CGTTTCTCTG	GGTCCGCGTG	GGGTGCTCCG	GTTCTCTCTG	4020
CCGCTGCTGC	CTTGTCTTTC	CGGCCGTGGC	GGCGTGGTGG	TCCGCCCCCC	CTGGCCTTCT	4080
GCTCGGGGTC	TGGCTGGTTG	CCGGTGGCCT	TGCGGGCGGT	CTTCTTCTCT	GTGGCTCTGG	4140
GCCCGGCCGG	TCTCGGGCGT	CTCGTGTTCG	CTCTTGTGCT	GTTCCGGCGG	CTCCTTCTCT	4200

TTCCGCCGCC	GCCGCTCC	GCCCGCTCGT	CGCCCTGGCC	CGGCCTCCTC	CTGGCCGCTG	4260
TCTCGGGCGG	CGGCCTTGGC	GCTCCGTTTG	GGGCTGCCTC	TGGCGCTTCC	GGCCCTCGGC	4320
CTGGGCGCTC	TCTTCCGCCT	GTGCTGGTGG	CCCTCGTGGG	CCCCTCCTGG	CCTCGGTGT	4380
CCTGTGGTCC	CCCGGCTGGT	GGCCGGGCGG	GTTGGGCGGG	CGTGGGCGCC	GGCGGGTCCT	4440
CCGGGCTGCC	CTTCTCGGCC	GGGGGTCCCG	CGCTCCTGCT	GTTCCCTGGG	CTCTTCTGCC	4500
TCTCTCCTGG	GTGGGTGCTG	GGTGCCGGGG	TCTCCGGGCT	TGCCCCGCGC	TGCTGGGCGT	4560
TCTGCGGTCT	TGGGGTTGTC	TGTGGCCCGG	CTCGTGTGCG	CCTCCGTGCG	CCGTGCGCCG	4620
CCTCGTCCCC	TCCTGGGTGC	CGCGCGGGCT	GGTCCTGGCG	TTTTGCTCCT	TCCTGGGCGT	4680
CTTGGGGTGC	BGGGCCCBTC	CTGCTGCGCC	TGGGCGCTGC	TGTGCGTCCG	TCTGCTGGGG	4740
GGCCGGGGTG	GCTGGGCCCT	GCTTGGCCGA	CGACCCCGGG	CCGACCCGAG	GCTCGGGGGG	4800
CTGTGTTCTG	GCGCTGGTGG	GCTTGGGCCC	CTCTGGGGGG	TGGGTTTCCT	GCTGCGCCTG	4860
GGCGCTGGCG	TCTTGGGGTG	CGGGGCCGGG	GGCCCGGGGG	GCCGCTGTTT	GTGGGCTTGG	4920
GGGTGCCTGT	GGCTGCCGGT	TGCCCCGGTT	GGTGGCGCCG	TCCTGCTGCC	GGTCGTTGGC	4980
TGGGTCCCCC	CGCCCGTTTC	CTGGGGTCCG	CGTGGGGTGC	TCCGGTTCCT	CGTGCCGCTG	5040
CTGCCTTGTC	TTTCCGGCCG	TGGCGGCGTG	GTGGTCCGCC	CCCCCTGGCC	TTCTGCTCGG	5100
GGTCTGGCTG	TGTGCCGGTG	CCCTTGGCGG	CGGTCTTCTT	CCTGGTGGCT	CTGGGCCCCG	5160
CCGGTCTCGG	GCGTCTCGTG	TTCCGTCTTG	TGCTGTTCCG	GCCGCTCCTT	CCTCTTCCGC	5220
CGCCGCGGCT	CCCCGCCCCG	TCGTGCGCCT	GGCCCGGCCT	CCTCCTGGCC	GCTGTCTCGG	5280
GCGGCGGCGT	TGGCGCTCCG	TTTGGGGCTG	CCTCTGGCGC	TTCCGGCCCT	CGGCCTGGGC	5340
GCTCTCTTCC	GCTGTGCTG	GTGGCCCTCG	TGGGCCCCCT	CTGGCCTCCG	GTGTCTGTG	5400
GTCCCCCGCG	TGGTGGCCGG	GCCGGTTGGG	CGCCGCTGGG	CGCCGCGGGG	TCCTCCGGGC	5460
TGCCCTTCTC	CGCCGGGGGT	CCCGCGCTCC	TGCTGTTCCC	TGGGCTCTTC	TGCTCTCTC	5520
CTGGGTGGGT	GCTGGGTGCC	GGGGTCTCCG	GGCTTGCCCC	GCGCTGCTGG	GCGTCTGCG	5580
GTCTTGGGGT	TGTCTGTGGC	CCCGCTCGTG	TCGCCCTCCG	TCGCCCGTCC	CCGGCCTCGT	5640
CCCCCTCTGG	TGCGCGGGCG	GGCTGGTCTT	GGCGTTTTCG	TCCTTCTTGG	CTGCCCCBGT	5700
TTTTGBTCCT	CBGBTGCCGT	GGGGBGBBCB	BTGGCTGCCT	CCCCGGGGTT	TCTGTGCTT	5760
GCTGCTTCTT	TCCCGTCTCC	CTTCTTTCCC	GTCTCCTTTT	TGCCCTCTTG	GGTTCCTGTT	5820
GTTTCTGGCC	TGCTTGGTGG	CGGCTTGTGC	GTTTCTCTC	TCTTCTCTTG	GGTCTCCGCT	5880
TCTGCTCCTG	CCTTTTCTCG	TCTCTGTGCG	GCCGTTCCTC	CTCCGGCGTC	CTCCTGCCCT	5940
GTGCTGTTTG	CTCGGGTGG	TGCGGGTCCC	GGTGTCTCCC	CGGCGGGCCG	GCTGTTGCC	6000
TGGGCTGTG	TGGTGGGGTG	TGGGGCCGCT	GGGTGGGGGG	TGTGGTGGGC	TCTTCTGTGG	6060
CCTGTGGGGG	TGTTGGGTGC	TCTGTGGGCG	TGTGCTGGGT	CTTGGGGCTT	CCTCCCTTGT	6120
GCTGGGTGCG	GCCTCCCCGC	CCCCCTTCTG	GGCCGGTGGC	CTGGCTCCTT	GTGGGCGCTT	6180
CTGGCTCTTG	CCCTGTCTTT	CTTGCCTCTG	TGGCTGCTGG	GCTGC		6225

## (2) INFORMATION FOR SEQ ID NO:2411:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7033 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2411:

CCTCCTTCTT	GGTCTGTCTG	CCBGBCBBBT	TTGGGBBGTG	BBGBGTTTTG	GBBCCBTGTT	60
TCCCBGTCTC	TGBGCTGTGG	CGCCCTGCTG	CTCTTTCTGC	TCCCTTGGT	GGGTGGGGCC	120
GCTGGTTGTT	CTGGGGTTCT	TGCTGCCCTT	TCTGTCCCTG	TTTGTGGTGG	TCTGCGCCCC	180
CBBCBGBBBG	BGCBGBCBBB	TTTGGGBBGT	GBBCCBTGTT	GGBBCCBTGT	TTCTGTGCG	240
CTGGCCTTGG	TCCCGGGGGT	CTCCTCTTGT	TGTGTCTTGC	GCCTCCTGCT	GGGGGTCCCT	300
CTGTTCTTGT	TTTGGGGGCG	GGCCCGGGCG	TTGTCTTGGT	TGGGGGTTT	CCGTGGGGT	360
TCTCCTGGCC	CGGGCCTTGC	CCGGCCGTGG	TCCCGCCTTC	GTTCTGTCT	CCGTCTCGGC	420
TCTTCTGGGG	CCTTGGCGTG	TCTTTGGTGG	CBCCGTCCBG	TGBTGGTGGC	GTBCTTGTCC	480
CTGCBGCGCT	CGGCCTGGTC	CCGGBGBGCG	CGCGGGCCGG	GGGCTGCTGG	GGGTGGGCC	540
GGGGTGGCCC	GCCGCTGGGT	GCCCTCGTCC	TCTGCGGTCC	TGTCTCCTGG	CTCTGGTTCC	600
CCGCTGCGCC	CGTTGTCTTC	TGGGGTGGCC	TTGCTTCCCG	GGTCTGTTTC	TTGTGTTGGG	660
GGTCCCTTTT	TGGGCTGTGT	GTGGCGTGGC	TTGTGTGTTT	GGTTTCTGCC	CTGTCTCCCG	720
GCGTCCCCCG	BGCCTCCCCG	GGGCBGBGTG	BCTTTTGBGG	GGGBCBGBG	TGTCTGGGCB	780
TGCCBGBGTC	CTGGGBBGBG	BGCCCCGBGC	BGBBCCBGBG	GTGCGGGCBG	CGCGGGCCCG	840
GGGCTGCTGG	BGGBCBTBGC	GBGGCTGBGC	CTCTTTTCTG	TTTTTCCCTT	CTGCCCTTGT	900
TGGGGTTGCG	TTCTTTTCTG	CTTCTTCCCT	GTGTCTCCTG	TCTCCGCTTT	TTTCTTCTGC	960
TTTGTGTTT	TCTCTTCTT	GCTGBGCBBG	BTBTCTBGBT	TCTGGGGTGG	TCTCBTTTT	1020
BBBGGCTTGB	GBBGGCTGCB	BCBTBTCCB	BBGTBTBT	GBGGCTCCBB	GBBCTCBGBC	1080
CBTCTTCCCB	GGCBTTTTBB	GTTGCTGTGC	TBBGTGBBGB	CTGBGBBGB	CTGTGBBGBG	1140
BTCTBTGCTT	CBGBGTTTCT	TTTCCBCCGT	TCTTGGCTTC	TTCTGTCCGT	TGCTTCTCG	1200
TTGTCCCTGT	GGGCTTCTCG	TTGTCCCCC	TTCCGGGGCT	GGTGGGGCCG	TCCTTGCCCTG	1260
CTGGGTCTT	GGCTTCTTCT	GTCCGTGGGC	TTCTCGTTGT	CCCTGTGGGC	TTCTCGTTGT	1320
CCCCCTTCCG	GGGGCTGGTG	GGGCGCTCCT	TGCTGCTGG	TTTTCTCTTT	CGCTTTCTTT	1380
TGCTCTCCTG	TTCTCCTTT	TTTGTGTTT	TTTCTCCTT	TTCTCTCCTT	TCTTTCTTT	1440
TCTCTTCTGC	TTTCTTTTCT	TCTCTGTGTC	CTCCTTTTTT	GCTGTTTTTT	CTCCTTCTTC	1500
TCTCCTTTCT	TTTCTCTCTG	CTTGTCTGTC	TCCTTCTGTC	GGCTCTGTGT	CGCGTGGGTG	1560
CGGCCGTGGC	CGGCGGBCCB	GGBTGTTGG	CBGGGBCCBG	BCGGGCBGGC	GGCTCBTGT	1620
TGGBTCGGCB	GGBGCBCBTC	CTCTGTTTGG	CTTCTTCTGC	CGGCBCTGTC	TBGCBBGBBG	1680
BBGBGBGGGG	GBBGBGTTG	GGBGGTGBBG	CCBTTBBTB	GGTGTGCBTC	CCTGTTTCCC	1740
CCCTTTCTGT	CTGCGTTTGC	CTTTGGCGTT	TTTTGTTTGT	TTTCTCTCTC	CGTCTTTCTT	1800
CTCCCCCTGT	GGBBTTTCTG	TGGGGTGGGC	BTBCCGTGTC	GCBGCTCCBB	GBGCTBGCBB	1860
BCTCBBTGTC	BGBBGCBTCC	TCBTGGCTCT	GBBECGGTGG	GAATTTCTGT	GGGGBTGCCA	1920
TACACGTAGG	CAGCTCCAAG	AGCTAGCAAA	CTCAAATGCA	GAAGCATCCT	CATGGCTCTG	1980

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AAACGGGGGG	TGGCTTCCTG	CCGCGTCTCT	GGGCGGTCCC	GTCCCTCGGC	CCCGCGCCGC	2040
GCTCGGCTCC	TCTCCCTCTG	GCCCGGCTCG	GGGCGGGGCG	GGGCGGTGGG	CGGGCGCGCG	2100
TGCCCTGCGC	GCGGCGCTGG	CCCTGCTGG	CCGTGCGCTG	CGCGCTGCTG	GCTGCCCTGC	2160
TGGCCGCGCC	GGGGCCTGTC	CGCCTCTGCG	GGCGCTGTCT	CCTGGCTTGT	CTTCCGGCTC	2220
TTCTGCTGGG	GTGGGGCTGG	GCGGCCGGGG	CGGTGCTGGG	GCTCCTCGGG	GGGGGGGGCT	2280
TTCCGGGCTT	GTCTCCCTCC	GGGGCGGGGG	TTTCTGGCCG	TGGGGGTCTT	GCCTTGGCTC	2340
CGGGCTCCTG	CTTGTCTTGC	CTTCTTCTC	TGGTGGGTTG	TGGCTCGGGG	CTCCGTGGGT	2400
CCCTGGCGCC	CGTTTGTGTT	TTGTCTTTTC	CCCTGGCGTC	CCTGTGCCCC	TCTCCTCTCC	2460
TTCTCTGCT	TCTCGCTCTC	CTTGTGGGG	CCCTCCCTGC	TGCTCTTGGT	TTTGGGCTTT	2520
TTTTCTCTCT	CTCCTTTTTC	GTGCGTGGGC	CTCCGCACGC	CTCTTGCCAC	CTCCTGCGCA	2580
GGGCAGCGCC	TTGGGGCCAG	CGCCGCTCCC	GGCGCGGCCA	GCAGGGCAGC	CAGCAGCGCG	2640
CAGCCGACGG	CCAGCATGCT	TCCTCCTCGG	CTACCACTCC	ATGGTCCCGC	AGAGGCGGAC	2700
AGGCGCBCGC	CTCTTGCCBC	CTCCTGCGCB	GGGCBGCGCC	TTGGGGCCBG	CGCCGCTCCC	2760
GGCGCGGCCB	GCBGGGCBGC	CBGCBGCGCG	CBGCCGBCGG	CCBGCBTGCT	TCCTCCTCGG	2820
CTBCCBCTCC	BTGGTCCCGC	BGBGGCGGBC	BGGCGGGGTG	GBBGGTTTGT	GBGTBTGTCT	2880
TTBTGCBCTG	BCBTCTBBGT	TCTTTBGCBC	TCTTGGCBB	BBCTGCBCTT	TCBCBCBGBG	2940
CTGCBGBBBT	CBGGBBGGCT	GCCBBBGBBG	CCBCGGCCBG	CTTGGBBGTC	BTGTTTBCBC	3000
BCBGTGBGBT	GGTTCCTTCC	GGGCTTGTGT	GCTCTGCTGT	CTCTTGGTTC	CTTCCGGTGG	3060
TTTCTTCTTG	GCTCTTGTCC	TTTCTTCTGG	CCCTTGGCCG	GGBTGGGGGG	TCCTGGBCGG	3120
CBCTGBBGGC	BTCCBGGGCT	CCCTTCCBGT	CCCTTCTGTC	CGCTGCCBGC	BCCCTTCTBT	3180
TCCBGBGGCT	GBTGGCCTCC	BCCBGGGBCB	TGBTTBGGTB	GBBBCTBGGG	GGCCGGCCTC	3240
CBCCBGGGBC	BTGGTCCCTC	TTGTCCGCTG	CCTCTCTGGG	GTTTTCGGTC	TGGGTGGGCT	3300
TTCTCCTCGG	GGCTGCTGCT	GGGCTCTTCT	TTTTGTCTCT	GGCCTGGTGC	TCTCTCGTGC	3360
CCCTTCCCTT	GGGTGTCTTG	TTTTGTGGGC	CTCCBCCBGG	GBCBTGGTCT	TTGTTTCTGG	3420
GCTCGTGCCC	CBTCCCGGCT	TCTCTCTGGT	TCCGTCTCTT	GTGGTGGTTG	GCCCTGCTTC	3480
CTTTTGCCCTG	TTGAGGGGGC	AGCAGTTGGG	CCCCAAAGGC	CCTCTCGTTC	ACCTTCTGGC	3540
ACGGAGTTGC	ATCCCCATAG	TCAAACCTCTG	TGGTCTGTCT	ATAGTCTCTT	GTGGTGGTTG	3600
GAGTTTCCAT	CCCGGCTTCT	CTCTGGTTCC	AAGGGAGBGG	GGGCBGCBGT	TGGGCCCCBB	3660
BGGCCCTCTC	GTTCBCTTTC	TGGCBGGBG	BTBGTCCBCC	TCTGTGGTCTG	TCTGTGGTCTG	3720
TGTCBTBGTG	CTCTGTGGTG	TTTGGBTGTT	CCBTGCCGGC	TTCTCTCTGG	TTCCBBGGGB	3780
GGGCBGCGGG	CBGTGGGCGG	GCBBTGTBGG	CBBBGCBGCB	GGGTGTGGTG	TCCBGGBBBT	3840
BTGGGGBGGC	BGBTGCBGGB	GCGCBGGBGG	CBGTBGCBBT	GBGGBTGBCB	GCGBGGCGTG	3900
CCGCGGBGBC	CTTCTBTGGT	CCTGTGGGBG	GGCTGTGCGG	GGGGGTGTGG	TGTCCGCTTG	3960
GCGGTTCTTT	CGGGTGTCTT	TTCTCTGGGT	TGGCCTGCTG	CTCGTCTGTC	TCCGCTCCGCT	4020
CCCGGGTTCG	TCTCGCTCTG	TGCCCCCTTC	CTTCTTGTCT	GTGTTCTCTC	CTTCTTGGCC	4080
TCTGBTGTTT	GTTBCCBBBG	CBTCCBGBBT	BGCTTTGCTB	TCTBBGGBTC	BCBTTTBGBG	4140
BTBGGBBBBC	GCTGTBGGTC	BGBBBGBTGT	GCTTBCTTTC	BCBCBGBGCT	GCBGBBBTCTB	4200
GGBBGGCTGC	CBGGBGCGCT	BCGGCCBGCT	TGBGTCBTG	TTTBCBCCBC	GTGBGGTCTG	4260
CCGGTGGCTT	TTTGTCTGTG	TGCTCTGCTG	TCTCTGTTCC	TTCCGGTGGT	TTCTTCTCTG	4320
CTCTTGTCTT	TTCTCTTGGC	CCTTGGCCCC	TTGBGCBGGB	BGCTCTGGGG	CBGGGBGCTG	4380
GCBGGGGCCB	GGGGGGTGGC	TTCTTGCBC	GTCBGBGCTG	CBCTGTGCCB	CBGCBGCBGC	4440
TGCBGGGCCB	TBCGCTTCBT	GGGGCTCTGG	GTGGCBGGTC	CBGCCBTGGG	TCTGGGTGGG	4500
GCTGGGCTGC	BGGCTCCGGG	CGGTCCBGCC	BTGGGTCTGG	GGGCTGGGCT	GCBGGCTCCG	4560
GGCGGGCGGG	TGCGGGCTGC	GTGCTGGGGG	CTGCCCGCA	GGCCCTGCGG	TCCBGGCBTG	4620
GGTCTGGGGG	CTGGGCTGCB	GGCTCCGGGC	GGGCGGGTGC	GGGCTGCGTG	CTGGGGGCTG	4680
CCCCGACGGC	CCTGCGCBCC	GCCTGGBGCC	CTGGGGCCCC	CCTGTCTTCT	TGGGGBGCGC	4740
CTCTCTGGCC	BGCTCCBCGT	CCCGGBTCBT	GCTTTCBGTG	CTCBTGGTGT	CCTTTCBGG	4800
GGBGBGBGGG	GCTGGTCTCT	TGCTGTCCCT	GCTTGTGCTC	BTGGTGTCTT	TTCCCGCCTG	4860
GGGCCCCCCT	GTCTTCTTGG	GGCCTCTTCC	CTCTGGGGGC	CGTCTCTCTC	CCTCTCTTGC	4920
GTCTCTCTCT	TTCTCTCTCT	CTCTTCCCCT	TTCCCGCTCT	TTCTGTCTCG	GTGTCTGGTT	4980
TTCTCTCTCC	GCTGGCTGCC	TGTCTGGCCT	GCGCTCTTGG	CCTGTGCTGT	TCCTCTCCG	5040
GTTCTCTGTC	TCTGTCTGTC	TGCCCCCTC	TGGGGTCTCC	CTCTGGGTGG	TGGTCTTGT	5100
GCTTGGGCTG	GGCTCCGTGT	CTCCBGTGCT	CBTGGTGTCC	GCTGBGGGBG	CGTCTGCTGG	5160
CGCTGGTCTT	CTGCTGTCTT	TGCTGGTGTG	CBTGGTGTCC	TTTCCGCCCT	GGGGCCCCCC	5220
TGTCTTCTTG	GGGCTCTTTC	CCTCTGGGGG	CCGTCTCTCT	CCCTCTCTTG	CGTCTCTCTC	5280
TTTCTCTCTC	TCTCTTCCCC	TTTCCCGCTC	TTTCTGTCTC	GGTGTCTGGT	TTTCTCTCTC	5340
CGTGGCTGTC	CTGTCTGGCC	TGCGCTCTTG	GCCTGTGCTG	TTCTCCTCTC	GGTTCCTGTC	5400
CTCTCTGTCT	GTCGCCCCCT	CTGGGGTCTC	CCTCTGGCGT	GGTGGTCTTG	TTGCTTGGGC	5460
TGGGCTCCGT	GTCTCCBGTG	CTCBTGGTGT	CCGCTGBGGG	BGCGTCTGCT	GGCCTGCTGB	5520
GGCTTGGGTC	TCCGGGCGBT	TCTCTGCBGB	BGBTGCTCBB	BGGGCTCCGG	CBGTTCTCTC	5580
TGTBCTTGGT	CGCTGTCTGT	CCBGTCCGBC	CBGTBBTTCB	GBTCTCBTTC	GGCTCCTBTT	5640
TCTTCTGCB	BCBGTCTBGT	GGBGBCBBGB	BBBBBGBCTG	CCBGGGCCBC	GBGGBTTTTT	5700
BTGTTGGBTT	TTGCGBCGGB	CBGTCCCGCG	GGGTGCTGAG	TTTCTCTGGT	TCCTCCGBGC	5760
GCBCGTGGTC	GCTCCGCGTT	TCTCTGGTTC	CTCCGCTCCC	GCGGGGTGCT	GTCTGGTCCG	5820
TGTCGTGGCT	TGGGTCTCCG	GCGGTTTCC	TTCTTTTTC	GCCGGCCCTT	CTCACTGGAG	5880
GCACCGGGCA	GTCTCCATG	GGAGGTTTGG	GCTTGGCCGG	GGCTGCCCGG	TGCCTCTCTT	5940
TGGCTGGTCC	CTCGTTGTCC	TTGGGGCCCC	CTCCCGCTGC	TGCGCCCTCC	TGTTCTTTGG	6000
CCTCTTGTCT	CGCCTGCTGT	CTTGTCCCGT	CCCTCCTCG	CTTGGCTTTC	CCTCTTCTCT	6060
GTCTTCCAGG	CCTTCTCTCG	CTTCCGCTGC	TGGGGCCCCG	GCCGGGGGGG	CGCTCGGCTC	6120
CGCGGCTTCC	TCCCCGGGCT	GGGGGTCTCT	GTCCTCCGGG	CCTGCGGCTC	GCGGGCTCGG	6180
GGCTGCGTGC	GCCGCGCGCG	GCGTCCGCGG	TGGGTGGCGC	TGTCCCGCCG	TGGTGTGTCT	6240
CCGTTCTCGT	CCTGCGCCGT	CCTGGTCTGC	CCGTGGGGTC	CTGGGCTGG	TGGGGGGCGT	6300
CTGGTGCCCT	GTCTGCCCCG	TGGGGCTTCG	GGCTCGGGGC	TGTTCTGCTC	CCCTGCCGCT	6360
CTGTGGCCTC	CGGGGCTCCT	CGTTTTCTGCT	GCTTCGGGTG	TCCTTCTCGG	CGTGTGGCCC	6420
CGGGTCCCGG	CCCTGCTGGG	CTGGGCGGGG	TGCTGCCCCT	GGGCTTCTGG	CCCGTCTGGT	6480

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TGTCTGTCGG	TGCTGTCTC	GGGTTTCTGG	CCTCTGTGCT	GGGCGCTTCT	CTGCCTCCTG	6540
CTCCGCCCTC	CTGGTGGCTC	GGCTGGGGGT	GCCCGTGCGG	GGGTGGGTGT	GGGGTGTTTT	6600
CGGGGTCTCT	CCCTTCCCGT	TTCATCTTGG	CTTTATCCTC	TCCCCTTGT	CCTCCCCTCT	6660
CCTGCTCTGG	RGTCTCCTCT	TCCCTCCCTC	CCCTGCCGTG	TGTCTGTGG	GTGTCGTTT	6720
GCTCTTGTG	CCCTGGGCCC	TCCCTGCTG	GGGGGGAGTT	TCATCTTGG	TTTCBTCTTG	6780
GCTTTBTCT	CTCCCCTTGT	TCTCCCCTC	TCCTGCTCTG	GRGTCTCCTC	TTCCCTCCCT	6840
CCCCTGCCGT	GTTGTCTGTG	GGTGTGCTT	CGCTCTTGT	GCCCTGGGCC	CTTCCCTGCT	6900
GGGGGGGBGT	TTTCTTGTG	GGGGGBGTT	CBTCTTGGCT	TCCCGTGTG	TCBGTGGTGC	6960
TGCCCGTTTG	BGGTBTGGCG	CTCCBCCBBT	TCCCTTTTCT	CCTTGTTTTC	CGTTTCTCTT	7020
GCCGTCTGTG	GTT					7033

## (2) INFORMATION FOR SEQ ID NO:2412:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2412:

GATGGAGGGC	GGCATGGCGG	G	21
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## (2) INFORMATION FOR SEQ ID NO:2413:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2413:

GCGGGTCGCC	GG		12
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## (2) INFORMATION FOR SEQ ID NO:2414:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2414:

GGCGGGCBCB	GGC		13
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## (2) INFORMATION FOR SEQ ID NO:2415:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2415:

GGCGGGCBC			9
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## (2) INFORMATION FOR SEQ ID NO:2416:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2416:

GCGGCCTGG			9
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## (2) INFORMATION FOR SEQ ID NO:2417:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2417:

GGBGGGCGGC			10
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## (2) INFORMATION FOR SEQ ID NO:2418:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2418:

GBTGGBGGG			9
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## (2) INFORMATION FOR SEQ ID NO:2419:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2419:

GGCTGGGC

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## (2) INFORMATION FOR SEQ ID NO:2420:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 961 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2420:

```
1 ATGCCGCCCT CCATCTCAGC TTTCCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC
61 CTGGTCTCTG TGCCCGGGAA CGTGCTGGTG ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG
121 CGGGATGCCA CTTCTGCTT CATCGTCTCG CTGGCGGTGG CTGATGTGGC CGTGGGTGCC
181 CTGGTCATCC CCCTCGCCAT CCTCATCAAC ATTGGGCCAC AGACCTACTT CCACACCTGC
241 CTCATGGTTG CTTGTCCGGT CCTCATCTC ACCCAGAGCT CCATCCTGGC CTTGCTGGCA
301 ATTGCTGTGG ACCGCTACCT CCGGGTCAAG ATCCCTCTCC GGTACAAGAT GGTGGTGACC
361 CCGCGGAGGG CGGCGGTGGC CATAGCCGGC TGCTGGATCC TCTCCTTCGT GGTGGGACTG
421 ACCCTATGT TTGGCTGGAA CAATCTGAGT GCGGTGGAGC GGGCCTGGGC AGCCAACGGC
481 AGCATGGGGG AGCCCGTGAT CAAGTGCAG TTCGAGAAGG TCATCAGCAT GGAGTACATG
541 GTCTACTTCA ACTTCTTTGT GTGGGTGCTG CCCCCGCTC TCCTCATGGT CCTCATCTAC
601 CTGGAGGTCT TCTACCTAAT CCGCAAGCAG CTCACAAGA AGGTGTCGGC CTCCTCCGGC
661 GACCCGCAGA AGTACTATGG GAAGGAGCTG AAGATCGCCA AGTCGCTGGC CCTCATCTC
721 TTCCTCTTTG CCCTCAGCTG GCTGCCTTTG CACATCTCA ACTGCATCAC CCTCTCTG
781 CCGTCCCTCC ACAAGCCAG CATCCTTACC TACATTGCCA TCTTCTCAC GCACGGCAAC
841 TCGGCCATGA ACCCCATTGT CTATGCCTTC CGCATCCAGA AGTTCCGCGT CACCTTCCTT
901 AAGATTTGGA ATGACCATT CCGCTGCCAG CCTGCACCTC CCATTGACGA GGATCTCCCA
961 GAAGAGAGGC CTGATGACTA G
```

## (2) INFORMATION FOR SEQ ID NO:2421:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2881 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2421:

```
1 ATGAGTGTCA GAAGTGTGAA GGGTGCCTGT TCTGAATCCC AGAGCCTCCT CTCCCTCTGT
61 GAGGCTGGCA GGTGAGGAAG GGTTTAACCT CACTGGAAGG AATCCCTGGA GCTAGCGGCT
121 GCTGAAGGCG TCGAGGTGTG GGGGCACTTG GACAGAACAG TCAGGCAGCC GGGAGCTCTG
181 CCAGCTTTGG TGACCTTGGG CCGGGCTGGG AGCGCTGCGG CGGGAGCCGG AGGACTATGA
241 GCTGCCGCGC GTTGTCAGA GCCCAGCCCA GCCCTACGGC CGCGGCCCGG AGCTCTGTTC
301 CCTGGAACTT TGGGCACTG CTCTGGGACC CCTGCCGGCC AGCAGGCGAG ATGGTGCTTG
361 CCTCGTGCCC CTTGGTGCCC GTCTGCTGAT GTGCCAGCC TGTGCCCGCC ATGCCCGCCT
421 CCATCTCAGC TTTCCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC CTGGTCTCTG
481 TGCCCGGGAA CGTGCTGGTG ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG CGGGATGCCA
541 CTTTCTGCTT CATCGTGTG CTGGCGGTGG CTGATGTGGC CGTGGGTGCC CTGGTCATCC
601 CCCTCGCCAT CCTCATCAAC ATTGGGCCAC AGACCTACTT CCACACCTGC CTCATGGTTG
661 CCTGTCCGGT CCTCATCTC ACCCAGAGCT CCATCCTGGC CCTGCTGGCA ATTGCTGTGG
721 ACCGCTACCT CCGGGTCAAG ATCCCTCTCC GGTACAAGAT GGTGGTGACC CCGCGGAGGG
781 CGGCGGTGGC CATAGCCGGC TGCTGGATCC TCTCCTTCGT GGTGGGACTG ACCCTATGT
841 TTGGCTGGAA CAATCTGAGT GCGGTGGAGC GGGCCTGGGC AGCCAACGGC AGCATGGGGG
901 AGCCCGTGAT CAAGTGCAG TTCGAGAAGG TCATCAGCAT GGAGTACATG GTCTACTTCA
961 ACTTCTTTGT GTGGGTGCTG CCCCCGCTC TCCTCATGGT CCTCATCTAC CTGGAGGTCT
1021 TCTACCTAAT CCGCAAGCAG CTCACAAGA AGGTGTCGGC CTCCTCCGGC GACCCGCAGA
1081 AGTACTATGG GAAGGAGCTG AAGATCGCCA AGTCGCTGGC CCTCATCTC TTCCTCTTTG
1141 CCCTCAGCTG GCTGCCTTTG CACATCTCA ACTGCATCAC CCTCTCTGC CCGTCTTGCC
1201 ACAAGCCAG CATCCTTACC TACATTGCCA TCTTCTCAC GCACGGCAAC TCGGCATGA
1261 ACCCCATTGT CTATGCCTTC CGCATCCAGA AGTTCCGCGT CACCTTCCTT AAGATTGGA
1321 ATGACCATT CCGCTGCCAG CCTGCACCTC CCATTGACGA GGATCTCCCA GAAGAGAGGC
1381 CTGATGACTA GACCCCGCCT TCCGCTCCCA CCAGCCACA TCCAGTGGGG TCTCAGTCCA
1441 GTCCTCATAT GCCCGCTGTC CCAGGGGTCT CCCTGAGCCT GCGCCAGCTG GGCTGTGGC
1501 TGGGGGCATG GGGGAGGCTC TGAAGAGATA CCCACAGAGT GTGGTCCCTC CACTAGGAGT
1561 TAACTACCCT ACACCTCTGG GCCCTGCAGG AGGCCTGGGA GGGCAAGGGT CCTACGGAGG
1621 GACCAGGTGT CTAGAGGCAA CAGTGTCTG AGCCCCACC TGCCTGACCA TCCCATGAGC
1681 AGTCCAGCGC TTCAGGGCTG GGCAGGTCTT GGGGAGGCTG AGACTGCAGA GGAGCCACCT
1741 GGGCTGGGAG AAGGTGCTTG GGCTTCTCG GTGAGGCAGG GGAGTCTGCT TGTCTTAGAT
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1801 GTTGGTGGTG CAGCCCCAGG ACCAAGCTTA AGGAGAGGAG AGCATCTGCT CTGAGACGGA  
 1861 TGGAAGGAGA GAGGTTGAGG ATGCACTGGC CTGTTCTGTA GGAGAGACTG GCCAGAGGCA  
 1921 GCTAAGGGGC AGGAATCAAG GAGCCTCCGT TCCCACCTCT GAGGACTCTG GACCCAGGC  
 1981 CATACCAGGT GCTAGGGTGC CTGCTCTCCT TGCCCTGGGC CAGCCCAGGA TTGTACGTGG  
 2041 GAGAGGCAGA AAGGGTAGGT TCAGTAATCA TTTCTGATGA TTTGCTGGAG TGCTGGCTCC  
 2101 AGCCCTGGG GAGTGAGCTT GGTGCGGTAG GTGCTGGCCT CAAACAGCCA CGAGGTGGTA  
 2161 GCTCTGAGCC CTCCTTCTTG CCCTGAGCTT TCCGGGGAGG AGCCTGGAGT GTAATTACCT  
 2221 GTCATCTGGG CCACCAGCTC CACTGGCCCC CGTTGCCGGG CCTGGACTGT CCTAGGTGAC  
 2281 CCCATCTCTG CTGCTTCTGG GCCTGATGGA GAGGAGAACA CTAGACATGC CAACTCGGGA  
 2341 GCATTCTGCC TGCTGGGAA CGGGGTGGAC GAGGGAGTGT CTGTAAGGAC TCAGTGTGA  
 2401 CTGTAGGCGC CCCTGGGGTG GGTTAGCAG GCTGCAGCAG GCAGAGGAGG AGTACCCCC  
 2461 TGAGAGCATG TGGGGGAAGG CTTGCTGTC ATGTGAATCC CTCAATACCC CTAGTATCTG  
 2521 GCTGGGTTTT CAGGGGCTTT GGAAGCTCTG TTGAGGTGT CCGGGGGTCT AGGACTTTAG  
 2581 GGATCTGGGA TCTGGGGAAG GACCAACCCA TGCCCTGCCA AGCCTGGAGC CCCTGTGTG  
 2641 GGGGGCAAGG TGGGGGAGCC TGGAGCCCCT GTGTGGGAGG GCGAGGCGGG GGAGCCTGGA  
 2701 GCCCTGTGT GGGAGGGCGA GCGGGGGAT CCTGGAGCCC CTGTGTCGGG GGGCGAGGGA  
 2761 GGGGAGGTGG CCGTCGGTTG ACCTTCTGAA CATGAGTGT AACTCCAGGA CTTGCTTCCA  
 2821 AGCCCTTCCC TCTGTTGGAA ATTGGGTGTG CCCTGGCTCC CAAGGGAGGC CCATGTGACT  
 2881 AATAAAAAAC TGTGAACCT

## (2) INFORMATION FOR SEQ ID NO:2422:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1921 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2422:

1 CGCATTGTG TTTTAATAAA AGAATCTGGA AGATAAATAG TCTTGAAGAG AGACAAAGGA  
 61 AGGAAAATTT AAATCCTTAG ATTCAAGCAG AAGAATTCCA TGTGGAAGGT TTGGGTGTG  
 121 GTTGTGTTG TTTGGTGTG TTTTGTGTTT TTTGTTTTTT TGTTTTTTT TGAGATGGAG  
 181 TCTCGCTGTG TTACCGGGAG CGACAGAGCC GCACGGCCGA GTCGAGTCCC AGCCAGCTAC  
 241 CATCCCTCTG GAGCTTACCG GCCGGCCTTG GCTTCCCCAG GAATCCCTGG AGCTAGCGGC  
 301 TGCTGAAGGC GTCGAGGTGT GGGGGCACTT GGACAGAACA GTCAGGCAGC CGGGAGCTCT  
 361 GCCAGCTTTG GTGACCTTGG GTGCTTGCCCT CGTGCCCTT GGTGCCCGTC TGCTGATGTG  
 421 CCCAGCCTGT GCCCGCATG CCGCCCTCCA TCTCAGCTT CCAGGCCGCC TACATCGGCA  
 481 TCGAGGTGCT CATCGCCCTG GTCTCTGTGC CCGGGAACGT GCTGGTGATC TGGGCGGTGA  
 541 AGGTGAACCA GGCGCTGCGG GATGCCACCT TCTGCTTCAT CGTGTGCTG GCGGTGGCTG  
 601 ATGTGGCCGT GGGTGCCCTG GTCATCCCC TCGCCATCCT CATCAACATT GGGCCACAGA  
 661 CCTACTTCCA CACCTGCCTC ATGGTTGCCT GTCCGGTCTT CATCCTCACC CAGAGCTCCA  
 721 TCCTGGCCCT GCTGCAATT GCTGTGGACC GCTACCTCCG GGTCAAGATC CCTCTCCGGT  
 781 ACAAGATGGT GGTGACCCCC CGGAGGCGCG CGGTGGCCAT AGCCGGCTGC TGGATCCTCT  
 841 CCTTCGTGGT GGGACTGACC CCTATGTTG GCTGGAACAA TCTGAGTGCG GTGGAGCGGG  
 901 CTGGGCGAGC CAACGGCAGC ATGGGGGAGC CCGTGATCAA GTGCGAGTTC GAGAAGGTCA  
 961 TCAGCATGGA GTACATGGTC TACTTCAACT TCTTGTGTG GGTGCTGCC CCGTTCTCC  
 1021 TCATGGTCTT CATCTACCTG GAGGTCTTCT ACCTAATCCG CAAGCAGCTC AACAAGAAGG  
 1081 TGTCGGCCTC CTCGGCGGAC CCGCAGAAGT ACTATGGGAA GGAGCTGAAG ATCGCCAAGT  
 1141 CGCTGGCCCT CATCTCTTC CTCTTTGCC TCAGCTGGCT GCCTTTGCAC ATCCTCAACT  
 1201 GCATCACCTT CTCTGCCCG TCCTGCCACA AGCCCAGCAT CCTTACCTAC ATTGCCATCT  
 1261 TCCTCACGCA CGGCAACTCG GCCATGAACC CCATTGTCTA TGCTTCCGC ATCCAGAAGT  
 1321 TCCGCGTCAC CTCTTTAAG ATTTGGAATG ACCATTTCG CTGCCAGCCT GCTCCACCG  
 1381 TTGACGAGGA TCTCCCAGAA GAGAGGCCTG ATGACTAGAC CCCGCTTCC GCTCCACCG  
 1441 CCCACATCCA GTGGGGTCTC AGTCCAGTCC TCACATGCCC GCTGTCCCAG GGGTCTCCCT  
 1501 GAGCCTGCCC CAGCTGGGCT GTTGGCTGGG GGCATGGGG AGGCTCTGAA GAGATACCCA  
 1561 CAGAGTGTGG TCCCTCCACT AGGAGTTAAC TACCCTACAC CTCTGGGCC TGCAGGAGGC  
 1621 CTGGGAGGGC AAGGGTCCTA CCGAGGGACC AGGTGTCTAG AGGCAACAGT GTTCTGAGCC  
 1681 CCCACCTGCC TGACCATCCC ATGAGCAGTC CAGAGCTTCA GGGCTGGGCA GGTCTGGGG  
 1741 AGGCTGAGAC TGCAGAGGAG CCACCTGGGC TGGGAGAAGG TGCTTGGGCT TCTGCGGTGA  
 1801 GGCAGGGGAG TCTGCTTGTG TTAGATGTTG GTGGTGAGC CCCAGGACCA AGCTTAAGGA  
 1861 GAGGAGAGCA TCTGCTCTGA GACGGATGGA AGGAGAGAGG TTGAGGATGC ACTGCGCTGT  
 1921 TCTGTAGGAG AGACTGGCCA GA

## (2) INFORMATION FOR SEQ ID NO:2423:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5904 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2423:

ATGCCGCCCT CCATCTCAGC TTTCCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC CTGGTCTCTG  
 TGCCCGGGAA CGTGCTGGTG ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG CGGGATGCCA CTTCTGCTT



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CATCGTCTCG	CTGGCGGTGG	CTGATGTGGC	CGTGGGTGCC	CTGGTCATCC	CCCTCGCCAT	CCTCATCAAC
ATTGGGCCAC	AGACCTACTT	CCACACCTGC	CTCATGGTTG	CCTGTCCGGT	CCTCATCCTC	ACCCAGAGCT
CCATCTGGC	CCTGTGGCA	ATTGCTGTGG	ACCGCTACCT	CCGGGTCAAG	ATCCCTCTCC	GGTACAAGAT
GGTGTGACC	CCCCGAGGG	CGGCGGTGGC	CATAGCCGGC	TGCTGGATCC	TCTCCTTCGT	GGTGGGACTG
TTGGCTGGAA	CAATCTGAGT	GCGGTGGAGC	GGGCCTGGGC	AGCCAAACGGC	AGCATGGGGG	AGCCCCGTGAT
CAAGTGCGAG	TTCGAGAAGG	TCATCAGCAT	GGAGTACATG	GTCTACTTCA	ACTTCTTTGT	GTGGGTGCTG
CCCCCGCTTC	TCCTCATGGT	CCTCATCTAC	CTGGAGTCTG	TCTACCTAAT	CCGCAAGCAG	CTCAACAAGA
AGGTGTCGGC	CTCCTCCGGC	GACCCGAGA	AGTACTATGG	GAAGGAGCTG	AAGATCGCCA	AGTCGTGGC
CCTCATCCTC	TTCCTCTTTG	CCCTCAGCTG	GCTGCCTTTG	CACATCCTCA	ACTGCATCAC	CCTCTTCTGC
CCGTCTGCC	ACAAGCCCAG	CATCCTTACC	TACATTGCCA	TCTTCTCAC	GCACGGCAAC	TCGGCCATGA
ACCCCATTTG	CTATGCCTTC	CGCATCCAGA	AGTTCGCGT	CACCTTCCTT	AAGATTTGGA	ATGACCATT
CCGTCTGCC	CCTGCACCTC	CCATTGACGA	GGATCTCCCA	GAAGAGAGGC	CTGATGACTA	G
GAAGTGTGAA	GGGTGCCTGT	TCTGAATCCC	AGAGCCTCCT	CTCCCTCTGT	GAGGTGGCA	GGTGAGGAAG
GGTTAACTT	CACCTGAAGG	AATCCCTGGA	GCTAGCGGCT	GCTGAAGGCG	TCGAGGTGTG	GGGGCACTTG
CACAGAAGC	TCAGGCAGCC	GGGAGCTCTG	CCAGCTTTGG	TGACCTTGGG	CCGGGCTGGG	AGCGCTCGCG
CGGGAGCCGG	AGGACTATGA	GCTGCCGCGC	GTTGTCCAGA	GCCCCAGCCA	GCCCTACGCG	CGCGGCCCGG
AGCTCTGTTC	CCTGGAACCT	TGGGCACTGC	CTCTGGGACC	CCTGCCGGCC	AGCAGGCAGG	ATGGTGCTTG
CCTCGTGCCC	CTTGGTGCCC	GTCTGCTGAT	GTGCCAGGCC	TGTGCCCGCC	ATGCCGCCCT	CCATCTCAGC
TTTCCAGGCC	GCCTACATCG	GCATCGAGGT	GCTCATCGCC	CTGGTCTCTG	TGCCCCGGAA	CGTGCTGGTG
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CCACACCTGC	CTCATGGTTG	CCTGTCCGGT	CCTCATCCTC	ACCCAGAGCT	CCATCCTGGC	CCTGTGGCA
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CGGCGGTGGC	CATAGCCGGC	TGCTGGATCC	TCTCCTTCGT	GGTGGGACTG	ACCCCTATGT	TTGGCTGGAA
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TTCGAGAAGG	TCATCAGCAT	GGAGTACATG	GTCTACTTCA	ACTTCTTTGT	GTGGGTGCTG	CCCCCGCTTC
TCCTCATGGT	CCTCATCTAC	CTGGAGTCTG	TCTACCTAAT	CCGCAAGCAG	CTCAACAAGA	AGGTGTGGGC
CTCCTCCGGC	GACCCGAGA	AGTACTATGG	GAAGGAGCTG	AAGATCGCCA	AGTCGTGGC	CCTCATCCTC
TTCCTCTTTG	CCCTCAGCTG	GCTGCCTTTG	CACATCCTCA	ACTGCATCAC	CCTCTTCTGC	CCGTCTCTGC
ACAAGCCAG	CATCCTTACC	TACATTGCCA	TCTTCTCAC	GCACGGCAAC	TCGGCCATGA	ACCCCATTTG
CTATGCCTTC	CGCATCCAGA	AGTTCGCGT	CACCTTCCTT	AAGATTTGGA	ATGACCATT	CCGCTGCCAG
CCTGCACCTC	CCATTGACGA	GGATCTCCCA	GAAGAGAGGC	CTGATGACTA	GACCCCGCCT	TCCGCTCCCA
CCAGCCACA	TCCAGTGGGG	TCTCAGTCCA	GTCTCACAT	GCCCCGTGTC	CCAGGGGTCT	CCCTGAGCCT
GCCCCAGCTG	GGCTGTTGGC	TGGGGGCATG	GGGGAGGCTC	TGAAGAGATA	CCCACAGAGT	GTGGTCCCTC
CACTAGGAGT	TAACCTACCT	ACACCTCTGG	GCCCTGCAGG	AGGCCTGGGA	GGGCAAGGGT	CCTACGGAGG
GACCAGGTGT	CTAGAGGCAA	CAGTGTCTG	AGCCCCCACC	TGCCCTGACCA	TCCCATGAGC	AGTCCAGCGC
TTCAGGCTGT	GGCAGGTCTT	GGGAGGCTG	AGACTGCAGA	GGAGCCACCT	GGGCTGGGAG	AAGGTGCTTG
GGCTTCTGCG	GTGAGGCAGG	GGAGTCTGCT	TGTCTTAGAT	GTTGGTGGTG	CAGCCCCAGG	ACCAAGCTTA
AGGAGAGGAG	AGCATCTGCT	CTGAGACGGA	TGGAAGGAGA	GAGGTTGAGG	ATGCACTGGC	CTGTTCTGTA
GGAGAGACTG	GCCAGAGGCA	GCTAAGGGGC	AGGAATCAAG	GAGCCTCCGT	TCCCACCTCT	GAGGACTCTG
GACCCAGGC	CATACCAGGT	GCTAGGCTGC	CTGCTCTCCT	TGCCCTGGGC	CAGCCCAGGA	TTGTACGTGG
GAGAGGCAGA	AAGGGTAGGT	TCAGTAATCA	TTTCTGATGA	TTTGCTGGAG	TGCTGGCTCC	ACGCCTGGG
GAGTGAAGT	GGTGCGGTAG	GTGCTGGCCT	CAAACAGCCA	CGAGGTGGTA	GCTCTGAGCC	CTCCTTCTTG
CCCTGAGCTT	TCCGGGAGG	AGCCTGGAGT	GTAATTACCT	GTCTCTGGG	CCACAGCTG	CACTGGCCCC
CGTTGCCGGG	CCTGGAAGT	CCTAGGTGAC	CCATCTCTG	CTGCTTCTGG	CTGCTTCTGG	GAGGAGAACA
CTAGACATGC	CAACTCGGGA	GCATTCTGCC	TGCTTGGGAA	CGGGGTGGAC	GAGGGAGTGT	CTGTAAAGAC
TCAGTGTGTA	CTGTAGGCGC	CCCTGGGGTG	GGTTTAGCAG	GCTGCAGCAG	GCAGAGGAGG	AGTACCCCCC
TGAGAGCATG	TGGGGGAAGG	CCTTGCTGTC	ATGTGAATCC	CTCAATACCC	CTAGTATCTG	GCTGGGTTTT
CAGGGGCTTT	GGAGGCTCTG	TTGCAGGTGT	CCGGGGGTCT	AGGACTTTAG	GGATCTGGGA	TCTGGGGAAG
GACCAACCCA	TGCCCTGCCA	AGCCTGGAGC	CCCTGTGTTG	GGGGGCAAGG	TGGGGGAGCC	TGGAGCCCCC
GTGTGGGAGG	GCGAGGCGGG	GGAGCCTGGA	GCCCTGTGT	GGGAGGGCGA	GGCGGGGGAT	CCTGGAGCCC
CTGTGTCCGG	GGGCGAGGGA	GGGGAGGTGG	CCGTGGTTG	ACCTTCTGAA	CATGAGTGTG	AACTCCAGGA
CTTGCTTCCA	AGCCCTTCCC	TCTGTTGGAA	ATTGGGTGTG	CCCTGGCTCC	CAAGGGAGGC	CCATGTGACT
AATAAAAAAC	TGTGAACCCT	CGCATTTGTG	TTTTAATAAA	AGAATCTGGA	AGATAAATAG	TCTTGAAGAG
AGACAAAGGA	AGGAAAATTT	AAATCCTTAG	ATTCAAGCAG	AAGAATTCCA	TGTGGAAGGT	TTGGGTGTGT
GTTGTTGTGT	TTTGGTGTGT	TTTTTGTGTT	TTTGTGTTTT	TGTTTTTTTT	TGAGATGGAG	TCTCGCTGTG
TTACCGGGAG	CGACAGAGCC	GCACGGCCGA	GTCGAGTCCC	AGCCAGCTAC	CATCCCTCTG	GAGCTTACCG
GCCGGCCCTG	GCTTCCCCAG	GAATCCCTGT	AGCTAGCGGC	TGCTGAAGGC	GTGAGGTGT	GGGGGCACTT
GGACAGACAA	GTCAGGCAGC	CGGAGCTCTG	GCCAGCTTTG	GTGACCTTGG	GTGCTTGCC	CGTGCCCTTT
GGTGCCCGTC	TGCTGATGTG	CCAGCCTGT	GCCGCCATG	CCGCCCTCCA	TCTCAGCTTT	CCAGGCCGCG
TACATCGGCA	TCGAGGTGCT	CATCGCCCTG	GTCTCTGTGC	CCGGGAACGT	GCTGGTGATC	TGGGCGGTGA
AGGTGAACCA	GGCGCTGCGG	GATGCCACCT	TCTGCTTCAT	CGTGTGCTG	GCGGTGGCTG	ATGTGGCCGT
GGGTGCCCTG	GTCATCCCCC	TCGCCATCCT	CATCAACATT	GGGCCACAGA	CCTACTTCCA	CACCTGCCTC
ATGGTTGCCT	GTCCGGTCTT	CATCCTCACC	CAGAGCTCCA	TCTTGGCCCT	GCTGGCAATT	GCTGTGGACC
GCTACCTCCG	GGTCAAGATC	CCTCTCCGGT	ACAAGATGGT	GGTGACCCCC	CGGAGGGCGG	CGGTGGCCAT
AGCCGGCTGC	TGGATCCTCT	CCTTCGTGGT	GGGACTGACC	CCTATGTTTG	GCTGGAACAA	TCTGAGTGCG
GTGGAGCGGG	CCTGGGCAGC	CAACGGCAGC	ATGGGGGAGC	CCGTGATCAA	GTGCGAGTTC	GAGAAGGTCA
TCAGCATGGA	GTACATGGTC	TACTTCAACT	TCTTGTGTG	GGTGTGCC	CCGCTTCTCC	TCATGGTCTT



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CATCTACCTG GACTCTTCT ACCTAATCCG CAAGCAGCTC AACAAAGAGG TGTCCGCCCTC CTCCGGCGAC  
 CCGCAGAAGT ACTATGGGAA GGAGCTGAAG ATCGCCAAGT CGCTGGCCCT CATCCTCTTC CTCTTTGCCC  
 TCAGCTGGCT GCCTTTGCAC ATCCTCAACT GCATCACCTT CTCTGCCCCG TCCTGCCACA AGCCCAGCAT  
 CTTACCTAC ATTGCCATCT TCCTACGCA CCGCAACTCG GCCATGAACC CCATTGTCTA TGCTTCCGC  
 ATCCAGAAGT TCCGCGTCAC CTTCTTAAG ATTTGGAATG ACCATTTCG CTGCCAGCCT GCACCTCCCA  
 TTGACGAGGA TCTCCAGAA GAGAGGCCTG ATGACTAGAC CCCGCCTTCC GCTCCACCG CCCACATCCA  
 GTGGGGTCTC AGTCCAGTCC TCACATGCCC GCTGTCCCAG GGGTCTCCCT GAGCCTGCCC CAGCTGGGCT  
 GTTGGCTGGG GGCATGGGGG AGGCTCTGAA GAGATACCCA CAGAGTGTGG TCCCTCCACT AGGAGTTAAC  
 TACCCTACAC CTCTGGGCCC TGCAGGAGGC CTGGGAGGGC AAGGGTCCCTA CGGAGGGACC AGGTGTCTAG  
 AGGCAACAGT GTTCTGAGCC CCCACCTGCC TGACCATCCC ATGAGCAGTC CAGAGCTTCA GGGCTGGGCA  
 GGTCTGGGG AGGCTGAGAC TGCAGAGGAG CCACCTGGGC TGGGAGAAGG TGCTTGGGCT TCTGCGGTGA  
 GGCAGGGGAG TCTGCTTGTC TTAGATGTTG GTGTGTCAGC CCCAGGACCA AGCTTAAGGA GAGGAGAGCA  
 TCTGCTCTGA GACGGATGGA AGGAGAGAGG TTGAGGATGC ACTGGCCTGT TCTGTAGGAG AGACTGGCCA GA GAT  
 GGA GGG CGG CAT GGC GGG G CGG GTC GCC GG GGC GGG CBC BGG C GGC GGG CBC GC GGC CTG G  
 GGB GGG CGG C GBT GGB GGG GG CTG GGC GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC  
 GGG CAC AGG CTG GGC

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## (2) INFORMATION FOR SEQ ID NO:2424:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1681 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2424:

1 CCCAGCCCCG AGGCTCAGAA GCGGCAGGCG GAGGCGCGGT CCGGGCGCTA TGGCCATGCC  
 61 CGGCGGGTCT CACGCGGCTG CCCCTCGCCC GCGCGCGCTT CGGTAGGGGG CGCCCCGGGG  
 121 CCAGCTGGCC CGGCCATGCT GCTGGAGACA CAGGACGCGC TGTACGTGGC GCTGGAGCTG  
 181 GTCATCGCCG CGCTTTCGGT GCGGGGCAAC GTGCTGGTGT GCGCCGCGGT GGGCAGGGCG  
 241 AACACTCTGC AGACGCCCAC CAACTACTTC CTGGTGTCCC TGGCTGCGGC GCACGTGGCC  
 301 GTGGGGCTCT TCGCCATCCC CTTTGCCATC ACCATCAGCC TGGGCTTCTG CACTGACTTC  
 361 TACGGCTGCC TCTTCCTCGC CTGCTTCGTG CTGGTGTCTA CGCAGAGCTC CATCTTCAGC  
 421 CTTCTGGCCG TGGCAGTCGA CAGATACCTG GCCATCTGTG TCCCGCTCAG GTATAAAAGT  
 481 TTGGTCACGG GGACCCGAGC AAGAGGGGTC ATTGCTGTCC TCTGGGTCTT TGCTTTTGGC  
 541 ATCGGATTGA CTCCATTCTT GGGGTGGAAC AGTAAAGACA GTGCCACCAA CAACTGCACA  
 601 GAACCCTGGG ATGGAACCAAC GAATGAAAGC TGCTGCCTTG TGAAGTGTCT CTTTGAGAAAT  
 661 GTGGTCCCCA TGAGCTACAT GGTATATTTC AATTTCTTTG GGTGTGTTCT GCGCCCACTG  
 721 CTTATAATGC TGGTGATCTA CATTAGATC TTCCTGGTGG CCTGCAGGCA GCTTCAGCGC  
 781 ACTGAGCTGA TGGACCACTC GAGGACCACC CTCCAGCGGG AGATCCATGC AGCCAAGTCA  
 841 CTGGCCATGA TTGTGGGGAT TTTTGCCCTG TGCTGGTTAC CTGTGCATGC TGTTAACTGT  
 901 GTCACTCTTT TCCAGCCAGC TCAGGGTAAA AATAAGCCCA AGTGGGCAAT GAATATGGCC  
 961 ATTCTTCTGT CACATGCCAA TTCAGTTGTC AATCCATTG TCTATGCTTA CCGGAACCGA  
 1021 GACTTCCGCT ACACCTTTCA CAAAATTATC TCCAGGTATC TTCTCTGCCA AGCAGATGTC  
 1081 AAGAGTGGGA ATGGTCAGGC TGGGGTACAG CCTGCTCTCG GTGTGGGCCT ATGATCTAGG  
 1141 CTCTCGCCTC TTCCAGGAGA AGATACAAAT CCACAAGAAA CAAAGAGGAC ACGGCTGGTT  
 1201 TTCATTGTGA AAGATAGCTA CACCTCACAA GGAATAGGAC TGCCTCTCTT GAGCACTTCC  
 1261 CTGGAGCTAC CACGTATCTA GCTAATATGT ATGTGTCACT AGTAGCACC AAGATTGACA  
 1321 AATATATTTA TGATCTATTG AGCTGCTTTT ACTGTGTGGA TTATGCCAAC AGCTTGAATG  
 1381 GATTCTAACA GACTCTTTTG TTTTAAAG TCTGCTTGT TTATGGTGG AATTACTGA  
 1441 AACTATTTTA CTGTGAAACA GTGTGAACTA TTATAATGCA AATACTTTTT AACTTAGAGG  
 1501 CAATGGAAAA ATAAAAGTTG ACTGTACTAA AAATGTATAC TTGTGCCAG GAAGGTGACC  
 1561 TCAAAAATTA AAAGTATAAT TATTCGGCCG GGCATGGTGG CTCACACCTG TAATTCCAGC  
 1621 ACTTTGGGAG GCCAAGGCAG GCGATCAGC AGGTGAGGAG TTCAAAACCA GCCTGTCCAA  
 1681 TATAGT

## (2) INFORMATION FOR SEQ ID NO:2425:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1681 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2425:

1 GGGCAATTTG TTAGTTATCC GCCGCCACCA AGACGCGGCA CGGCGCCTGG ACCGGAGGGG  
 61 CCCGCGCGCG GCGCGAACTT TGGGCTCGGG CGAGTGGGTG GTGCTCCGCC CAGCCCGAGA  
 121 CGGGCGGGCG CGCGGGCCAA TGGGTGCCG CTCTTGGCCG CCGGGGGCCC CGACCCGTGG  
 181 GTCCCGGCCA CCAGCGCCCC AGCCCCGAGG CTCAGAAGCG GCAGGCGGAG GCGCGGTCCG  
 241 GCGCTATGG CCATGCCCGG CGGGTCTCAC GCGGCTGCC CTGCGCCGGC GCGCTTCCG  
 301 TAGGGGGCGC CCGGGGCCCA GCTGGCCCG CCATGCTGCT GGAGACACAG GACGCGTGT  
 361 ACGTGGCGCT GGAGCTGGTC ATCGCCGCGC TTTCCGTGGC GGGCAACGTG CTGGTGTGCG  
 421 CCGCGGTGGG CACGGCGAAC ACTCTGCAGA CGCCACCAA CTACTTCTG GTGTCCCTGG

481 CTGCGGCCGA CGTGGCCGTG GGGCTCTTCG CCATCCCCTT TGCCATCACC ATCAGCCTGG  
541 GCTTCTGCAC TGACTTCTAC GGCTGCCTCT TCCTCGCCTG CTTCGTGCTG GTGCTCACGC  
601 AGAGCTCCAT CTTAGCCTT CTGGCCGTGG CAGTCGACAG ATACCTGGCC ATCTGTGTCC  
661 CGCTCAGGTA TAAAAGTTTG GTCACGGGGA CCCGAGCAAG AGGGGTCAAT GCTGTCTCT  
721 GGGTCCTTGC CTTTGGCATC GGATTGACTC CATTCTGGG GTGGAACAGT AAAGACAGTG  
781 CCACCAACAA CTGCACAGAA CCCTGGGATG GAACCACGAA TGAAAGCTGC TGCCTTGTGA  
841 AGTGTCTCTT TGAGAAATGTG GTCCCCATGA GCTACATGGT ATATTTCAAT TTCTTTGGGT  
901 GTGTTCTGCC CCCACTGCTT ATAATGCTGG TGATCTACAT TAAGATCTTC CTGGTGGCCT  
961 GCAGGCAGCT TCAGGCCACT GAGCTGATGG ACCACTCGAG GACCACCCCTC CAGCGGGAGA  
1021 TCCATGCAGC CAAGTCACTG GCCATGATTG TGGGGATTTT TGCCCTGTGC TGGTTACCTG  
1081 TGCATGCTGT TAACTGTGTC ACTCTTTTCC AGCCAGCTCA GGGTAAAAAT AAGCCCAAGT  
1141 GGGCAATGAA TATGGCCATT CTTCTGTAC ATGCCAATTC AGTTGTCAAT CCCATTGTCT  
1201 ATGCTTACCG GAACCGAGAC TTCCGCTACA CTTTTACAA AATTATCTCC AGGTATCTTC  
1261 TCTGCCAAGC AGATGTCAAG AGTGGGAATG GTCAGGCTGG GGTACAGCCT GCTCTCGGTG  
1321 TGGGCCTATG ATCTAGGCTC TCGCCTCTTC CAGGAGAAGA TACAAATCCA CAAGAAACAA  
1381 AGAGGACACG GCTGGTTTTC ATTGTGAAAG ATAGCTACAC CTCACAAGGA AATCGGATG  
1441 CTCTCTTGAG CACTTCCCTG GAGCTACCAC GTATCTAGCT AATATGTATG TGTCAGTAGT  
1501 AGGCTCCAAG GATTGACAAA TATATTTATG ATCTATTAG CTGCTTTTAC TGTGTGGATT  
1561 ATGCCAACAG CTTGAATGGA TTCTAACAGA CTCTTTTGT TTTAAAGTC TGCCTTGTTC  
1621 ATGGTGGAAA ATTACTGAAA CTATTTTACT GTGAAACAGT GTGAACTATT ATATGCAAA  
1681 TACTTTTTTAA CTTAGAGGCA ATGGAAAAAT AAAAGTTGAC TGTACTAAAA ATG

## (2) INFORMATION FOR SEQ ID NO:2426:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2461 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2426:

1 GAATTCCAG ATGGGCAGAG GTGGCTGGGC TGGTGACCCT AAGTGTGTCT CCTGCCTTTA  
61 TTCTCTCTAG TGGGTATTTC TTTCATGTGG TATCTTGCCCT ACAGCATGCT GTGTTGGAC  
121 ACAAACCCCT TTCCTTGGTT TCTCTGACCC AGCTGAGATG GACTGATTCC AAAAGAATC  
181 ACCTATGTAC TGGGGTAGGG GAGGGAGGGT TTTTGCAGT ATTTAACTAA GGTTCAAAGA  
241 GTGCTATATA GTGAGAAAGG CTTCTTTTTC TTTTGTGCTG TTTTGTGCTG GAGTGTGCTG  
301 TCCTAGAAAT TTCTCTTGGT AACTTCCCTTC TCTGAAGCAC AGATAAAGAA AACAATTACA  
361 GTAGAAACAT TTATGAGGGA CACATTGGAG GCCGATGAAG CTTTTCAGT TCCAGCAGTG  
421 CAGGGATGTG GGCAGAACTG ACATTGGAAA ATACTAGAAT GATGGAAAT CAGTTGGAGA  
481 GGAATGCCCT TTTTAATGTC TGGGGAGTCT GCTCAGGGAG AAATGACAAG TCTGGCGGGG  
541 ACAAGTATGG GATTGGTAA GACTTGGATC AACTTGGGAT ACAGGGTGGG GGTGGGGAGT  
601 GGAATCAATG AATGATGCCA GAGCAGATCA ACTAACAAGA GGACCCTGAT GAGCCCCAGG  
661 CAGAGGCGTC TCCCTTATGC CCCACTCTGA AGTGTGTTGT AGTAAACACC AGAACGCCAT  
721 TGTGTGTTACT GCTGAATTTT ATTTTGGGCT GTACATATT AGATGCTTAA GGTAAATATG  
781 ATAAAGCCCT CAAGCCACTG TGTGGGTTTG GGTCCAAGTG TTCCTTCTTG CTGCCTCTCT  
841 AACACGCCCT GTTAAATATA TCCCTTTGGA TGGTGCTGAG AAGCACCTGA ACCAAGTGGG  
901 TCCCCAAATA ACAATGGCGT GCAAGTGTCT GGTTCACAGA AGTTGGTGAC TAGGTAAGCA  
961 GCTTCAGGGA GAGGGGGCTG ATTCCCAGAC AGTCGCCTGT TCCTGCCGGG ATGGGGCTGA  
1021 GGCTTGGGGA ATGTGGGCAG GAGGATATGC CATTTGATTG TGTGTCACAC GTTCTTTTCC  
1081 CTTCTTCTG TATGTCTGGT CATTCTGCTA TTCTGTCTGT CCTCACATG GTTGACATT  
1141 GGCCGCGTGC CAGCATAAGT GCCAGTGTGA TTTTGCTAGG TGTGAGCTGA GAAAGAGAGG  
1201 TGGAGGCTAA GCAGGTGTGA TGCTTCTCAG AGGTGCTGAG TTTTGGCCCT TCTGAGCAGG  
1261 GAATCTTTGC TTATCCCTTT GACCAAGGAT CTTTGCTGCA AAGGCTGGGT ATCGGCTGTG  
1321 CTCAGCAAAG CGTCAACTCG TGCAAGAACT TAGCAGGAAT AGTTCTGGCT AAGGTTAGGA  
1381 GGCTGCCACC AAAGTCTCTT TTTTGTTCCT CTGCTTCTCC CGTTTGCCCT CTTATCATGA  
1441 GATCTTTTTG CTAAGCTGGC AGAAAGATTG CATAGTCAGT GCTTCCAGCT CTGCTCCAC  
1501 CTGATCCTGC ACTGCTCTCT GGTCCCTGAA TGAATGAAT CTGATACCCA ATCTGTCTC  
1561 GAGCTTCTC TATGCCACTC ATGGCTCCTC TCTGCTCTT TCCATCTTT TGCTGAGAGT  
1621 TCTGAGCTCT GTACTTCTC TTGGCCCATC TCACTTCTG AAACACCCCT GAAGAGGTT  
1681 GCTTATCTTG ATGGAATCA AAAAGCCAAA AAGCTGCAGG CAGAGGCGTT GAGGACATCT  
1741 GTTTGGGGAA CTAAGAGCAG CAGCACTTTC AGATTGATC CATATAGAGC TGTCTACAG  
1801 CATTCTGGAA ACTTGAGGAT GTGCGGTGCA TAAAGGGGCT GGAAGTGACC CACCTGTGAT  
1861 GAGCCCTTTC TAAGGAGAAG GGTTCCTCAAG AGATCACCCC ACCAGAAAAG GGTAGGAATG  
1921 AGCAAGTTGG GAATTTTAGA CTGTCACTGC ACATGGACCT CTGGGAAGAC GTCTGGCGAG  
1981 AGCTAGGCCC ACTGGCCCTA CAGACGGATC TTGCTGGCTC ACCTGTCCCT GTGGAGGTTT  
2041 CCCTGGGAAG GCAAGATGCC CAACAACAGC ACTGCTCTGT CATTGGCCAA TGTACCTAC  
2101 ATCACCATGG AAATTTTCAT TGGACTCTGC GCCATAGTGG GCAACGTGCT GTTCATCTGC  
2161 GTGGTCAAGC TGAACCCAG CCTGCAGACC ACCACCTTCT ATTTTATTGT CTCTCTAGCC  
2221 CTGGCTGACA TTGCTGTTGG GGTGCTGGTC ATGCTTTTGG CCATTGTTGT CAGCCTGGGC  
2281 ATCACAATCC ACTTCTACAG CTGCCTTTTT ATGACTTGCC TACTGCTTAT CTTTACCCAC  
2341 GCCTCCATCA TGTCTTGTCT GGCCATCGCT GTGGACCGAT ACTTGGGGT CAAGCTTACC

2401 GTCAGGTAGC CTGCGGCGTG GGGTGGGCAG CAATTGAGGC AGCTGGGAAA TGAGGCTACA  
2461 AAGCCAGAGC

## (2) INFORMATION FOR SEQ ID NO:2427:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1741 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2427:

1 CGAATTCGGG GGACATCTGT TTGGGGAAGT AAGAGCAGCA GCACTTTCAG ATTCAGTCCA  
61 TATAGAGCTG TCCTACAGCA TTCTGGAAAC TTGAGGATGT GCGGTGCATA AACGGGCTGG  
121 AAGTGACCCA CCTGTGATGA GCCCTTTCTA AGGAGAAGGG TTTCCAAGAG ATCAGCCAC  
181 CAGAAAAGGG TAGGAATGAG CAAGTTGGGA ATTTTAGACT GTCAGTGCAC ATGGACCTCT  
241 GGGAAAGACGT CTGGCGAGAG CTAGGCCAC TGGCCCTACA GACGGATCTT GCTGGCTCAC  
301 CTGTCCCTGT GGAGGTTCCT CTGGGAAGGC AAGATGCCCA ACAACAGCAC TGCTCTGTCA  
361 TTGGCCAATG TTACCTACAT CACCATGGAA ATTTTCATG GACTCTGCGC CATAGTGGGC  
421 AACGTGCTGG TCATCTGCGT GGTCAAGCTG AACCCAGCC TGACAGCCAC CACCTTCTAT  
481 TTCATTGTCT CTCTAGCCCT GGCTGACATT GCTGTTGGGG TGCTGGTCAT GCCTTTGGCC  
541 ATTGTTGTCA GCCTGGGCAT CACAATCCAC TTCTACAGCT GCCTTTTAT GACTTGCTTA  
601 CTGCTTATCT TTACCCAGCG CTCATCATG TCCTTGCTGG CCATCGCTGT GGACCGATAC  
661 TTGCGGGTCA AGCTTACCGT CAGATACAAG AGGGTCACCA CTCACAGAAG AATATGGCTG  
721 GCCCTGGGCC TTTGCTGGCT GGTGTCATTC CTGGTGGGAT TGACCCCAT GTTTGGCTGG  
781 AACATGAAAC TGACCTCAGA GTACCACAGA AATGTCACCT TCCTTTCATG CCAATTGTGT  
841 TCCGTCATGA GGATGGACTA CATGGTATAC TTCAGCTTCC TCACCTGGAT TTTCATCCCC  
901 CTGGTTGTCA TGTGCGCCAT CTATCTTGAC ATCTTTTACA TCATTCGGAA CAAACTCAGT  
961 CTGAACCTAT CTAACCTCAA AGAGACAGGT GCATTTTATG GACGGGAGTT CAAGACGGCT  
1021 AAGTCCTTGT TTCTGGTTCT TTTCTTGTTT GCTCTGTCAT GGCTGCCTTT ATCTCTCATC  
1081 AACTGCATCA TCTACTTTAA TGGTGAGGTA CCACAGCTTG TGCTGTACAT GGGCATCCTG  
1141 CTGTCCCATG CCAACTCCAT GATGAACCCT ATCGTCTATG CCTATAAAAT AAAGAAGTTC  
1201 AAGGAAACCT ACCTTTTGAT CCTCAAAGCC TGTGTGCTCT GCCATCCCTC TGATTCTTTG  
1261 GACACAAGCA TTGAGAAGAA TTCTGAGTAG TTATCCATCA GAGATGACTC TGTCTCATTG  
1321 ACCTTCAGAT TCCCCATCA CAAACACTTG AGGGCCTGTA TGCTGGGCC AAGGGATTTT  
1381 TACATCCTTG ATTACTTCCA CTGAGGTGGG AGCATCTCCA GTGCTCCCCA ATTATATCTC  
1441 CCCCACTCCA CTAATCTCTT CCTCCACTTC ATTTTCTCTT TGCTCTTCT CTCTAATTCA  
1501 GTGTTTTGGA GGCCTGACTT GGGGACAACG TATTATTGAT ATTATTGTCT GTTTTCTTTC  
1561 TTCCCAATAG AAGAATAAGT CATGGAGCCT GAAGGGTGCC TAGTTGACTT ACTGACAAAA  
1621 GGCTCTAGTT GGGCTGAACA TGTGTGTTGG GGTGACTCAT TTCCATGCCA TTGTGGAATT  
1681 GAGCAGAGAA CCTGCTCTCG GAGGATGCCT AGGAGATGTT GGAACAGAA GAAATAAACT  
1741 GAGTTTAAGG GGGACTTAAA CTGCTGAATT C

## (2) INFORMATION FOR SEQ ID NO:2428:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2041 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2428:

1 GCCGCCGCCG CCAAGATGGC GGACCTGGAG GCGGTGCTGG CCGACGTGAG CTACCTGATG  
61 GCCATGGAGA AGAGCAAGGC CACGCCGGCC GCGCGCGCCA GCAAGAAGAT ACTGCTGCCC  
121 GAGCCCAGCA TCCGCACTGT CATGCAGAAG TACCTGGAGG ACCGGGGCGA GGTGACCTTT  
181 GAGAAGATCT TTTCCAGAA GCTGGGGTAC CTGCTCTTCC GAGACTTCTG CCTGAACCAC  
241 CTGGAGGAGG CCAGGCCCTT GGTGGAATTC TATGAGGAGA TCAAGAAGTA CGAGAAGCTG  
301 GAGACGGAGG AGGAGCGTGT GGCCCGCAGC CGGGAGATCT TCGACTCATA CATCATGAAG  
361 GAGCTGCTGG CCTGCTCGCA TCCCTTCTCG AAGAGTGCCA CTGAGCATGT CCAAGGCCAC  
421 CTGGGGAAGA AGCAGGTGCC TCCGGATCTC TTCCAGCCAT ACATCGAAGA GATTGTCAA  
481 AACCTCCGAG GGGACGTGTT CCAGAAATTC ATTGAGAGCG ATAAGTTCAC ACGGTTTTGC  
541 CATGTGGAAGA ATGTGGAGCT CAACATCCAC CTGACCATGA ATGACTTCA CGTGATCGC  
601 ATCATTGGGC GCGGGGCTT TGGCGAGGTC TATGGGTGCC GGAAGGTCGA CACAGGCAAG  
661 ATGTACGCCA TGAAGTGCTT GGACAAAAG CGCATCAAGA TGAAGCAGGG GGAGACCCTG  
721 GCCCTGAACG AGCGCATCAT GCTCTCGCTC GTCAGCACTG GGGACTGCCC ATTCATTGTC  
781 TGCATGTCAT ACGCGTTCCA CACGCCAGAC AAGCTCAGCT TCATCCTGGA CCTCATGAAC  
841 GGTGGGGACC TGCATACCA CCTCTCCCAG CACGGGTCT TCTCAGAGGC TGACATGCGC  
901 TTCTATGCGG CCGAGATCAT CCTGGGCTCT GAGCACATGC ACAACCGCTT CGTGGTCTAC  
961 CCGGACCTGA AGCCAGCCAA CATCCTTCTG GACGAGCATG GCCACGTGCG GATCTCGGAC  
1021 CTGGGCTGCG CCTGTGACTT CTCCAAGAAG AAGCCCCATG CCAGCGTGGG CACCCAGGGG  
1081 TACATGGCTC CGGAGGTCCT GCAGAAGGGC GTGGCCTACG ACAGCAGTGC CGACTGGTTC  
1141 TCTCTGGGT GCATGCTCTT CAAGTTGCTG CCGGGGCACA GCGCTTCCG GCAGCACAAG  
1201 ACCAAAGACA AGCATGAGAT CGACCGCATG ACGCTGACGA TGGCCGTGGA GCTGCCCGAC

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1261 TCCTTCTCCC CTGAACTACG CTCCCTGCTG GAGGGGTTGC TGCAGAGGGA TGTCAACCGG  
 1321 AGATTGGGCT GCCTGGGCCG AGGGGCTCAG GAGGTGAAAG AGAGCCCCTT TTTCCGCTCC  
 1381 CTGGACTGGC AGATGGTCTT CTTGCAGAAG TACCCTCCCC CGCTGATCCC CCCACGAGGG  
 1441 GAGGTGAACG CGGCCGACGC CTTGACATT GGCTCCTTCG ATGAGGAGGA CACAAAAGGA  
 1501 ATCAAGTTAC TGGACAGTGA TCAGGAGCTC TACCGCAACT TCCCCCTCAC CATCTCGGAG  
 1561 CCGTGGCAGC AGGAGGTGGC AGAGACTGTC TTCGACACCA TCAACGCTGA GACAGACCGG  
 1621 CTGGAGGCTC GCAAGAAAGC CAAGAACAAG CAGCTGGGCC ATGAGGAAGA CTACGCCCTG  
 1681 GGCAAGGACT GCATCATGCA TGGCTACATG TCCAAGATGG GCAACCCCTT CCTGACCCAG  
 1741 TGGCAGCGGC GGTACTTCTA CCTGTTCCCC AACCGCCTCG AGTGGCGGGG CGAGGGCGAG  
 1801 GCCCCGCGAGA GCCTGCTGAC CATGGAGGAG ATCCAGTCGG TGGAGGAGAC GCAGATCAAG  
 1861 GAGCGCAAGT GCCTGCTCCT CAAGATCCGC GGTGGGAAAC AGTTCATTTT GCAGTGCAT  
 1921 AGCGACCCCTG AGCTGGTGCA GTGGAAGAAG GAGCTGCGCG ACGCCTACCG CGAGGCCAG  
 1981 CAGCTGCTGC AGCGGGTGCC CAAGATGAAG AACAAGCCGC GCTCGCCCGT GGTGGAGCTG  
 2041 AGCAAGGTGC CGCTGGTCCA GCGCGGCAGT GCCAACGGCC TCTGACCCGC CCACCCGCCT

## (2) INFORMATION FOR SEQ ID NO:2429:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2341 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2429:

1 CCAGGAAGCT ACCTGGAGGA GGTGAGTCTT AGCGGATGAG TAGGAGTTGT CCACGGAGGA  
 61 AGGTACACAG AAGGGCTTCC AGGCCAGGA AACAGCAGAG GCACAGAAGT GAGAATGGGT  
 121 GGGTGAGTTG GTGGGGAAAC TCCAGGTGCA GAGGATGGTA GCGAAACAAA CTGGAGCATT  
 181 AAGGTCCAAG TCCTCCAAGA TCTTGACTTG CAGATTAAGG AGTTTGTTCA CCTAATCTGC  
 241 TTTGGGCAGA GTGTGGTGAG TCCTAGAGAC CCCTCTAGGT CTCTCCTCTC AGTAGCCCCA  
 301 GAAGGCCTGG AGAGCTGCTT CTGGGTGCCA AGCAGGCAGT GACTCCATCA GATCTAGATT  
 361 TGGGAAAAGC ATCCCTGGTC AGGGCCTGCA TCAGGGCAGT GGCTGGCCAT GAGGACCCCTG  
 421 AGAAGTAGAC AGATTACCGG AGATTCTCAG GAGGCCAGAC AGGAGACTAT GGTGACAAAT  
 481 TAGATTAGAG AAGGGGAGAG AATGAAGGAG CAGTTGGGGT AAAAGAAAAC TGAGGCTGAC  
 541 ATGGGTATAT GGGTGGCGAG TGAATCAGCA CCCACTGAGA GGAGAACCTC ACAAGCTCTG  
 601 ACATGCTCTG GTTCCAGGTT CTGTTGGGGC TGATCCAAGA TGGTAGCCTA GAGGTGCACA  
 661 GAGATGGGGG CCTTGCTTTG CAAAAGGATG CTGGCTGCTG GCGGCAGCA TGGTAATGAG  
 721 ATTTGAGCTT TATGTGCCCA GGGCTGGGAG GAGGGTCTCT TCACTTTGAA AGCAAAGAGA  
 781 GGCTCTAGAG AGGGGCATGT TGAGATAGGA ATGCTGCCTT GAGACACCTG GCTTCCCCA  
 841 CTCTGGGTGG CTCTCAGCAG GGTGGGTTTC CCCTGCCAGG CAGCACTGAA CCTCTGTGCG  
 901 CTTCCGGCTG GGAGAGTTTT TACCGTAACT ACATGTGGAA CCATCCTGAA GGAACATCTG  
 961 GATGGGATGG GGTACAGGGA AGGGAGCTGC CAAGAGTGCT GGCCAGGGAC CTGGGTCTAT  
 1021 GAGCTGGTTG GGGGGTGGGG TTGGGTGCAG GGTACTTGAT CCTGAGTGGG CTTTCTGCGG  
 1081 CCAGGATTGG TTCTAGAGTA GGAGGGGTGG GATCGGGGAT GGGGGAAGCC TGTAACTGCG  
 1141 CTGCAAGTTG CAGGTCCCAG GTTCTGGGTG ACCTACTAAG GATTCTGGGT CCAGTGTGGG  
 1201 TCCAGGTTA GACGTCCTAG TCCTGAGTCC GTGTCCACAG TTCTGGGTGT TGAGTCTAGG  
 1261 ACAGTGATCT GGAGTTGACA GTCCAATCTA GGTCTGAGTC CTGACCCCAA GTCTAGAGTT  
 1321 CAGGSTCATG GTAGTAGCCT AGGGTCAGAA TCAAGGTTGG GGTCAAGTAA CAGGATGGGA  
 1381 TCGAGGTCAT GGTCCAAAAT CTGGATCTGG GGACCTGTG GGGGTCTGAG GTGAGTGTG  
 1441 CAGTCTGGGT ATGGCGTTGG AGACCCAGGG CTGTGATCTG AGGTCATGGT TAGAGTCTCA  
 1501 GGTGGTGGGC CAAGGTTTGA GTCTGGGGTC CTGTTTGGAG TCTGGTGTCA GGTCTGTGGC  
 1561 TGCGTCCAAG GTCAGGGAGT CCGGGGTTAT AGCCAGGGTC TGAGATGAA GTCCCAGATG  
 1621 GTGTTTCAGAG GTCTGAATCT GTGTCTTGGT GAGCGTCCAG GTTCCCTGTG ATCAGGTTTG  
 1681 GTGTCAGGGC TGCGGCCCGA CTGGGGAGCC TGGGATCCAG AGATGTGACC CGAGGTTGTG  
 1741 GTCAGAGAAT GGGTCTCGGG TCGTCTTCGT GCGGGTCCC TGTCGTGTT CAGGCCCGGG  
 1801 TCTCCGTCCA GCATCGAGGG CCGAGGTCAC GGCCAGGGTC TGAGCCCGCG GTCCGAGGTC  
 1861 TGTTTCGGGG TCAGATTCCG CGCGGCTCC AGGGGGCGCC GTCGCGCGCC GGCTCGGCC  
 1921 CTCGCGGGCT CGCTGGCGTT GTGCGCGGCA GGCGGGGCGG GAGGCGGGCG CGGCTCCGGG  
 1981 GCGCGGGGCC GGGCGGGCGG GCGGGCGGCG CCGGAGTGC AGTCCCGGCG GGAGCGGAGC  
 2041 GCGAAGCGCG GGGCGGGCGG CCGAGCGGCG GCGATGGGG GCGCGCGCT GTGAGCGGCG  
 2101 GCGAGCGGAG CCGCGGGCGG CCGAGCGGCG CAGGCGGGAG CTGCGGCGG CGAGGCGGAG  
 2161 CGAGCGCGCG CCGGGCGGGG CCGAGCGGCG AGCGAGCAGG AGCGGCGGCG GCGGCGGCGG  
 2221 CGGCGGGAGG AGGCGAGCGG GCGGCAAGA TGGCGGACCT GGAGGCGGTG CTGGCGGAGC  
 2281 TGAGCTACCT GATGGCCATG GAGAAGAGCA AGGCCACGCC GCGCGCGCGC GCCAGCAAGA  
 2341 AGATACTGCT GCCGAGCCCC AGGTGAGGAG AAGCT

## (2) INFORMATION FOR SEQ ID NO:2430:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4382 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2430:

GCCGCCGCCG	CCAAGATGGC	GGACCTGGAG	GCGGTGCTGG	CCGACGTGAG	CTACCTGATG	GCCATGGAGA
AGAGCAAGGC	CACGCCGGCC	GCGCGCGCCA	GCAAGAAGAT	ACTGCTGCCC	GAGCCCAGCA	TCCGCAGTGT
CATGCAGAAG	TACCTGGAGG	ACCGGGGCGA	GGTGACCTTT	GAGAAGATCT	TTTCCCAGAA	GCTGGGGTAC
CTGCTCTTCC	GAGACTTCTG	CCTGAACCAC	CTGGAGGAGG	CCAGGCCCTT	GGTGAATTTC	TATGAGGAGA
TCAAGAAGTA	CGAGAAGCTG	GAGACGGAGG	AGGAGCGTGT	GGCCCGCAGC	CGGGAGATCT	TCCACTCATA
CATCATGAAG	GAGCTGCTGG	CCTGCTCGCA	TCCCTTCTCG	AAGAGTGCCA	CTGAGCATGT	CCAAGGCCAC
CTGGGGAAGA	AGCAGGTGCC	TCCGGATCTC	TTCCAGCCAT	ACATCGAAGA	GATTTGTCAA	AACCTCCGAG
GGGACGTGTT	CCAGAAATTC	ATTGAGAGCG	ATAAGTTCAC	ACGTTTTTGC	CAGTGAAGA	ATGTGGAGCT
CAACATCCAC	CTGACCATGA	ATGACTTCAG	CGTGCATCGC	ATCATTGGGC	GCGGGGGCTT	TGGCGAGGTC
TATGGGTGCC	GGAAGGCTGA	CACAGGCAAG	ATGTACGCCA	TGAAGTGCC	GGACAAAAG	CGCATCAAGA
TGAAGCAGGG	GGAGACCCTG	GCCCTGAACG	AGCTCGCTC	GCTCTCGCTC	GTCAGCACTG	GGGACTGCCC
ATTGATTGTC	TGCATGTCAT	ACGCGTTCCA	CACGCCAGAC	AAGCTCAGCT	TCATCTGGA	CCTCATGAAC
GGTGGGGACC	TGCACTACCA	CCTCTCCAG	CACGGGGTCT	TCTCAGAGGC	TGACATGCGC	TTCTATGCGG
CCGAGATCAT	CCTGGGCCTG	GAGCACATGC	ACAACCGCTT	CGTGGTCTAC	CGGGACCTGA	AGCCAGCCAA
CATCCTTCTG	GACGAGCATG	GCCACGTGCG	GATCTCGGAC	CTGGGCCTGG	CCTGTGACTT	CTCCAAGAAG
AAGCCCCATG	CCAGCGTGGG	CACCCACGGG	TACATGGCTC	CGGAGGTCTT	GCAGAGGGGC	GTGGCCTACG
ACAGCAGTGC	CGACTGGTTC	TCTCTGGGT	GCATGCTCTT	CAAGTTGCTG	CGGGGGCACA	GCCCCTTCCG
GCAGCACAAG	ACCAAAGACA	AGCATGAGAT	CGACCGCATG	ACGCTGACGA	TGGCCGTGGA	GCTGCCCGAC
TCCTTCTCCC	CTGAACACG	CTCCCTGCTG	GAGGGGTTGC	TGCAGAGGGA	TGTCAACCGG	AGATTGGGCT
GCCTGGGCGG	AGGGGCTCAG	GAGGTGAAAG	AGAGCCCTTT	TTTCCGCTCC	CTGGACTGGC	AGATGGTCTT
CTTGACAGAAG	TACCCTCCCC	CGCTGATCCC	CCCACGAGGG	GAGGTGAACG	CGGCCGACGC	CTTCGACATT
GGCTCCTTCG	ATGAGGAGGA	CACAAAAGGA	ATCAAGTTAC	TGGACAGTGA	TCAGGAGCTC	TACCGCAACT
TCCCCCTCAC	CATCTCGGAG	CGGTGGCAGC	AGGAGGTGGC	AGAGACTGTC	TTCCGACACCA	TCACGCTGA
GACAGACCGG	CTGGAGGCTC	GCAAGAAAGC	CAAGAACAAG	CAGCTGGGCC	ATGAGGAAGA	CTACGCCCTG
GGCAAGGACT	GCATCATGCA	TGGCTACATG	TCCAAGATGG	GCAACCCCTT	CCTGACCCAG	TGGCAGCGGG
GGTACTTCTA	CCTGTTCCCC	AACCGCCTCG	AGTGGCGGGG	CGAGGGCGAG	GCCCCGACGA	GCCTGCTGAC
CATGGAGGAG	ATCCAGTCGG	TGGAGGAGAC	GCAGATCAAG	GAGCGCAAGT	GCCTGCTCCT	CAAGATCCGC
GGTGGGAAC	AGTTCAATTT	GCAGTGCGAT	AGCGACCTTG	AGCTGGTGCA	GTGGAAGAAG	GAGCTGCGCG
ACGCCTACCG	CGAGGCCACG	CAGCTGGTGC	AGCGGGTGCC	CAAGATGAAG	AACAAGCCGC	GCTCGCCCGT
GGTGGAGCTG	AGCAAGGTGC	CGCTGGTCCA	GCGCGGCAGT	GCCAACGGCC	TCTGACCCGC	CCACCCGCCT
CCAGGAAGCT	ACCTGGAGGA	GGTGAGTCTT	AGCGGATGAG	TAGGAGTTGT	CCACGGAGGA	AGGTACACAG
AAGGGCTTCC	AGGCCACAGG	AACAGCAGAG	GCACAGAAGT	GAGAATGGTG	GGGTGAGTTG	GTGGGGAAAC
TCCAGGTGCA	GAGGATGGTA	GCGAAACAAA	CTGGAGCATT	AAGGTCCAAG	TCCTCCAAGA	TCTTGACTTG
CAGATTAAGG	AGTTTGTTC	CCTAATCTGC	TTTGGGCAGA	GTGTGGTGAG	TCCTAGAGAC	CCCTCTAGGT
CTCTCCTCTC	AGTAGCCCCA	GAAGGCCTGG	AGAGCTGCTT	CTGGGTGCCA	AGCAGGCAGT	GACTCCATCA
GATCTAGATT	TGGGAAAAGC	ATCCCTGGTC	AGGGCCTGCA	TCAGGGCAGT	GGCTGGCCAT	GAGGACCCTG
AGAAGTAGAC	AGATTACGGC	AGATTCTCAG	GAGGCCAGAC	AGGAGACTAT	GGTGACAAAT	TAGATTAGAG
AAGGGGAGAG	AATGAAGGAG	CAGTTGGGGT	AAAAGAAAAC	TGAGGCTGAC	ATGGGTATAT	GGGTGGCGAG
TGACTACCA	CCCACTGAGA	GGAGAACCTC	ACAAGCTCTG	ACATGCTCTG	GTTCCAGGTT	CTGTTGGGGC
TGATCCAAGA	TGGTAGCCTA	GAGGTGCACA	GAGATGGGGG	CCTTGCTTTG	CAAAAGGATG	CTGGCTGCTG
GCCCACAGCA	TGGTAATGAG	ATTTGAGCTT	TATGTGCCCA	GGGCTGGGAG	GAGGGTCTCG	TCACTTTGAA
AGCAAAGAGA	GGCTCTAGAG	AGGGGCATGT	TGAGATAGGA	ATGCTGCCTT	GAGACACCTG	GCTTTCCCCA
CTCTGGGTGG	CTCTCAGCAG	GGTGGGTTTC	CCCTGCCAGG	CAGCACTGAA	CCTCTGTGCG	CTTCCGGCTG
GGAGAGTTTT	TACCGTAACT	ACATGTGGAA	CCATCCTGAA	GGAACATCTG	GATGGGATGG	GGTACAGGGA
AGGGAGCTGC	CAAGAGTGCT	CTGGGTCTAT	CTGGGTCTAT	GAGCTGGTTG	GGGGGTGGGG	TTGGGTGCAG
GGTACTTGAT	CCTGAGTGGG	CCTTCTGCGG	CCAGGATTGG	TTCTAGAGTA	GGAGGGGTGG	GATCGGGGAT
GGGGGAAGCC	TGTAAGTGCG	CTGCAGTTGT	CAGGTCCCAG	GTTCTGGGTG	ACCTACTAAG	GATTCTGGGT
CCAGTGTGGG	TCCCAGGTTA	GACGTCTCTAG	TCCTGAGTCC	GTGTCCACAG	TTCTGGGTGT	TGAGTCTAGG
ACAGTGATCT	GGAGTTGACA	GTCCAATCTA	GGTCTGAGTC	CTGACCCCAA	GTCTAGAGTT	CAGGGTCATG
GTAGTAGCCT	AGGGTCAGAA	TCAAGGTTGG	GGTCAGTAAC	CAGGATGGGA	TCGAGGTCAT	GGTCCAAAAT
CTGGATCTGG	GGACCTGTTG	GGGTCTGAG	GTGAGTGTCG	CAGTCTGGGT	ATGGCGTTGG	AGACCCAGGG
CTGTGATCTG	AGGTGATGGT	TAGAGTCTCA	GGTGGTGGGC	CAAGGTTTGA	GTCTGGGGTC	CTGTTTGGAG
TCTGGTGTC	GCTCGTGGAC	TGCGTCCAAG	GTCAGGGAGT	CCGGGGTTAT	AGCCAGGGTC	TGAGATGAAA
GTCCAGATG	GTGTTACAG	GTCTGAATCT	GTGTCTTGGT	GAGCGTCCAG	GTTCCCTGTG	ATCAGGTTTG
GTGTCAAGGC	TGCGGCCCGA	CTGGGGAGCC	TGGGATCCAG	AGATGTGACC	CGAGGTTGTG	CTCAGAGAA
GGGTCTCGGG	TCGTCTTCGT	GCCGGGTCCC	TGTCGTGTTT	CAGGCCCGGG	TCTCCGTCCA	GCATCGAGGG
CCGAGGTCAC	GCCAGGCTC	TGAGCCCGCG	GTGCGCAGTC	TGGTTCGGGG	TCAGATTCCG	CGCGGCCTCC
AGGGGGCGCC	GTCGCGGCC	GGCTCGGCC	CTGCGGGGCT	CGCTGGCGTT	GTGCGCGGCA	GGCGGGGCGG
GAGGCGGCGG	CGGCTCCGGG	GGCGCGGGCC	GCGCGCGGCG	GGCGCGGGCG	CCCCGACTGC	AGTCCCGGCG
GGAGCGGAGC	GCGAAGCGCG	GGGCGGGGCC	CGGAGCGGGC	GCCATGGGGC	GGGCGCGGCT	GTGAGCGGCG
GCGAGCGGAG	CCGCGGGCGC	CGAGCAGGGC	CAGGCGGGAG	CGTCCGGCGC	CGAGGCGGAG	CGAGCCGCGG
CCGGGCGGGG	CCGAGCGCGG	AGCGAGCAGG	AGCGGCGGCG	GCGGCGGGCG	CGGCGGGAGG	AGGCAAGGCC
GCCGCCAAGA	TGGCGGACCT	GGAGGCGGTG	CTGGCCGACG	TGAGCTACCT	GATGGCCATG	GAGAAGAGCA
AGGCCACGCC	GGCGCGCGCG	GCCAGCAAGA	AGATACTGCT	GCCCCAGCCC	AGGTGAGGAG	AAGCT

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(2) INFORMATION FOR SEQ ID NO:2431:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2581 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2431:

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1 CAGATTACACA AACTGCAGGA CTGGGCAGGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT
61 GCTGTGAATT TGTGAAGGA TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC
121 AAGGAGACAT CTATGCACGA CCTTGGGAAA TGAGTTGATG TCTCCGGTAA AACACCGGAG
181 ACTAATTCCT GCCCTGCCCA ATTTTGCAGG GAGCATGGCT GTGAGGATGG GGTGAATCA
241 CGCACAGCCA AGGACTCCAA AATCACAACA GCATTACTGT TCTTATTTGC TGCCACACCT
301 GAGCCAGCCT GCTCCTTCCC AGGAGTGGAG GAGGCCTGGG GGGAGGGAGA GGAGTGACTG
361 AGCTTCCCTC CCGTGTGTTT TCCGTCCCTG CCCAGCAAG ACAACTTAGA TCTCCAGGAG
421 AACTGCCATC CAGCTTTGGT GCAATGGCTG AGTGCACAAG TGAGTTGTTG CCCTGGGTTT
481 CTTTAATCTA TTCAGCTAGA ACTTTGAAGG ACAATTTCTT GCATTAATAA AGGTTAAGCC
541 CTGAGGGGTC CCTGATAACA ACCTGGAGAC CAGGATTTTA TGGCTCCCCT CACTGATGGA
601 CAAGGAGGTC TGTGCCAAAG AAGAATCCAA TAAGCACATA TTGAGCACTT GCTGTATATG
661 CAGTATTGAG CACTGTAGGC AAGACCCAAG AAAGAGAAGG AGCCATCTCC ATCTTGAAGG
721 AACTCAAAGA CTCAAGTGGG AACGACTGGG CACTGCCACC ACCAGAAAGC TGTCGACGA
781 GACGGTGCAG CAGGGTGCTG TGGGTGATAT GGACAGCAGA AGGGGGAGAC CAAGGTTCCA
841 GCTCAACCAA TAACTATTGC ACAACCACCT GTCCTGCCT CAGTTCCTT TTATGTAACA
901 TGAAGTCGTT GTGAGGGTTA AAGGCAGTAA CAGGTATAAA GTACTTAGAA AAGCAAAGGG
961 TGCTACGTAC ATGTGAGGCA TCATTACGCA GACGTAACG GGATATGTTT ACTATAAGGA
1021 AAAGACACTG AGGTCTAGAA ATAGCTCCGT GGAGCAGAA CAGTATTGGG AGCCGGTGGC
1081 GGTGTGAAGC ACCAGTGTCT GGCACACAGT AGGTGCTCAT TGGCTCCCCT CCACCTGTCA
1141 TTCCCACCAC CCTGAGGCCC CAACCGCCAC ACACACAGGA GCATTTGGAG AGAAGGCCAT
1201 GTCTTCAAAG TCTGATTGTG GATGAGGCAG AGGAAGATAT TTCTAATCGG TCTTGCCCAG
1261 AGGATCACAG TGCTGAGACC CCCCACACC AGCCGGTACC TGGGAAGGGG GAGAGTGCAG
1321 GCCTGCTCAG GGACTGTTCC TGTCTCAGCA ACCAAGGGAT TGTTCTGTG AATCAATGGT
1381 TTATTGGAAG GTGGCCAGT ATGAGCCCTA GAAGAGTGTG AAAAGGAATG GCAATGGTGT
1441 TCACCATCGG CAGTGCCAGG GCAGCACTCA TTCATTGAT AAATGAATAT TTATTAGCTG
1501 GTTGAGAGC TAGAACCTGG AGAGCTAGAA CCTGGAGAAC TAGAACCTGG AGGGCTAGAA
1561 CCTGGAGAGG CTAGAACCAA GAAGGGCTAG AACCTGGAGG GGCTAGAACC TAGAGAAGCT
1621 AAAACCTGAG CTAGAAGCTG GAGGACTAGA ACCTGGAGGG CTGGAATCTG AAGGGCTAGA
1681 ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG GAGGGCTAGA
1741 ACCTAGAAGG GCTAGAACCT GGAGGGCTGG AATCTGGAGA GCTAGAACCT GGAGGGCTAG
1801 AACCTGGAGG GCTAGAACCT AGAAGGGCTA GAACCTGGAG GGCTAGAACC TGGCAGGTTA
1861 GAACCTAGAA GGGCTAGAAC CTGGAGAGCC AGAACCTGGA GGGCTAGAAC CTGGAAGGGC
1921 TAGAACCTGT AGAGCTAGAA CATGGAGAGC TAGAACCCGG CAGGCTAGAA CCTGGCAAGC
1981 TAGAACCTGG AGGGAATGAA CCTGGAGGGC TAGAACCTGG AGAATGAGAA AAATTTACAT
2041 GGCAAGAGC CCATAAATCC TGACCAATCC AACTCTGAAT TTTAAAGCAA AAGCGTGAAA
2101 AAAAAGATT CTTCTTACC CCAAACCCAC TCTTTTTC CACCACCCAC TCTCCTCTGC
2161 CTCAGTAAGT ATCTGGAGGA AGAAAACAGG TGAAAAGAAG AGTAAAAACC ATTTAGTATT
2221 AGTATTAGAA TGAAGTCAA CTGTGCCACA CATGGTGAAT GAAAAAAGG AAAAAAGAGG
2281 TGTGTTTTGT CACACAGGGC AGTCATTGAG CACCAGAGCA CGTGATGGTC TGAGACTCTC
2341 TTAGGAGCAG AGCTCTGCCG CAATGGCCAT GTGGGGATCC ACACCTGGTC TGAGGGGCAA
2401 CTGAGTCTGC GGGAGAAGAG CGGCCCTATG CATGGTGTAG ATGCCCTGAT AAAGAACATC
2461 TGTCTGTGTA AAGACTCAAT GAGCTGTTAT GTTGTAACA GGAAGCATTT CACATCCAAA
2521 CGAGAAATC ATGTAACAT GTGTCTTTT TGTAGAGCAT AATAATGGA TGAGGTTTTT
2581 GCAAAAAAAA AAAAAAAA

```

## (2) INFORMATION FOR SEQ ID NO:2432:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 961 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2432:

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1 ATGCCGCCCT CCATCTCAGC TTTCCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC
61 CTGGTCTCTG TGCCCGGGAA CGTGCTGGTG ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG
121 CGGGATGCCA CCTTCTGCTT CATCGTCTCG CTGGCGGTGG CTGATGTGGC CGTGGGTGCC
181 CTGGTCATCC CCCTCGCCAT CCTCATCAAC ATTGGGCCAC AGACCTACTT CCACACCTGC
241 CTCATGGTTG CCTGTCCGGT CCTCATCTC ACCCAGAGCT CCATCCTGGC CCTGCTGGCA
301 ATTGCTGTGG ACCGCTACCT CCGGGTCAAG ATCCCTCTCC GGTACAAGAT GGTGGTGACC
361 CCCCAGAGGG CGGCGGTGGC CATAGCCGGC TGCTGGATCC TCTCCTTCGT GGTGGGACTG
421 ACCCCTATGT TTGGCTGGAA CAATCTGAGT GCGGTGGAGC GGGCCTGGGC AGCCAACGGC
481 AGCATGGGGG AGCCCGTAT CAAGTGCAG TTCGAGAAGG TCATCAGCAT GGAGTACATG
541 GTCTACTTCA ACTTCTTTGT GTGGGTGCTG CCCCCTTC TCCTCATGGT CCTCATCTAC

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581

601 CTGGAGGTCT TCTACCTAAT CCGCAAGCAG CTCAACAAGA AGGTGTCGGC CTCCTCCGGC  
661 GACCCGCGAGA AGTACTATGG GAAGGAGCTG AAGATCGCCA AGTCGCTGGC CCTCATCCTC  
721 TTCCTCTTTG CCCTCAGCTG GCTGCCTTTG CACATCCTCA ACTGCATCAC CCTCTTCTGC  
781 CCGTCCTGCC ACAAGCCCAG CATCCTTACC TACATTGCCA TCTTCCTCAC GCACGGCAAC  
841 TCGGCCATGA ACCCATTTGT CTATGCCTTC CGCATCCAGA AGTTCGCGT CACCTTCCTT  
901 AAGATTGGA ATGACCATT CCGCTGCCAG CCTGCACCTC CCATTGACGA GGATCTCCCA  
961 GAAGAGAGGC CTGATGACTA G

## (2) INFORMATION FOR SEQ ID NO:2433:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2881 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2433:

1 ATGAGTGTCA GAAGTGTGAA GGGTGCCTGT TCTGAATCCC AGAGCCTCCT CTCCTCTGT  
61 GAGGCTGGCA GGTGAGGAAG GGTTTAACCT CACTGGAAGG AATCCCTGGA GCTAGCGGCT  
121 GCTGAAGGCG TCGAGGTGTG GGGGCACTTG GACAGAACAG TCAGGCAGCC GGGAGCTCTG  
181 CCAGCTTTGG TGACCTTGGG CCGGGCTGGG AGCGCTGCGG CGGAGCCGG AGGACTATGA  
241 GCTGCCGCGC GTTGTCCAGA GCCAGCCCA GCCCTACGGC CGCGGCCCG AGCTCTGTTC  
301 CCTGGAACTT TGGGCACTGC CTCTGGGACC CCTGCCGGCC AGCAGGCAGG ATGGTGCTTG  
361 CCTCGTGCCC CTTGGTGCCC GTCTGCTGAT GTGCCAGCC TGTGCCCGCC ATGCCGCCCT  
421 CCATCTCAGC TTTCCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC CTGGTCTCTG  
481 TGCCCGGGAA CGTGTGGTG ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG CGGGATGCCA  
541 CCTTCTGTCT CATCGTGTG CTGGCGGTGG CTGATGTGGC CGTGGGTGCC CTGGTCATCC  
601 CCCTCGCCAT CCTCATCAAC ATTGGGCCAC AGACCTACTT CCACACCTGC CTCATGGTTG  
661 CCTGTCCGGT CCTCATCCTC ACCCAGAGCT CCATCCTGGC CCTGCTGGCA ATTGCTGTGG  
721 ACCGCTACCT CCGGGTCAAG ATCCCTCTCC GGTACAAGAT GGTGGTGACC CCCCAGAGGG  
781 CGGCGGTGGC CATAGCCGGC TGCTGGATCC TCTCCTCGT GGTGGGACTG ACCCCTATGT  
841 TTGGCTGGAA CAATCTGAGT GCGGTGGAGC GGGCCTGGG AGCCAACGGC AGCATGGGGG  
901 AGCCCGTGAT CAAGTGCAG TTCGAGAAGG TCATCAGCAT GGAGTACATG GTCTACTTCA  
961 ACTTCTTTGT GTGGGTGCTG CCCCCTCTC TCCTCATGGT CCTCATCTAC CTGGAGGTCT  
1021 TCTACCTAAT CCGCAAGCAG CTCAACAAGA AGGTGTCGGC CTCCTCCGGC GACCCGCGAGA  
1081 AGTACTATGG GAAGGAGCTG AAGATCGCCA AGTCGCTGGC CCTCATCCTC TTCTCTTTG  
1141 CCCTCAGCTG GCTGCCTTTG CACATCCTCA ACTGCATCAC CCTCTTCTGC CCGTCTGCC  
1201 ACAAGCCCAG CATCCTTACC TACATTGCCA TCTTCCTCAC GCACGGCAAC TCGGCCATGA  
1261 ACCCATTTGT CTATGCCTTC CGCATCCAGA AGTTCGCGT CACCTTCCTT AAGATTGGA  
1321 ATGACCATT CCGCTGCCAG CCTGCACCTC CCATTGACGA GGATCTCCCA GAAGAGAGGC  
1381 CTGATGACTA GACCCCGCT TCCGCTCCCA CCAGCCACA TCCAGTGGG TCTCAGTCCA  
1441 GTCCTCACAT GCGCGCTGTC CCAGGGGTCT CCCTGAGCCT GCGCCAGCTG GGCTGTTGGC  
1501 TGGGGGCATG GGGGAGGCTC TGAAGAGATA CCCACAGAGT GTGGTCCCTC CACTAGGAGT  
1561 TAACTACCCT ACACCTCTGG GCCCTGCAGG AGGCCTGGGA GGGCAAGGCT CCTACGGAGG  
1621 GACCAGGTGT CTAGAGGCAA CAGTGTCTG AGCCCCACC TGCCTGACCA TCCATGAGC  
1681 AGTCCAGCGC TTCAGGGCTG GGCAGGTCCT GGGGAGGCTG AGACTGCAGA GGAGCCACCT  
1741 GGGCTGGGAG AAGGTGCTTG GGCTTCTGCG GTGAGGCAGG GGAGTCTGCT TGTCTTAGAT  
1801 GTTGGTGGTG CAGCCCCAGG ACCAAGCTTA AGGAGAGGAG AGCATCTGCT CTGAGACGGA  
1861 TGAAGGAGA GAGGTTGAGG ATGCACTGGC CTGTTCTGTA GGAGAGACTG GCCAGAGGCA  
1921 GCTAAGGGGC AGGAATCAAG GAGCCTCCGT TCCACCTCT GAGGACTCTG GACCCAGGC  
1981 CATACCAGGT GCTAGGGTGC CTGCTCTCCT TGCCCTGGG CAGCCCAGGA TTGTACGTGG  
2041 GAGAGGCAGA AAGGGTAGGT TCAGTAATCA TTTCTGATGA TTTGCTGGAG TGCTGGCTCC  
2101 ACGCCCTGGG GAGTGAGCTT GGTGCGGTAG GTGCTGGCCT CAAACAGCCA CGAGGTGGTA  
2161 GCTCTGAGCC CTCCTTCTTG CCCTGAGCTT TCCGGGGAGG AGCCTGGAGT GTAATTACCT  
2221 GTCATCTGGG CCACAGCTC CACTGCCCC CGTTGCCGGG CTGGACTGT CTTAGGTGAC  
2281 CCCATCTCTG CTGCTTCTGG GCCTGATGGA GAGGAGAACA CTAGACATGC CAACTCGGGA  
2341 GCATTCTGCC TGCCCTGGGA CCGGGTGGAC GAGGAGTGT CTGTAAGGAG TCAGTGTGTA  
2401 CTGTAGGCGC CCCTGGGGTG GGTTAGCAG GCTGCAGCAG GCAGAGGAG AGTACCCCC  
2461 TGAGAGCATG TGGGGGAAGG CCTTGCTGTC ATGTGAATCC CTCAATACCC CTAGTATCTG  
2521 GCTGGGTTTT CAGGGGCTTT GGAAGCTCTG TTGCAGGTGT CCGGGGGTCT AGGACTTTAG  
2581 GGATCTGGGA TCTGGGGAAG GACCAACCCA TGCCCTGCCA AGCCTGGAGC CCCTGTGTTG  
2641 GGGGGCAAGG TGGGGGAGCC TGGAGCCCT GTGTGGGAGG GCGAGGCGGG GGAGCCTGGA  
2701 GCCCTGTGT GGGAGGGCGA GCGGGGGAT CCTGGAGCCC CTGTGTCGGG GGGCGAGGGA  
2761 GGGGAGGTGG CCGTCGGTGG ACCTTCTGAA CATGAGTGTG AACTCCAGGA CTTGCTTCCA  
2821 AGCCCTTCCC TCTGTTGGAA ATTGGGTGTG CCCTGGCTCC CAAGGAGGC CCATGTGACT  
2881 AATAAAAAAC TGTGAACCT

## (2) INFORMATION FOR SEQ ID NO:2434:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1921 base pairs



(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2434:

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1 CGCATTGTG TTTAATAAA AGAATCTGGA AGATAAATAG TCTTGAAGAG AGACAAAGGA
61 AGGAAAATT AAATCCTTAG ATTCAAGCAG AAGAATTCCA TGTGGAAGST TTGGGTGTGT
121 GTTGTGTGT TTTGGTGTGT TTTTGTTTT TTTTGTTTT TGTTTTTT TGAGATGGAG
181 TCTCGCTGTG TTACCGGGAG CGACAGAGCC GCACGGCCGA GTCGAGTCCC AGCCAGCTAC
241 CATCCCTCTG GAGCTTACCG GCCGGCCTTG GCTTCCCCAG GAATCCCTGG AGCTAGCGGC
301 TGCTGAAGGC GTCGAGGTGT GGGGGCACTT GGACAGAACA GTCAGGCAGC CGGGAGCTCT
361 GCCAGCTTTG GTGACCTTGG GTGCTTGCCT CGTGCCCTT GGTGCCCGTC TGCTGATGTG
421 CCCAGCCTGT GCGCCCATG CCGCCCTCCA TCTCAGCTTT CCAGGCCGCC TACATCGGCA
481 TCGAGGTGCT CATCGCCCTG GTCTCTGTGC CCGGGAACGT GCTGGTGATC TGGGCGGTGA
541 AGGTGAACCA GCGCTGCGG GATGCCACCT TCTGCTTCAT CGTGTGCTG CCGGTGGCTG
601 ATGTGGCCGT GGTGCGCCTG GTCATCCCC TCGCCATCCT CATCAACATT GGGCCACAGA
661 CCTACTTCCA CACCTGCCTC ATGGTTGCCT GTCCGGTCTT CATCTCACC CAGAGCTCCA
721 TCCTGGCCCT GCTGGCAATT GCTGTGGACC GCTACCTCCG GGTCAAGATC CCTCTCCGGT
781 ACAAGATGTT GGTACCCCC CGGAGGGCGG CGGTGCCAT AGCCGGCTGC TGGATCCTCT
841 CTTTCGTGGT GGGACTGACC CCTATGTTT GCTGGAACAA TCTGAGTGGC GTGGAGCGGG
901 CCTGGGCAGC CAACGGCAGC ATGGGGGAGC CCGTGATCAA GTGCGAGTTC GAGAAGGTCA
961 TCAGCATGGA GTACATGGTC TACTTCAACT TCTTTGTGTG GGTGCTGCCC CCGCTTCTCC
1021 TCATGGTCTT CATCTACCTG GAGGTCTTCT ACCTAATCCG CAAGCAGTC AACAAAGAGG
1081 TGTCGGCCTC CTCCGGCGAC CCGCAGAAGT ACTATGGGAA GGAGCTGAAG ATCGCCAAGT
1141 CGCTGGCCCT CATCCTCTTC CTCTTGGCCC TCAGCTGGCT GCCTTGCAC ATCTCAACT
1201 GCATACCCTT CTTCTGCCCG TCCTGCCACA AGCCAGCAT CCTTACCTAC ATTGCCATCT
1261 TCCTCACGCA CGGCAACTCG GCCATGAACC CCATTGTCTA TGCCTTCCGC ATCCAGAAGT
1321 TCCGCGTAC CTTCCTTAAG ATTTGGAATG ACCATTTCG CTGCCAGCCT GCACCTCCCA
1381 TTGACGAGGA TCTCCAGAA GAGAGGCCCTG ATGACTAGAC CCCGCCTTCC GCTCCACCG
1441 CCCACATCCA GTGGGGTCT AGTCCAGTCC TCACATGCC GCTGTCCCAG GGTCTCTCT
1501 GAGCCTGCCC CAGCTGGGCT GTTGGCTGGG GGCATGGGG AGGCTCTGAA GAGATACCCA
1561 CAGAGTGTGG TCCCTCCACT AGGAGTTAAC TACCCTACAC CTCTGGGCCC TGCAGGAGGC
1621 CTGGGAGGGC AAGGGTCTTA CGGAGGGACC AGGTGTCTAG AGGCAACAGT GTTCTGAGCC
1681 CCCACCTGCC TGACCATCCC ATGAGCAGTC CAGAGCTTCA GGGCTGGGCA GGTCTGGGG
1741 AGGCTGAGAC TGACAGGAG CCACCTGGGC TGGGAGAAGG TGCTTGGGCT TCTGCGGTGA
1801 GGCAGGGGAG TCTGCTTGT TTAGATGTT GTGGTGACG CCCAGGACCA AGCTTAAGGA
1861 GAGGAGAGCA TCTGCTCTGA GACGGATGGA AGGAGAGAGG TTGAGGATGC ACTGGCCTGT
1921 TCTGTAGGAG AGACTGGCCA GA
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(2) INFORMATION FOR SEQ ID NO:2435:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1681 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2435:

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1 CCCAGCCCCG AGGCTCAGAA GCGGCAGGCG GAGGCGCGGT CCGGGCGCTA TGGCCATGCC
61 CGGCGGGTCT CACGCGGCTG CCCCTCGCCC GCGCGCCTT CCGTAGGGGG CGCCCGGGGG
121 CCAGCTGGCC CGGCCATGCT CTGGAGACA CAGGACGCGC TGTACGTGGC GCTGGAGCTG
181 GTCATCGCCG CGCTTTCGGT GCGGGGCAAC GTGCTGGTGT GCGCCGCGGT GGGCACGGCG
241 AACACTCTGC AGACGCCAC CAACTACTTC CTGGTGTCCC TGGCTGCGGC CGACGTGGCC
301 GTGGGGTCTT TCGCCATCCC CTTTGCCATC ACCATCAGCC TGGGCTTCTG CACTGACTTC
361 TACGGCTGCC TCTTCTCGC CTGCTTCGTG CTGGTGCTCA CGCAGAGCTC CATCTTCAGC
421 CTTCTGGCCG TGGCAGTCGA CAGATACCTG GCCATCTGTG TCCCGCTCAG GTATAAAAGT
481 TTGGTCACGG GGACCCGAGC AAGAGGGGTC ATTGCTGTCC TCTGGGTCC TGCCTTTGGC
541 ATCGGATTGA CTCCATTCTT GGGGTGGAAC AGTAAAGACA GTGCCACCAA CAACTGCACA
601 GAACCTGGG ATGGAACCAC GAATGAAGC TGCTGCCTT TGAAGTGTCT CTTTGAGAA
661 GTGGTCCCCA TGAGCTACAT GGTATATTTC AATTTCTTTG GGTGTGTTCT GCGCCACTG
721 CTTATAATGC TGGTGATCTA CATTAGATC TTCCTGGTGG CCTGCAGGCA GCTTCAGCGC
781 ACTGAGCTGA TGGACCACTC GAGGACCACC CTCAGCGGG AGATCCATGC AGCCAAGTCA
841 CTGGCCATGA TTGTGGGGAT TTTTGCCCTG TGCTGGTTAC CTGTGCATGC TGTTAACTGT
901 GTCACTCTTT TCCAGCCAGC TCAGGGTAAA AATAAGCCCA AGTGGGCAAT GAATATGGCC
961 ATTCTTCTGT CACATGCCAA TTCAGTTGTC AATCCCATG TCTATGCTTA CCGGAACCGA
1021 GACTTCCGCT ACACTTTTCA CAAAATTATC TCCAGGTATC TTCTCTGCCA AGCAGATGTC
1081 AAGAGTGGGA ATGGTCAGGC TGGGGTACAG CCTGCTCTCG GTGTGGCCCT ATGATCTAGG
1141 CTCTCGCCTC TTCCAGGAGA AGATACAAAT CCACAAGAAA CAAAGAGGAC ACGGCTGGTT
1201 TTCATTGTGA AAGATAGCTA CACCTCACAA GGAAATGGAC TGCCTCTCTT GAGCACTTCC
1261 CTGGAGCTAC CACGTATCTA GCTAATATGT ATGTGTGAGT AGTAGACCA AGGATTGACA
1321 AATATATTTA TGATCTATTC AGCTGCTTTT ACTGTGTGGA TTATGCCAAC AGCTTGAATG
1381 GATTCTAACA GACTCTTTTG TTTTAAAG TCTGCCTTGT TTATGGTGA AAATTACTGA
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1441 AACTATTITA CTGTGAAACA GTGTGAACTA TTATAATGCA AATACTTTTT AACTTAGAGG  
 1501 CAATGGAAAA ATAAAAGTTG ACTGTACTAA AAATGTATAC TTGTTGCCAG GAAGGTGACC  
 1561 TCAAAAATTA AAAGTATAAT TATTCGGCCG GGCATGGTGG CTCACACCTG TAATTCACAG  
 1621 ACTTTGGGAG GCCAAGGCAG GCGGATCAG AGGTGAGGAG TTCAAACCA GCCTGTCCAA  
 1681 TATAGTG

## (2) INFORMATION FOR SEQ ID NO:2436:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1681 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2436:

1 GGGCAATTG TTAGTTATCC GCCGCCACCA AGACGCGGCA CGGCGCCTGG ACCGGAGGGG  
 61 CCCCGCGCGG GCGCGAACTT TGGGCTCGGG CGAGTGGGTG GTGCTCCGCC CAGCCCAGAG  
 121 CGGCGGGGCG CGCGGGCCAA TGGGTGCCGC CTCTTGCCG CGGGGGGCCG CGACCCGTGG  
 181 GTCCCGGCCA CCAGCGCCCC AGCCCCGAGG CTCAGAAGCG GCAGGCGGAG GCGCGGTCCG  
 241 GGCCTATGG CCATGCCCGG CGGGTCTCAC GCGGCTGCCC CTCGCCCGGC GCGCCTTCGG  
 301 TAGGGGGGCG CCGGGGCCCA GCTGGCCCGG CCATGCTGCT GGAGACACAG GACGCGCTGT  
 361 ACGTGGCGCT GGAGCTGGTC ATCGCCGCGC TTTCGGTGGC GGGCAACGTG CTGGTGTGCG  
 421 CGCGGTGGG CACGGCGAAC ACTCTGCAGA CGCCACCAA CTACTTCTG GTGTCCCTGG  
 481 CTGCGGCCGA CGTGGCCGTG GGGCTCTTCG CCATCCCCTT TGCCATCACC ATCAGCCTGG  
 541 GCTTCTGCAC TGACTTCTAC GGCTGCCTCT TCCTCGCTG CTTCTGTGCT GTGCTCACGC  
 601 AGAGCTCCAT CTTAGCCTT CTGGCCGTGG CAGTCGACAG ATACCTGGCC ATCTGTGCTC  
 661 CGCTCAGGTA TAAAAGTTG GTCACGGGGA CCCGAGCAAG AGGGGTCATT GCTGTCTCT  
 721 GGGTCCTTGC CTTTGGCATC GGATTGACTC CATTCTGGG GTGGAACAGT AAAGACAGTG  
 781 CCACCAACAA CTGCACAGAA CCCTGGGATG GAACCACGAA TGAAAGCTGC TGCCTTGTGA  
 841 AGTGTCTCTT TGAGAATGTG GTCCCATGA GCTACATGGT ATATTTCAAT TTCTTTGGGT  
 901 GTGTTCTGCC CCCACTGCTT ATAATGCTGG TGATCTACAT TAAGATCTTC CTGGTGGCCT  
 961 GCAGGCAGCT TCAGCGCACT GAGCTGATGG ACCACTCGAG GACCACCCTC CAGCGGGAGA  
 1021 TCCATGCAGC CAAGTCACTG GCCATGATTG TGGGGATTTT TGCCCTGTGC TGGTTACCTG  
 1081 TGCATGCTGT TAACTGTGTC ACTCTTTTCC AGCCAGCTCA GGGTAAAAAT AAGCCCAAGT  
 1141 GGGCAATGAA TATGGCCATT CTTCTGTAC ATGCCAATC AGTTGTCAAT CCCATTGTCT  
 1201 ATGCTTACCG GAACCGAGAC TTCCGCTACA CTTTTCACAA AATTATCTCC AGGTATCTTC  
 1261 TCTGCCAAGC AGATGTCAAG AGTGGGAATG GTCAGGCTGG GGTACAGCCT GCTCTCGGTG  
 1321 TGGGCTATG ATCTAGGCTC TCGCCTCTTC CAGGAGAAGA TACAAATCCA CAAGAAACAA  
 1381 AGAGGACACG GCTGGTTTTT ATTGTGAAAG ATAGCTACAC CTCACAAGGA AATGGACTGC  
 1441 CTCTTTGAG CACTTCCCTG GAGCTACCAC GTATCTAGCT AATATGTATG TGTGAGTAGT  
 1501 AGGTCCAAG GATTGACAAA TATATTTATG ATCTATTCAG CTGCTTTTAC TGTGTGGATT  
 1561 ATGCCAACAG CTTGAATGGA TTCTAACAGA CTCTTTTGT TTTAAAAGTC TGCCTTGTTC  
 1621 ATGGTGAAA ATTACTGAAA CTATTTTACT GTGAAACAGT GTGAACATT ATAATGCAAA  
 1681 TACTTTTTAA CTTAGAGGCA ATGGAATAAT AAAAGTTGAC TGTACTAAA ATG

## (2) INFORMATION FOR SEQ ID NO:2437:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2461 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2437:

1 GAATTCCCAG ATGGGCAGAG GTGGCTGGGC TGGTGACCCT AAGTGTGTCT CCTGCCTTTA  
 61 TTCTCTCTAG TGGGTTATTC TTTCTATGTT TATCTTGCCT ACAGCATGCT GTGTTTGGAC  
 121 ACAAACCCCT TTCCTTGTT TCTCTGACCC AGCTGAGATG GACTGATTCC AAAAGAACTC  
 181 ACCTATGTAC TGGGGTAGGG GAGGGAGGGT TTTTTCAGT ATTTAACTAA GGTTCAAAGA  
 241 GTGCTATATA GTGAGAAAGG CTTCTTTTTT TTTTTTTTTT TTTTTTGGCA GAGTGCTGCC  
 301 TCCTAGAAAT TTCTCTTGGT AACTTCCTTC TCTGAAGCAC AGATAAAGAA AACAATTACA  
 361 GTAGAAACAT TTATGAGGGA CACATTGGAG GCGGATGAAG CTTTTCAAGT TCCAGCAGTG  
 421 CAGGGATGTG GGCAGAACTG ACATTGGAAG ATACTAGAAT GATGGAAATT CAGTTGGAGA  
 481 GGACTGCCCT TTTAATGTC TGGGGAGTCT GCTCAGGGAG AAATGACAAG TCTGGCGGGG  
 541 ACAAGTATGG GATTGGTAA GACTTGGATC AACTTGGGAT ACAGGGTGGG GGTGCGGGAGT  
 601 GGAATCAATG AATGATGCCA GAGCAGATCA ACTAACAAGA GGACCCTGAT GAGCCCCAGG  
 661 CAGAGGCGTC TCCCTTATGC CCCACTCTGA AGTGTGTTGT AGTAAACACC AGAACGCCAT  
 721 TGTGTTACT GCTGAATTTT ATTTTGGGCT GTACATATTT AGATGCTTAA GGTAAAAATG  
 781 ATAAAGCCCT CAAGCCACTG TGTGGGTTTG GGTCCAAGTG TTCCTTCTTG CTGCCTCTCT  
 841 AACACGCCCT GTTAAATAA TCCCTTGGGA TGGTGCTGAG AAGCACCTGA ACCAAGTGGG  
 901 TCCCCAATA ACAATGGCGT GCAAGTGTCT GGTTCACAGA AGTTGGTGAC TAGGTAAGCA  
 961 GCTTCAGGGA GAGGGGGCTG ATTCCAGAC AGTCGCCCTG TCCTGCGGGG ATGGGGCTGA  
 1021 GGCTTGGGGA ATGTGGGCGAG GAGGATATGC CATTGATTC TGTGTCACAC GTTCTTTTCC  
 1081 CTTCTTTCTG TATGTCTGGT CATTCTGCTA TTCTGCTGTT CCTCACATAG GTTGACATT

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1141 GGCCGGCTGC CAGCATAAGT GCCAGTGTGA TTTTGCTAGG TGTGAGCTGA GAAAGAGAGG
1201 TGGAGGCTAA GCAGGTGTGA TGCTTCTCAG AGGTGCTGAG TTTTGGCCCT TCTGAGCAGG
1261 GAATCTTTGC TTATCCCTTT GACCAAGGAT CTTTGCTGCA AAGGCTGGGT ATCGGCTGTG
1321 CTCAGCAAAG CGTCAACTCG TGCAAGAACT TAGCAGGAAT AGTTCTGGCT AAGGTTAGGA
1381 GGCTGCCACC AAAGTCTCTT TTTTGTTCCT CTGCTTCTCC CGTTTGCCTC CTTATCATGA
1441 GATCTTTTTG CTAAGCTGGC AGAAAGATTG CATAGTCAGT GCTTCCAGCT CTGCTCCCAC
1501 CTGATCCTGC ACTGTCCTCT GGTCCCTGAA TGAATGAACT CTGATACCCA ATCTTGCTCTC
1561 GAGCCTTCTC TATGCCACTC ATGGCTCCTC TTCTGCTCTT TCCATCTTTT TGCTGAGAGT
1621 TCTGAGCTCT GACTTCTCTC TTGGCCCATC TCACTTCTCG AAACACCCCT GAAGAGGGTT
1681 GCTTATCTTG ATGGAAGTCA AAAAGCCAAA AAGCTGCAGG CAGAGGCGTT GAGGACATCT
1741 GTTTGGGGAA CTAAGAGCAG CAGCACTTTC AGATTGAGTC CATATAGAGC TGTCCTACAG
1801 CATTCTGGAA ACTTGAGGAT GTGCGGTGCA TAAAGGGGCT GGAAGTGACC CACCTGTGAT
1861 GAGCCCTTTC TAAGGAGAAG GGTTTCCAAG AGATCACCCC ACCAGAAAAG GGTAGGAATG
1921 AGCAAGTTGG GAATTTTAGA CTGTCACTGC ACATGGACCT CTGGGAAGAC GTCTGGCGAG
1981 AGCTAGGCCC ACTGGCCCTA CAGACGGATC TTGCTGGCTC ACCTGTCCCT GTGGAGGTTT
2041 CCCTGGGAAG GCAAGATGCC CAACAACAGC ACTGCTCTGT CATTGGCCAA TGTTACCTAC
2101 ATCACCATGG AAATTTTCAT TGGACTCTGC GCCATAGTGG GCAACGTGTG GGTCTAGTGC
2161 GTGGTCAAGC TGAACCCAG CCTGCAGACC ACCACCTTCT ATTTTCATTG CTCTCTAGCC
2221 CTGGCTGACA TTGCTGTTGG GGTGCTGGTC ATGCCTTTGG CCATTGTTGT CAGCCTGGGC
2281 ATCACAATCC ACTTCTACAG CTGCCTTTTT ATGACTTGCC TACTGCTTAT CTTTACCCAC
2341 GCCTCCATCA TGTCTTGGCT GGCCATCGCT GTGGACCGAT ACTTGCGGGT CAAGCTTACC
2401 GTCAGGTAGC CTGCGGCGTG GGGTGGGCAG CAATTGAGGC AGCTGGGAAA TGAGGCTACA
2461 AAGCCAGAGC

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## (2) INFORMATION FOR SEQ ID NO:2438:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2438:

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1 CTGCTGAATT TTATTTTGA CTGTACATAT TTAGATGCTT AAGGTAAAAA TGATAAAGCC
61 CTCAAGCCAC TGTGTGGGTT GGGTCCAAGT GTTCTTGCT GCTGCCTCTC TAACACGCCT
121 GGTTAAATA ATCCCTTGG ATGGTGTGA GAAGCACCTG AACCAAGTGG GTCCCAAAT
181 AACTATGGCG TGCAAGTGTG TGGTCCCAG AAGTTGGTGA CTAGGTAAGC GACTCAGGGA
241 GAGGGGCTGA TTCCAGACA GTCGCCTGTT CCTGCTGGGA TGGGGCTGAG GCTTGGGGAA
301 TGTGGGCAGG AGGATATGCC ATTTGATTCT GTTGACACG TTCTTTTCCC TTCTTTCTGT
361 ATGTCTGGTC ATTCTGCTAT TCTGTCGTT CTCACATAGG TTGGACATTG GCCGGCTGCC
421 AGCATAAGTG CCAAGTGTGAT TTTGCTAGG TGTGAGCTGA GAAAGAGAGG TGGAGGCTAA
481 GCAGGTGTGA TGCTTCTCAG AGGTGCTGAG TTTTGGCCCT TCTGAGCAGG GAATCTTTGC
541 TTATCCCTTT GACCAAGGAT CTTTGCTCCA AAGGCTGGGT ATCGGCTGTG CTCAGCAAAG
601 CGTCAACTCG TGCAAGAACT TAGCAGGAAT AGTTCTGGCT AAGGTTAGGA GGCTGCCACC
661 AAAGTCTCTT TTTGTTTCCT CTGCTTCTCC CGTTTGCTC CTTATCATGA GATCTTTTGT
721 CTAAGCTGGC AGAAAGATTG CATAATCAGT GCTTCCAGCT CCGCTCCCAC CTGATCCTGC
781 ACTGTCCTCT GGTCCCTGAA TGAATGAACT CTGATACCCA ATCTTGCTCTC GAGCCTTCTC
841 TATGCCACTC ATGGCTCCTC TTCTGCTCTT TCCATCTTTT TGCTGAGAGT TACTGAGCTC
901 TGTACTTCCT CTGGCCCAT CTCATTCTCT GAAACACCCC TGAAGAGGGT TGCTTATCTT
961 GATGGAATC AAAAAGCCAA AAAGCTGCAG GCAGAGGCGT TGAGGACATC TGTTTGGGGA
1021 ACTAAGAGCA GCAGCACTT CAGATTGAGT CCATATAGAG CTGTCCTACA GCATTCTGGA
1081 AACTTGAGGA TGTGCGGTGC ATAAAGGGGC TGGAAAGTGC CCACCTGTGA TGAGCCCTTT
1141 CTAAGGAGAA GGGTTTCCAA GAGATCACCC CACCAGAAAA GGGTAGGAAT GAGCAAGTTG
1201 GGAATTTTAG ACTGTCCTG CACATGGACC TCTGGGAAGA CGTCTGGCGA GAGCTAGGCC
1261 CACTGGCCCT ACAGACGGAT CTTGCTGGCT CACCTGTCCC TGTGAGAGTT CCCCTGGGAA
1321 GGCAAGATGC CCAACAACAG CACTGCTCTG

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## (2) INFORMATION FOR SEQ ID NO:2439:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1741 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2439:

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1 CGAATTCGGG GGACATCTGT TTGGGGAAGT AAGAGCAGCA GCACTTTCAG ATTCACTCCA
61 TATAGAGCTG TCCTACAGCA TTCTGGAAAC TTGAGGATGT GCGGTGCATA AACGGGCTGG
121 AAGTGACCCA CCTGTGATGA GCCCTTCTA AGGAGAAGGG TTTCCAAGAG ATCACCCAC
181 CAGAAAAGGG TAGGAATGAG CAAGTTGGGA ATTTTAGACT GTCACTGCAC ATGGACCTCT
241 GGAAGACGT CTGGCGAGAG CTAGGCCAC TGGCCCTACA GACGGATCTT GCTGGCTCAC
301 CTGTCCTGT GGAGGTTCCC CTGGGAAGGC AAGATGCCA ACAACAGCAC TGCTCTGTCA
361 TTGGCCAATG TTACCTACAT CACCATGGAA ATTTTCATTG GACTCTGCGC CATAGTGGGC

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421 AACGTGCTGG TCATCTGCGT GGTCAGCTG AACCCAGCC TGCAGACCAC CACCTTCTAT  
481 TTCATTGTCT CTCTAGCCCT GGCTGACATT GCTGTTGGGG TGCTGGTCAT GCCTTTGGCC  
541 ATTGTTGTCA GCCTGGGCAT CACAATCCAC TTCTACAGCT GCCTTTTAT GACTTGCTTA  
601 CTGCTTATCT TTACCCACGC TCCTCATATG TCCTTGCTGG CCATCGCTGT GGACCGATAC  
661 TTGCGGGTCA AGCTTACCGT CAGATACAAG AGGGTCACCA CTCACAGAAG AATATGGCTG  
721 GCCCTGGGCC TTTGCTGGCT GGTGTCATTC CTGGTGGGAT TGACCCCAT GTTTGGCTGG  
781 AACATGAAAC TGACCTCAGA GTACCACAGA AATGTCACCT TCCTTTCATG CCAATTTGTT  
841 TCCGTCAATG GGATGGACTA CATGGTATAC TTCAGCTTCC TCACCTGGAT TTTTCATCCC  
901 CTGGTTGTCA TGTGCGCCAT CTATCTTGAC ATCTTTTACA TCATTGCGAA CAAACTCAGT  
961 CTGAACCTAT CTAACCTCAA AGAGACAGGT GCATTTTATG GACGGGAGTT CAAGACGGCT  
1021 AAGTCCTTGT TTCTGGTTCT TTTCTTGTTC GCTCTGTCAT GGCTGCCTTT ATCTCTCATC  
1081 AACTGCATCA TCTACTTTAA TGGTGAGGTA CCACAGCTTG TGCTGTACAT GGGCATCCTG  
1141 CTGTCCCATG CCAACTCCAT GATGAACCTT ATCGTCTATG CCTATAAAAT AAAGAAGTTC  
1201 AAGGAAACCT ACCTTTTGTAT CCTCAAAGCC TGTGTGGTCT GCCATCCCTC TGATTCTTTG  
1261 GACACAAGCA TTGAGAAGAA TTCTGAGTAG TTATCCATCA GAGATGACTC TGTCTCATTG  
1321 ACCTTCAGAT TCCCACATCA CAAACACTTG AGGGCCTGTA TGCCTGGGCC AAGGGATTTT  
1381 TACATCCTTG ATTACTTCCA CTGAGGTGGG AGCATCTCCA GTGCTCCCCA ATTATATCTC  
1441 CCCCACCTCA CTACTCTCTT CCTCCACTTC ATTTTTCCTT TGCTCTTCT CTCTAATTCA  
1501 GTGTTTGGGA GGCCTGACTT GGGGACAACG TATTATTGAT ATTATTGTCT GTTTTCTTCT  
1561 TTCCAATAG AAGAATAAGT CATGGAGCCT GAAGGGTGCC TAGTTGACTT ACTGACAAA  
1621 GGCTCTAGT GGGCTGAACA TGTGTGGT GGTGACTCAT TTCCATGCCA TTGTGGAATT  
1681 GAGCAGAGAA CCTGCTCTCG GAGGATGCCT AGGAGATGTT GGGAACAGAA GAAATAAACT  
1741 GAGTTTAAGG GGGACTTAAA CTGCTGAATT C

## (2) INFORMATION FOR SEQ ID NO:2440:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2041 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2440:

1 GCCGCCGCCG CCAAGATGGC GGACCTGGAG GCGGTGCTGG CCGACGTGAG CTACCTGATG  
61 GCCATGGAGA AGAGCAAGGC CACGCCGGCC GCGCGCGCCA GCAAGAAGAT ACTGCTGCCC  
121 GAGCCAGCA TCCGAGTGT CATGCAGAAG TACCTGGAGG ACCGGGGCGA GGTGACCTTT  
181 GAGAAGATCT TTTCCAGAA GCTGGGTAC CTGCTCTTCC GAGACTTCTG CCTGAACCAC  
241 CTGGAGGAGG CCAGGCCCTT GGTGGAATTC TATGAGGAGA TCAAGAAGTA CGAGAAGCTG  
301 GAGACGGAGG AGGAGCGTGT GGCCCGCAGC CGGAGATCT TCGACTCATA CATCATGAAG  
361 GAGTGCTGG CCTGCTCGCA TCCCTTCTCG AAGAGTGCCA CTGAGCATGT CCAAGGCCAC  
421 CTGGGGAAGA AGCAGGTGCC TCCGGATCTC TTCCAGCCAT ACATCGAAGA GATTGTCAA  
481 AACCTCCGAG GGGACGTGTT CCAGAAATTC ATTGAGAGCG ATAAGTTCAC ACGTTTTTGC  
541 CAGTGAAGA ATGTGGAGCT CAACATCCAC CTGACCATGA ATGACTTCAG CGTGATCGC  
601 ATCATTGGGC GCGGGGGCTT TGGCGAGGTC TATGGGTGCC GGAAGGCTGA CACAGGCAAG  
661 ATGTACGCCA TGAAGTGCTT GGACAAAAG CGCATCAAGA TGAAGCAGGG GGAGACCCTG  
721 GCCCTGAACG AGCGCATCAT GCTCTCGCTC GTCAGCACTG GGGACTGCCC ATTCATTGTC  
781 TGATGTCAT ACGCGTTCCA CACGCCAGAC AAGCTCAGCT TCATCCTGGA CCTCATGAAC  
841 GGTGGGACC TGCATACCA CCTCTCCAG CACGGGTCT TCTCAGAGG TGACATGCGC  
901 TTCTATGCGG CCGAGATCAT CCTGGGCTG GAGCAGATGC ACAACCGCTT CGTGGTCTAC  
961 CGGGACCTGA AGCCAGCCAA CATCTTCTG GACGAGCATG GCCACGTGCG GATCTCGGAC  
1021 CTGGGCTTG CCTGTGACTT CTCCAAGAAG AAGCCCATG CCAGCGTGGG CACCCACGGG  
1081 TACATGGCTC CGGAGTCCCT GCAGAAGGC GTGGCCTACG ACAGCAGTGC CGACTGTTC  
1141 TCTCTGGGGT GCATGCTCTT CAAGTTGCTG CCGGGGCACA GCCCTTCCG GCAGCACAAG  
1201 ACCAAAGACA AGCATGAGAT CGACCGCATG ACCTGACGA TGGCCGTGGA GCTGCCCGAC  
1261 TCCTTCTCCC CTGAATACG CTCCTGCTG GAGGGGTTC TGCAGAGGGA TGTCAACCGG  
1321 AGATTGGGCT GCCTGGGCCG AGGGGCTCAG GAGGTGAAAG AGAGCCCTT TTTCCGCTCC  
1381 CTGGAAGTGC AGATGGTCTT CTTGCAGAAG TACCCTCCCC CGCTGATCCC CCCACGAGGG  
1441 GAGGTGAACG CGGCCGACGC CTTGCACATT GGCTCCTTCG ATGAGGAGGA CACAAAAGGA  
1501 ATCAAGTTAC TGGACAGTGA TCAGGAGCTC TACCGCAACT TCCCCCTCAC CATCTCGGAG  
1561 CGGTGGCAGC AGGAGGTGGC AGAGACTGTC TTCGACCA TCAACGCTGA GACAGACCGG  
1621 CTGGAGGCTC GCAAGAAAGC CAAGAACAAG CAGCTGGGCC ATGAGGAAGA CTACGCCCTG  
1681 GGCAAGGACT GCATCATGCA TGGCTACATG TCCAAGATGG GCAACCCCTT CCTGACCCAG  
1741 TGGCAGCGGC GGTACTTCTA CCTGTTCCCC AACCGCCTCG AGTGGCGGGG CGAGGGCGAG  
1801 GCGCCGAGA GCCTGCTGAC CATGGAGGAG ATCCAGTCCG TGGAGGAGAC GCAGATCAAG  
1861 GAGCGCAAGT GCCTGCTCCT CAAGATCCGC GGTGGGAAAC AGTTCAATTT GCAGTGCAT  
1921 AGCGACCTG AGCTGGTGCA GTGGAAGAAG GAGCTGCGCG ACGCTACCG CGAGGCCAG  
1981 CAGCTGGTGC AGCGGGTGCC CAAGATGAAG AACAAGCCGC GCTCGCCCGT GGTGGAGCTG  
2041 AGCAAGGTGC CGCTGGTCCA GCGCGGCACT GCCAAGCGCC TCTGACCCGC CCACCCGCT

## (2) INFORMATION FOR SEQ ID NO:2441:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7321 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2441:

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1 AAATGATAGA CCGTCAATAA TTTGTTAAAT GCTTTTAAAT ATGAATGCTT TAAGCCGGGT
61 GCAGTGCCTC ACATCTGTAA TCCCAGCACT TTGGAGCCGA GCGGGTGGAT TGTGTAGGT
121 CAGGAGTTCG AGACCAACCT GGCCAACATG GCAAAACCTC ACTCTCTACC AAAAATACAA
181 AAATTAGCCA GGCATGGTGG CAGGCACCTG TGATCCCAGC TACTCAGGAG GCTGAGACAG
241 GAGAAATCGCT TGAACCCGGG AGGCAAGGTT GCAGTGAGCC AAGATTACGC CATTGTACTC
301 CAGCCTGGGT GACAGAGAGA GACTCCGTCT CAAAAAATAA AAAAAAATAA AAAAAATTAC
361 GCTTCAAACA CATGATCTCT CACCACTGTT GAATTTTCTT TCTATGAGCC CAGGAGGGCC
421 TCTCAGAGAG GAAAGCTCCT AGGTCTTCTT TTCCCTCTGC AAATCCCTG CTTTGAAGGT
481 TCAGAAGGAC TGTGCGTGCT CGTTGCATCC TTTGCAAGTG TCCAAACCTT GATCCCAGCT
541 GTGCTTAGGG GTTCTTGCAA ACCTTTTCCA GGTGTTAATT ACCTCCCACT TCATTCTCTG
601 TTTACCAACT CAGCTTTTGG TTTTAGTGTG TTTGAATTCC CTGAAGTAC CGTTGTCTGA
661 TCTCCACCTC CCAACTGAAT TAGGGGAGCT GGGCTTCTGG AAACCCAGGT GCCGGGTGTT
721 GCAGAGTGGC TGAAAGCTGG GATGTGGCAG ATCCGTGGCT ACATTCATGC ACACACACAC
781 ACCCACATAC CCACACATGC ACACACACAC ACACACCCGC ACTCACACAC TTGGACATGC
841 ATAGACCACA GCTTTCCACA CCCTTCCTAG ACAGGGGTCA CTTGGTATCC TGGAGAGAGT
901 GTGAAGTCCT GGAATGGAAA GAGGGGGGAT TAAGCCCACT CTCTAGCCAT GGGACTGAGA
961 CAAGTCACCA CCAACCCATC TGCCTCTGTT TTACCTCTCT TGTGAGGCAA GCACAGAGCC
1021 CATGCCTGCC CCCCTGGATG GGAGTGATGT GAAACTTGAA GGGCGGTGAG AGCAAGGGTC
1081 GGAATGGGAA GGCCCTTGGG AAAAAGGCC CTTTCAACTA GGGGCACAGA GGAGGCCCTG
1141 GGCTGAGAAC TTGACAGCAC CTTGTAATTG GTAAGCCAAG CCCGAAGGGA CTGGAATATC
1201 TCAGATGTGT CTGTCTCCCT TATTAGGTTT AAAGTCCCTC AAGACCTGT CTCCATCACA
1261 GTGCTCCAGT CCAGACCCCT CCTCTGAGCT CCAGACCCCTG CTGGACCCAA CCAGCCCTAT
1321 GGGGTGCGAT CCCCACCTGC CTGGAATTCT CCAAAGAACC TCCCCTTTAA CAGTTCCAGC
1381 CTTTAACAGT TCCAGTCTAA ACACATGACC TTTCTCTCTT AAATCAGCCC CCCATCTCTG
1441 CCTTTGCAGG AGATGGAAGC CATGACACCT GCCTCGCCCC TGTCCTCACC CCATCCATGT
1501 CCAATCAAGC ACTAGGCATG TCAGGTTTAC CCTCTAAACT CCTCTGGAAT CCAGTCTCTC
1561 AGTCTCCATC ATCCCAGGTC GAAGCTAATG GGCTAACTGG TCCTTGCTTC CACTCTACCC
1621 CCACTGCAGT CTTGACTTCC TGAGCAGCAG CCAGGGCCTA ATCGATATTC ACACCAAGCG
1681 CCAACCTGAC TGAGATATCC TCCTGCACCA TCATCCCTCC ACCCTGTTTA GTTCTGCTCA
1741 CCGTCAGTGT TCTCATCAAT AATCCACTCC CCTCAGAGC GCGTTTGGGA CCCCATGTTT
1801 TATGCTCTCA CAGGACCTTT TGCTTGATTT TTCACGTGAC TTAGGTCAGT TTGCAAGTAT
1861 TAAGTGACTG AGCAATGTCT GGCTTCTCCA GTAGACTGTC AGCTCCTAGC CATTGTATAC
1921 CTAGCACCAG TGTGTGGGAG CACGTGACAA ACCTCCAGTG AGTCAGGGAC TCAGCAGTCT
1981 CCATTTCTCC GCCCTGCTGG AGAATGCGTG TATTTGGCAA TCCCAGAGCC CTGTGCCATC
2041 TAACCATCTT TTCTTCTCTG TTCAGCCCAG GTGTGGCCTC ACTCACATCC CACTCTGAGT
2101 CCAAATGTTT TCTCCCTGGA AGATATCAAT GTTTCTGTCT GTTCGTGAGG ACTCCGTGCC
2161 CACCACGGCC TCTTTCAGGT GAGTCAAAGG GATTCCTCAG TTCCTAGTT AGGGGAGGTG
2221 GGCAGACACC CTGGAGAACT CCCTGGAAAG CTCAACTCTC ATGCCCCGGA CAACAGTTGA
2281 AGGAACCATG GTGATGTTAA GCCCAAAGAC AAAACCTCTC AGGTGTCCAA GTCCCTGTTG
2341 GAATCTTGGG AGCAGAGGGA ATGTTCTGTG GTCTAGAGGA AGAGGGGGCTC AGGGAGGAGA
2401 AGGGCACATT CCTGTTGTTT ATATGTTTCT ATCTATCCCA GATGAAGTGT GAAGTGAAGG
2461 GAAGAGAGTT AAACATTAAT GTAAATACCC AGTGGATCAG ACAGCAATGT GCCAGATTGC
2521 CTTGGAAACA AAATATCTCC AACACATGGC TGACATTGGT TGGGAGATCA GAACACCCTA
2581 AAGAGAGAAT TTAAGGGGAG GGGGAGGAGG ACCTGAGCCA GAGTAGAAGC AGAGGATAGG
2641 GAGATCTGTT CTTGGGGACA GCATTTGCAA GAAACAAGGC TGAGGGGTCC ACTCCAACCT
2701 CTCCACCCCTG CTGCAGGTGC TGCCTATGAT GAAGATGAGC AGATGGCCAT CTCAGCTGGG
2761 GCCACAGTGC ACTGGACCTA TAGTTTCCAA TTCCGCACTC AGCAGGCATC TTTCTGATGA
2821 TCCGATGGCT TCTCAGAGCC AGGGATGGGC CAGGATCCAT CCCCTTGGCT ACTGTCTTGC
2881 TGAGAAATTT ATAAGCAGCA TCTGGTGCTA TACTTTGGTC TCTAGTGAGT TAGCTCATGA
2941 AAGATGATAG ACTCTCCAAG CCAGGGGTAT GCAGGAAATG GGTTTTCTGT AGCTACAGAA
3001 ATGGGGTTGA GGGTTGGACC AAGGGACTAC CCAGGGGAAG TCTTACCTTC AGAGGACTCT
3061 GGAAGAGGAG GTGCAAGTTT TCATGGGTCA AGAATTCAGA GCCCAGTAGA GACAGCTTAT
3121 CTCTGTTCCT AGATGTCTGG GGCCTTGGTT GGAAGATTCA AAGGCTAGGA AACCAGGAGC
3181 CACCAAAAGC GTAACCTGGG CCAGAGGATC CACTTTCAAG GTGGCAAGTT GGTTCCTCCC
3241 ATGTGGCTGC TTGAGTATCC TCACATGGCG GCTCACATCC TTCCAAGTAA GCAATGCAAA
3301 AGGCCAAGAA AGATGCTGCA AAGATGTTAT GACCTAGCCT CAGAAATCAC ACACCATCCC
3361 TGCCACCATT AGTAAGAAGT CCAGCCCACG TCCAGGAGAA GAGGAAGCAG ATTCTCTCTT
3421 TTGAAATGAA GAATATCAAG TAATTCGGGG GGCATATGAA AGCCACCACA CACCACAGGG
3481 ATCTTTTGTG AGCATACTTC TTATACCATC ACTGTAGTTC CTTAAGACTC AGGGGCAAGG
3541 CCTCACTTCC TTAGCACCCA GTGAAGACCA CGCTTACTCC CTCACCTAAC CTCTTGCTAC
3601 TTCCACCTC TCCTGTCCAA CATCTAGTGT CACTTTCCAG AACATACCAA CAGCTTCCCC
3661 AGTTCTGTGC CTCTGCTCAG GCTGTTCCCC CTGCCTGGTC CACTTGTCTT CTTCTTGTG
3721 CGGTCAAAAT GCTTCTTATC CTTCAAGACC CAGCTCTAGA GTCACCTCCA ACCCCTTACC
3781 CACCAGCCCC CTCTCCAAGT CTGTGTCCCA CAACCCCTCT GTCCTCTCCA GGGCACCCTC
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3841 CACCCCTCTGG GCCACAGTTG TCAGGAGTCA GGCAGGGCAG GGGCCGGGTG GTGTCTTCTT
3901 TGTGTTCTTG CACTCAGGGC AGAGCTCAGC ACAGAGCAGA CGCTCAAAAA ACATTTAAAG
3961 GATAGAAGCA TTGATTGTG GGTCCCCCAG TCTGGCTCCA GGATGCCAGC CAGCTGCTCC
4021 TAGAAGCAAA CGGACTTTTC CTGGGAAATC CCAGAGGTGA TGATCAGTAA TCTCTCCCGT
4081 GACTCGTAGT TCAGCTCTTC CTCCATGAGC CTGACTATCA GTGGACCTTC CAGAAAGAGC
4141 CCCTTTTCCT TCTCTCACC ACAGCACAGG GCACTGGGAA AATGCCCAAT GAGTCCTGCC
4201 TCTGGGTGTG GCTTTGGACT TTTCACTGTG TCTCGCATCC ACTCTTCAAC TTGAATGTTG
4261 CAACAGCCAT GAAAAAGAA ATGCAAGCG ATTCAAGATG AGAGCAATAC CCTACTCCAA
4321 AGAAGGCAAC ATAGAAGCTC AGAGAGATCA AGCAATTTGC CCAAGACCAC ACAGCTAGGA
4381 GTGGAACCTCA TGGCTGTCCA AGCCCCATGC CTCTGCTGAA GGTAGAGATG AATTACAGCA
4441 ACAAGTCTAG AAAGGTGCCT GCCCTATGGT CTGTGAGTCT TGCTAAGAA TGAAGAGGA
4501 GCCAGTGGGT TAAAGATGAG GTCACCAACA ACGGTGGTGT TGGAGTTTAC CACTGATAAT
4561 AAGGGTGCAA AATGTAAAT ACTAATGTTT ATTGAGCCTA GTGCAGTGGC TGGGGCATTT
4621 TGCACATTGT CTCTGATCCC TATGACAACC CTGAGAGGTA GTGGTTTTAA CTGCCATGTT
4681 ACAGGTGAGG TCATTGTGGT TCAAGGACGT TAAGTAACTT CCCCAGCGTG ACACGGCTTA
4741 TAAGTAAGGC AGCCAGGATG TGAACCCAGT AGGACTATCT GGCTGCAAAG TCCCCACCCC
4801 CCTCGCCATC TGTATCCTCC AATCACTTCA GTGCTTTGCT GCATAGAAGG TAACGGAAAT
4861 CACGATGCCA CAGACTGTCC AGGAAGACAG AAACTAGGCA GATGGGCTGG CCATGGTCTC
4921 CAAGCCAGAC TGGAACTCTCC AGGTCTGGAA TGATATCATT TTTCTCTTTT AATAAATTAA
4981 CTACCCACC ACACGGCTTT GAGAGGCTCA AAGTTGACCA ACTCCCTTGG GAGGGCCCCG
5041 GTTGATAAGG AAGGAACGTG AATCTCCCA TCACGGAAGC TTCAAGGAGG TCAAGGGTCC
5101 AACACTTGAG ATTGTTAGTG CTGTTGGTGG ATACTGGCCA AGGAAATATC CCAGTGGAGC
5161 CTCGAGATGA AGAATCATGAG GCCCCGTTT AGAACCAAGG ATCAGAGGGG GCTCTGTAAAG
5221 ACCCAGGGGA GTCAGGTGCA CTGGAGCGCG GGCATGCAGA AAACAGCCTG AGCTCCACCT
5281 CGGCTTCTCC TTGTCTGGC TGGTTGTCTT TAACCCCTGT CTCCTTCTGG ACCAGTTTTT
5341 GTCCTTCCCT TGTGACCGCT GAGGGGTAAC AGCCTCTTTC CACTTTCTTT CAGCGCCGAC
5401 ATGCTCAATG TCACCTTGCA AGGGCCACT CTTAACGGGA CCTTTGCCCA GAGCAAATGC
5461 CCCCAGTGG AGTGGCTGGG CTGGCTCAAC ACCATCCAGC CCCCCTTCTT CTGGGTGCTG
5521 TTCGTGCTGG CCACCCTAGA GAACATCTTT GTCCTCAGCG TCTTCTGCCT GCACAAGAGC
5581 AGCTGCACGG TGGCAGAGAT CTACCTGGGG AACCTGGCCG CAGCAGACCT GATCCTGGCC
5641 TGCGGGCTGC CCTTCTGGGC CATCACCATC TCCAACAAC TCGACTGGCT CTTTGGGGAG
5701 ACGCTCTGCC GCGTGGTGAA TGCCATTATC TCCATGAACC TGTACAGCAG CATCTGTTTC
5761 CTGATGCTGG TGAGCATCGA CCGCTACCTG GCCCTGGTGA AAACCATGTC CATGGCCCGG
5821 ATGCGCGGCG TCGCTGGGC CAAGCTCTAC AGCTTGGTGA TCTGGGGGTG TACGCTGCTC
5881 CTGAGCTCAC CCATGCTGGT GTTCCGGACC ATGAAGGAGT ACAGCGATGA GGGCCACAAC
5941 GTCACCGCTT GTGTCATCAG CTACCCATCC CTCATCTGGG AAGTGTTCAC CAACATGCTC
6001 CTGAATGTCG TGGGCTTCCT GCTGCCCTG AGTGTCACTA CCTTCTGCAC GATGCAGATC
6061 ATGCAGGTGC TCGGGAACAA CGAGATGCAG AAGTTCAAGG AGATCCAGAC GGAGAGGAGG
6121 GCCACGGTGC TAGTCCTGGT TGTGCTGCTG CTATTCACTA TCTGCTGGCT GCCCTTCCAG
6181 ATCAGCACCT TCCTGGATAC GCTGCATCGC CTCGGCATCC TCTCCAGCTG CCAGGACGAG
6241 CGCATCATCG ATGTAATCAC ACAGATCGCC TCCTTCATGG CCTACAGCAA CAGCTGCCTC
6301 AACCCTACTG TGTACGTGAT CGTGGGCAAG CGCTTCCGAA AGAAGTCTTG GGAGGTGTAC
6361 CAGGGAGTGT GCCAGAAAGG GGGCTGCAGG TCAGAACCQA TTCAGATGGA GAACTCCATG
6421 GGCACACTGC GGACCTCCAT CTCCGTGGAA CGCCAGATTG ACAAATGCA GGACTGGGCA
6481 GGGAGCAGAC AGTGAGCAAA CGCCAGCAGG GCTGCTGTGA ATTTGTGTAA GGATTGAGGG
6541 ACAGTTGCTT TTCAGCATGG GCCCAGGAAT GCCAAGGAGA CATCTATGCA CGACCTTGGG
6601 AAATGAGTTG ATGTCTCCGG TAAAACACCG GAGACTAATT CCTGCCCTGC CCAATTTTGC
6661 AGGGAGCATG GCTGTGAGGA TGGGGTGAAC TCACGCACAG CCAAGGACTC CAAAATCACA
6721 ACAGCATTAC TGTCTTATT TGCTGCCACA CCTGAGCCAG CCTGCTCTT CCCAGGAGTG
6781 GAGGAGGCCT GGGGGCAGGG AGAGGAGTGA CTGAGCTTCC CTCCCCTGTG TTCTCCGTCC
6841 CTGCCCCAGC AAGACAACCT AGATCTCCAG GAGAACTGCC ATCCAGCTTT GGTGCAATGG
6901 CTGAGTGCAC AAGTGAGTTG TTGCCCTGGG TTTCTTTAAT CTATTAGCT AGAATTTGA
6961 AGGACAATTT CTTGCATTAA TAAAGTTAA GCCTGAGGG GTCCCTGATA ACAACCTGGA
7021 GACCAGGATT TTATGGCTCC CCTCACTGAT GGACAAGGAG GTCTGTGCCA AAGAAGAATC
7081 CAATAAGCAC ATATTGAGCA CTTGCTGTAT ATGCAGTATT GAGCACTGTA GGCAAGAGGG
7141 AAGAAAGAGA AGGAGCCATC TCCATCTTGA AGGAACCTCA AGACTCAAGT GGAACGACT
7201 GGGCACTGCC ACCACCAGAA AGCTGTTCTGA TGAGACGGTC GAGCAGGGTG CTGTGGGTGA
7261 TATGGACAGC AGAAGGGGGA GCCAGGTTCC AGCTACCAA TACTATTGCA CACCACCTGT
7321 CCTGCCTC

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## (2) INFORMATION FOR SEQ ID NO:2442:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2442:

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1 GCCCTTCAAA GATGAGCTGT TCCGCGCCGCT ACTCCAGCTC TGGCTTCTGG GCTCCGAGGA
61 GGGGTGGGGA CGGTGGTGAC GGTGGGGACA TCAGGCTGCC CCGCAGTACC AGGGAGCGAC

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121 TGAAGTGGCC ATGCCGCTTG CTCGGAGAA GGTGGGTGCC GGGCAGGGGC TGCTCCAGCC  
181 GCCTCACCTC TGCTGGGAGG ACAAAGTCTC CCAGCACAGA GGGAGGGAGG GAGGGCAGGC  
241 AGCGGGGAGA AGTTTCCCTG TGGTCGTGGG GAGTT

## (2) INFORMATION FOR SEQ ID NO:2443:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1441 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2443:

1 GAGCTCTTCA ATATTTTAGT GAAAGCTATA GATGAGGCTC CATAGGGGAT AAAGCACAGA  
61 CACACCTTTT CAGAGGGCTT GTGGACTCTG GGCAGCCTGT CCATAGACCT CTGTCCCCAA  
121 CTGGCAAGTC AGGAACTCC AGATTAAGGA GCCCCAATGT GGTGGAACAG CCAGGTGCAC  
181 AGATGAGTCA ACCACACAGC CAGGCCAGGG AGGGCCTTCA CTCAAGAGCC TACAGCCAGT  
241 TCACAGCCAA GCCAGGGCTA GCGCCAGGCC ACCCATAAAC TGATCTGAGA CTCTGTTTCC  
301 CTGTCTCCAT GATGATGGGA TCAGGCTTGA TTGCTGTTT GTAGGCTTGT TATGAATCAA  
361 GTCACAGGGA AGAGGAGCTG ATGGGCTGGG GGGACGTCCT CTGGCCCTCC TGTCTCTTCC  
421 CCAGATCCAC TGGGCCCCACT CTTATCTGTT CTCTTCTGAA GGAAGGGTTT TAAGGCTTCA  
481 AAAAAAATG TTTGAAAGT CCCTGCCCTT TCCAGCTCCT ACCGTCTCAG CCCTGGGAGT  
541 GTAAAGTGCT GCAGATAGTT AGTAAGTCTT TGAGCAAAAC TGAGAAAGCC AGCCTGAGCC  
601 TTGACATGGG AGAAACCTCC GCCATACATC TCCGAAGAAA CGGCCGCGTG TCTCAGGGGA  
661 GCGCAAAAC CCGTACCCAG GAAACAGGAC AGCTTCTGCC ACTGTGCGCC TTGGGAGCCG  
721 TACGTGGCAT GACAAAGAAA TCCCAGGACT CCGCCTGCCC ACCTGGCCAC CCTCTGTTTA  
781 CACCTTCCGC GTAAACGCCC ACTGTTTACA TCCAAAATC AGACACAAA TAACCACCTC  
841 AAGAAGATAA ATAATGATAA GAAATAAATG TTACGCGAGG CAAATTTATT CACATGGGGC  
901 TTCCAGGCC ACTTTGTGGT CAGCCGGGAG GGACGTTTTT GCCGTCCCAC GACTCCAACG  
961 GGCAGCCGGG CCTACGCAA CATGGAAATC TTCCAAGAGC CTCCTGGGCC CCCAGGGCTC  
1021 AGAGGGTGGC AGAGCGGAGA GCGAAGGTGG CCGCAGCCTT CCCGCCCCCA CAGCCAGCCT  
1081 GGCTCCAGCT GGGCAGGAGT GCAGAGCTCA GCTGGAGGCG AGGGGGAAGT GCCCAGGAGG  
1141 CTGATGACAT CACTACCCAG CCCTTCAAAG ATGAGCTGTT CCCGCCGCA CTCCAGCTCT  
1201 GGCTTCTGGG CTCCGAGGAG GGGTGGGGAC GGTGGTGACG GTGGGGACAT CAGGCTGCCC  
1261 CGCAGTACCA GGGAGCGACT GAAGTGCCCA TGCCGCTTGC TCCGAGAAG GTGGGTGCCG  
1321 GGCAGGGGCT GCTCCAGCCG CCTCACCTCT GCTGGGAGGA CAACTGTCC CAGCACAGAG  
1381 GGAGGGAGGG AGGGCAGGCA GCGGGAGAA GTTCCCTGT GGTGCTGGG AGTTGGGAAA  
1441 AGTTCCCTTC CTTCCGAGG GAGG

## (2) INFORMATION FOR SEQ ID NO:2444:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2581 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2444:

1 CAGATTACA AACTGCAGGA CTGGGCAGGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT  
61 GCTGTGAATT TGTGTAAGGA TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC  
121 AAGGAGACAT CTATGCACGA CCTTGGGAAA TGAGTTGATG TCTCCGGTAA AACACCGGAG  
181 ACTAATTCCT GCCCTGCCA ATTTTGCAAG GAGCATGGCT GTGAGGATGG GGTGAATCA  
241 CGCACAGCCA AGGACTCAA AATCACAACA GCATTACTGT TCTATTTGCG TGCCACACCT  
301 GAGCCAGCCT GCTCCTCCC AGGAGTGGAG GAGGCCTGGG GGGAGGGAGA GGAGTGACTG  
361 AGCTTCCCTC CCGTGTGTTT TCCGTCCCTG CCCCAGCAAG ACAACTTAGA TCTCCAGGAG  
421 AACTGCCATC CAGCTTTGGT GCAATGGCTG AGTGCACAAG TGAGTTGTTG CCCTGGGTTT  
481 CTTAATCTA TTCAGCTAGA ACTTTGAAGG ACAATTTCTT GCATTAATAA AGGTTAAGCC  
541 CTGAGGGGTC CCTGATAACA ACCTGGAGAC CAGGATTTTA TGGCTCCCTC CACTGATGGA  
601 CAAGGAGGTC TGTGCCAAG AAGAATCCAA TAAGCACATA TTGAGCACTT GCTGTATATG  
661 CAGTATTGAG CACTGTAGGC AAGACCCAAG AAAGAGAAGG AGCCATCTCC ATCTTGAAGG  
721 AACTCAAAGA CTCAAGTGGG AACGACTGGG CACTGCCACC ACCAGAAAGC TGTTCCGACG  
781 GACGGTCGAG CAGGGTGCTG TGGGTGATAT GGACAGCAGA AGGGGGAGAC CAAGGTTCCA  
841 GCTCAACCAA TAACTATTGC ACAACACCT GTCCCTGCCT CAGTTCCCTT TTATGTAACA  
901 TGAAGTCGTT GTGAGGTTA AAGGCAGTAA CAGGTATAAA GTACTTAGAA AAGCAAAGGG  
961 TGCTACGTAC ATGTGAGGCA TCATTACGCA GACGTAACG GGATATGTT ACTATAAGGA  
1021 AAAGACACTG AGGTCTAGAA ATAGCTCCGT GGAGCAGAAT CAGTATTGGG AGCCGGTGGC  
1081 GGTGTGAAGC ACCAGTGTCT GGCACACAGT AGGTGCTCAT TGGCTCCCTT CCACCTGTCA  
1141 TTCCCACCAC CCTGAGGCCC CAACCGCCAC ACACACAGGA GCATTGAGG AGAAGGCCAT  
1201 GTCTTCAAAG TCTGATTTGT GATGAGGCAG AGGAAGATAT TTCTAATCGG TCTTGGCCAG  
1261 AGGATCACAG TGCTGAGACC CCCCACCACC AGCCGGTACC TGGGAAGGGG GAGAGTGCAG  
1321 GCCTGCTCAG GGAAGTGTCC TGTCTCAGCA ACCAAGGGAT TGTTCTGTG AATCAATGGT  
1381 TTATTGGAAG GTGGCCAGT ATGAGCCCTA GAAGAGTGTG AAAAGGAATG GCAATGGTGT  
1441 TCACCATCGG CAGTGCCAGG GCAGCACTCA TTCACCTGAT AAATGAATAT TTATTAGCTG

1501 GTTGGAGAGC TAGAACCTGG AGAGCTAGAA CCTGGAGAAC TAGAACCTGG AGGGCTAGAA  
1561 CCTGGAGAGG CTAGAACCAA GAAGGGCTAG AACCTGGAGG GGCTAGAACC TAGAGAAGCT  
1621 AAAACCTGAG CTAGAAGCTG GAGGACTAGA ACCTGGAGGG CTGGAATCTG AAGGGCTAGA  
1681 ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG GAGGGCTAGA  
1741 ACCTAGAAGG GCTAGAACCT GGAGGGCTGG AATCTGGAGA GCTAGAACCT GGAGGGCTAG  
1801 AACCTGGAGG GCTAGAACCT AGAAGGGCTA GAACCTGGAG GGCTAGAACC TGGCAGGTTA  
1861 GAACCTAGAA GGGCTAGAAC CTGGAGAGCC AGAACCTGGA GGGCTAGAAC CTGGAAGGGC  
1921 TAGAACCTGT AGAGCTAGAA CATGGAGAGC TAGAACCCGG CAGGCTAGAA CCTGGCAAGC  
1981 TAGAACCTGG AGGGAATGAA CCTGGAGGGC TAGAACCTGG AGAATGAGAA AAATTACAT  
2041 GGCAAGAGC CCATAAATCC TGACCAATCC AACTCTGAAT TTAAAGCAA AAGCGTGAAA  
2101 AAAAAGATTCT CCTCCTTACC CCCAACCCAC TCTTTTTTCC CACCACCCAC TCTCCTCTGC  
2161 CTCAGTAAGT ATCTGGAGGA AGAAAACAGG TGAAAGAAGA AGTAAACC ATTATGATT  
2221 AGTATTAGAA TGAAGTCAAA CTGTGCCACA CATGGTGAAT GAAAAAAGG AAAAAAGAGG  
2281 TGTGTTTTGT CACACAGGGC AGTCATTGAG CACAGAGCA CGTGATGGTC TGAGACTCTC  
2341 TTAGGAGCAG AGCTCTGCCG CAATGGCCAT GTGGGGATCC ACACCTGGTC TGAGGGGCAA  
2401 CTGAGTCTGC GGGAGAAGAG CGGCCCTATG CATGGGTGAG ATGCCCTGAT AAAGAACATC  
2461 TGTCTGTGA AAGACTCAAT GAGCTGTTAT GTTGTAAACA GGAAGCATT CACATCCAAA  
2521 CGAGAAAATC ATGTAAACAT GTGTCTTTTC TGAGAGCAT AATAAATGGA TGAGGTTTTT  
2581 GCAAAAAA AAAAAA

## (2) INFORMATION FOR SEQ ID NO:2445:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7321 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2445:

1 AAATGATAGA CCGTCAATAA TTGTATAAT GCTTTTTAAA ATGAATGCTT TAAGCCGGGT  
61 GCAGTGCCTC ACATCTGTAA TCCCAGCACT TTGGAGCCGA GCGGGTGGAT TGTGTGAGGT  
121 CAGGAGTTCT AGACCAACCT GGCCAACATG GCAAAACCTC ACTCTCTACC AAAAATACAA  
181 AAATTAGCCA GGCATGGTGG CAGGCACCTG TGATCCAGC TACTCAGGAG GCTGAGACAG  
241 GAGAATCGCT TGAACCCGGG AGGCAAGGTT GCAGTGAGCC AAGATTACGC CATTGTACTC  
301 CAGCCTGGGT GACAGAGAGA GACTCCGTCT CAAAAAAGG AAAAAAAGG AAAAAATTAC  
361 GCTTCAACA CATGATCTCT CACCACTGTT GAATTTTCTT TCTATGAGCC CAGGAGGGCC  
421 TCTCAGAGAG GAAAGCTCCT AGGTCTTCTT TCCCTCTGC AACTCCCTG CCTTGAAGGT  
481 TCAGAAGGAC TGTGCGTGCT CGTTGCATCC TTTGCAAGTG TCCAAACCTT GATCCAGCT  
541 GTGCTTAGGG GTTCTGCAA ACCTTTTCCA GGTGTTAATT ACCTCCCTT TCATTTCCTG  
601 TTTACCAACT CAGCTTTTTG TTTTAGTGTG TTTGAATTCC CTGAAGTAC CGTTGTCTGA  
661 TCTCCACCTC CCAACTGAAT TAGGGGAGCT GGGCTTCTG AAACCCAGGT GCCGGGTGTT  
721 GCAGAGTGGC TGAAAGCTGG GATGTGGCAG ATCCGTGGCT ACATTCTATG ACACACACAC  
781 ACCACATAC CCACACATG ACACACACAC ACACACCCG ACTCACACAC TTGGACATGC  
841 ATAGACCACA GCTTCCACA CCCTTCTAG ACAGGGGTCA CTGGGTATCC TGGAGAGAGT  
901 GTGAAGTCCT GGAATGGAAA GAGGGGGGAT TAAGCCCCAC CTCTAGCCAT GGGACTGAGA  
961 CAAGTACCA CCAACCCATC TGCGCCTTGT TTACCTCTC TGTGAGGCAA GCACAGAGCC  
1021 CATGCCTGCC CCCCTGGATG GGAGTGATGT GAAACTTGAA GGGCGGTGAG AGCAAGGGTC  
1081 GGAATGGAA GGCCTTGGG AAAAAAGGCC CTTTCAACTA GGGGCACAGA GGAGGCCCTG  
1141 GGCTGAGAAC TTGACAGCAC CTTGTAATTG GTAAGCCAAG CCCGAAGGGA CTGGAATATC  
1201 TCAGATGTGT CTGTCTCCCT TATTAGGTTT AAAGTCCCTC AAGACCTGT CTCCATCACA  
1261 GTGCTCCAGT CCAGACCCCT CCTCTGAGCT CCAGACCTG CTGGACCCAA CCAGCCCTAT  
1321 GGGGTGCGAT CCCACCTGC CTGGAATTCT CCAAGAACC TCCCCTTTAA CAGTTCACG  
1381 CTTTAACAGT TCCAGTCTAA ACACATGACC TTTCTCTCT AAATCAGCCC CCCATCTCTG  
1441 CTTTGCAGG AGATGGAAGC CATGACACCT GCCTCGCCCC TGTCCTCACC CCATCCATGT  
1501 CCAATCAAGC ACTAGGCATG TCAGGTTTAC CCTCTAACT CCTCTGGAAT CCAGTCTCTC  
1561 AGTCTCCATC ATCCAGGTC GAAGCTAATG GGCTAACTGG TCCTTGCTTC CACTCTACCC  
1621 CCACTGCAGT CCTGACTTCC TGAGCAGCAG CCAGGGCCTA ATCGATATTC ACACCAAGCG  
1681 CCAACCTGAC TGAGATATCC TCCTGCACCA TCATCCCTCC ACCCTGTTTA GTTCTGCTCA  
1741 CCTCAGTGT TCTCATCAAT AATCCACTCC CCTCACAGG CCGTTTGGGA CCCCATGTTT  
1801 TATGCTCTCA CAGGACCTTT TGCTTGATTT TCACTGTAT TTAGGTGAGT TTGCAATTAT  
1861 TAAGTGACTG AGCAATGTCT GGCTTCTCCA GTAGACTGTC AGCTCCTAGC CATTGTATAC  
1921 CTAGCACCAG TGTGTGGGAG CAGTGACAA ACGTCCAGTG AGTCAGGGAC TCAGCAGTCT  
1981 CCATTTCTCC GCCCTGCTGG AGAATGCGTG TATTGGCAA TCCCCAGCCC CTGTGCCATC  
2041 TAACCATCTT TTCTTCTCTG TTCAGCCAG GTGTGGCCTC ACTCATATCC CACTCTGAGT  
2101 CCAATGTTC TCTCCCTGGA AGATATCAAT GTTCTGTCT GTTCGTGAGG ACTCCGTGCC  
2161 CACCACGGCC TCTTTCAGT GAGTCAAGG GATTCTCAG TCACTAGTT AGGGGAGGTG  
2221 GGCAGACACC CTGGAGAAT CCCTGGAAAG CTCAACTCTC ATGCCCGGA CAACAGTTGA  
2281 AGGAACCATG GTGATGTTAA GCCCAAAGAC AAAACCTCTC AGGTGTCCAA GTCCCTGTG  
2341 GAATCTTGGG AGCAGAGGGA ATGTTCTGTG GTCTAGAGGA AGAGGGGCTC AGGGAGGAGA  
2401 AGGGCACATT CTGGTTGTT ATATGTTTCT ATCTATCCA GATGAAGTTG GAAGTGAAGG  
2461 GAAGAGAGTT AAACATTAAT GTAAATACCC AGTGATCAG ACAGCAATGT GCCAGATTGC



2521 CTTGGAACA AAATATCTCC AACACATGGC TGACATTTGG TGGGAGATCA GAACACCCTA  
2581 AAGAGAGAAT TTAAGGGGAG GGGGAGGAGG ACCTGAGCCA GAGTAGAAGC AGAGGATAGG  
2641 GAGATCTGTT CTTGGGGACA GCATTGCAAA GAAACAAGGC TGAGGGGTCC ACTCCAACCT  
2701 CTCCACCCTG CTGCAGGTGC TGCCTATGAT GAAGATGAGC AGATGGCCAT CTCAGCTGGG  
2761 GCCACAGTGC ACTGACCTA TAGTTTCCAA TTCCGCACTC AGCAGGCATC TTTCTGATGA  
2821 TCCGATGGCT TCTCAGAGCC AGGGATGGGC CAGGATCCAT CCCCTTGGCT ACTGTCTTGC  
2881 TGAGAAATTT ATAAGCAGCA TCTGGTGCTA TACTTTGGTC TCTAGTGAGT TAGCTCATGA  
2941 AAGATGATAG ACTCTCCAAG CCAGGGGTAT GCAGGAAATG GGTTTTCTGT AGCTACAGAA  
3001 ATGGGGTTGA GGGTTGGACC AAGGGACTAC CCAGGGGAAG TCTTACCTTC AGAGGACTCT  
3061 GGAAGGAGG CTGCAAGTTT TCATGGGTCA AGAATTCAGA GCCCAGTAGA GACAGCTTAT  
3121 CTCTGTTCCTA AGATGTCTGG GGCCTTGGTT GGAAGATTCA AAGGCTAGGA AACCAGGAGC  
3181 CACCAAAAGC GTAACCTGGG CCAGAGGATC CACTTTCAAG GTGGCAAGTT GGTTCACCCC  
3241 ATGTGGCTGC TTGAGTATCC TCACATGGCG GCTCACATCC TTCCAAGTAA GCATGCAAA  
3301 AGGCCAAGAA AGATGCTGCA AAGATGTTAT GACCTAGCCT CAGAAATCAC ACACCATCCC  
3361 TGCCACCATT AGTAAGAAGT CCAGCCCAGG TCCAGGAGAA GAGGAAGCAG ATTCTCTCTT  
3421 TTGAAATGAA GAATATCAAG TAATTCCGGG GGCATATGAA AGCCACCACA CACCACAGG  
3481 ATCTTTTCTAG AGCATACTTC TTATACCATC ACTGTAGTTC CTTAAGACTC AGGGGCAAG  
3541 CCTCACTTCC TTAGCACCCA GTGAAGACCA CGCTTACTCC CTCACCTAAC CTCTTGCTAC  
3601 TTCCCACTC TCCTGTCCAA CATCTAGTGT CACTTTCCAG AACATACCAA CAGCTTCCCC  
3661 AGTTCTGTGC CTCTGCTCAG GCTGTTCCCC CTGCCTGGTC CACTTGCTCT CTCTCTTGTG  
3721 CGGTCAAAT GCTTCTTATC CTTCAGAGCC CAGCTCTAGA GTCACCTCCA ACCCCTTACC  
3781 CACCAGCCCC CTCTCCAAGT CTGTGTCCCA CAACCCCTCT GCTCCCTCCA GGGCACCCTC  
3841 CACCCTCTGG GCCACAGTTG TCAGGAGTCA GGCAGGGCAG GGGCCGGGTG GTGTCTTCTT  
3901 TGTGTTCTTG CACTCAGGCG AGAGCTCAGC ACAGAGCAGA CGCTCAAAAA ACATTTAAAG  
3961 GATAGAAGCA TTGATTTGTG GGTCCCCCAG TCTGGCTCCA GGATGCCAGC CAGCTGCTCC  
4021 TAGAAGCAAA CGGACTTTTC CTGGGAAATC CCAGAGGTGA TGATCAGTAA TCTCTCCCGT  
4081 GACTCGTAGT TCAGCTCTTC CTCCATGAGC CTGACTATCA GTGGACCTTC CAGAAAGAGC  
4141 CCCTTTTCTT TCTCTACCCC ACAGCAACAG GCACTGGGAA AATGCCCAAT GAGTCCTGCC  
4201 TCTGGGTTGT GCTTTGGACT TTTCAGTGTG TCTCGCATCC ACTCTTCAAC TTGAATGTTG  
4261 CAACAGCCAT GAAAAAGAA ATGCAAGCGG ATTCAGGATG AGAGCAATAC CCTACTCCAA  
4321 AGAAGGCAAC ATAGAAGCTC AGAGAGATCA AGCAATTTGC CCAAGACCAC CAGCTAGGA  
4381 GTGGAATCA TGGCTGTCCA AGCCCCATGC CTCTGCTGAA GGTAGAGATG AATTACAGCA  
4441 ACAAGTCTAG AAAGGTGCCT GCCCTATGGT CTGTGAGTCT TGCCTAAGAA TGAAAGAGGA  
4501 GCCAGTGGGT TAAAGATGAG GTCACCAACA ACGGTGGTGT TGGAGTTTAC CACTGATAAT  
4561 AAGGGTGCAA AATGTAATTT ACTAATGTTT ATTGAGCCTA GTGCAGTGCG TGGGGCATTT  
4621 TGCACATTGT CTCTGATCCC TATGACAACC CTGAGAGGTA GTGGTTTTAA CTGCCATGTT  
4681 ACAGGTGAGG TCATTGTGGT TCAAGGACGT TAAGTAACCT CCCAGCGTG ACACGGCTTA  
4741 TAAGTAAGGC AGCCAGGATG TGAACCCAGT AGGACTATCT GGCTGCAAG TCCCCACCCC  
4801 CCTCGCCATC TGTATCCTCC AATCACTTCA GTGCTTTGCT GCATAGAAG TAACGGAAAT  
4861 CACGATGCCA CAGACTGTCC AGGAAGACAG AAACCTAGGCA GATGGGCTGG CCATGGTCTC  
4921 CAAGCCAGAC TGGAATCTCC AGGTCTGGAA TGATATCATT TTTCTCTTTT AATAAATTAA  
4981 CTCACCCACC ACACGGCTTT GAGAGGCTCA AAGTTGACCA ACTCCCTTGG GAGGGCCCCG  
5041 GTTGATAAGG AAGGAACGTG AATCCTCCCA TCACGGAAGC TTCAAGGAGG TCAAGGTGCC  
5101 AACACTTGAG ATTGTTAGTG CTGTTGGTGG ATACTGGCCA AGGAAATATC CCAGTGGAGC  
5161 CTCGAGATGA AGAACATGAG GCCCCCGTTT AGAACCAAGG ATCAGAGGGG GCTCTGTAAG  
5221 ACCCAGGGGA GTCAGGTGCA CTGGAGCGCG GGCATGCAGA AAACAGCCTG AGCTCCACCT  
5281 CGGCTTCTCC TTGTCTTGGC TGGTTGTCTT TAACCCCTGT CTCCTTCTGG ACCAGTTTTT  
5341 GTCTTCCCT TGTGACCGCT GAGGGGTAAC AGCCTCTTTC CACTTTCTTT CAGCGCCGAC  
5401 ATGCTCAATG TCACCTTGCA AGGCCCCACT CTTAACGGGA CCTTTGCCCA GAGCAATGC  
5461 CCCCAAGTGG AGTGGCTGGG CTGGCTCAAC ACCATCCAGC CCCCTTCTCT CTGGGTGCTG  
5521 TTCGTGCTGG CCACCTAGA GAACATCTTT GTCCTCAGCG TCTTCTGCCT GCACAAGAGC  
5581 AGCTGCACGG TGGCAGAGAT CTACCTGGGG AACCTGGCCG CAGCAGACCT GATCCTGGCC  
5641 TGGGGGCTGC CTTTCTGGGC CATCACCATC TCCAACAAC TCGACTGGCT CTTTGGGGAG  
5701 ACGCTCTGCC GCGTGGTGAA TGCCATTATC TCCATGAACC TGTACAGCAG CATCTGTTTC  
5761 CTGATGCTGG TGAGCATCGA CCGTACCTG GCCCTGGTGA AAACCATGTC CATGGGCCGG  
5821 ATGCGCGGCG TGGCTGGGC CAAGCTCTAC AGCTTGGTGA TCTGGGGGTG TACGCTGCTC  
5881 CTGAGCTCAC CCATGCTGGT GTTCCGGACC ATGAAGGAGT ACAGCGATGA GGGCCACAAC  
5941 GTCACCGCTT GTGTCATCAG CTACCCATCC CTCATCTGGG AAGTGTTCAC CAACATGCTC  
6001 CTGAATGCTG TGGGCTTCTT GCTGCCCTG AGTGTATCA CCTTCTGCAC GATGCGATC  
6061 ATGCAGGTGC TGGGGAACAA CGAGATGCAG AAGTTCAAGG AGATCCAGAC GGAGAGGAGG  
6121 GCCACGGTGC TAGTCTGGT TGTGCTGCTG CTATTCATCA TCTGCTGGCT GCCCTTCCAG  
6181 ATCAGCACCT TCCTGGATAC GCTGCATCGC CTCGGCATCC TCTCCAGCTG CCAGGACGAG  
6241 CGCATCATCG ATGTAATCAC ACAGATCGCC TCCTTCATGG CCTACAGCAA CAGCTGCCCTC  
6301 AACCACCTGG TGTACGTGAT CGTGGGCAAG CGCTTCCGAA AGAAGTCTTG GGAGGTGTAC  
6361 CAGGGAGTGT GCCAGAAAGG GGGCTGCAGG TCAGAACCCA TTCAGATGGA GAACTCCATG  
6421 GGCACACTGC GGACCTCCAT CTCCGTGGAA CGCCAGATTC ACAAATGCA GGAATGGGCA  
6481 GGGAGCAGAC AGTGAGCAAA CGCCAGCAGG GCTGCTGTGA ATTTGTGTAA GGATTGAGGG  
6541 ACAGTTGCTT TTCAGCATGG GCCCAGGAAT GCCAAGGAGA CATCTATGCA CGACCTTGGG



6601 AAATGTTG ATGTCTCCGG TAAACACCG GAGACTAATT CCAGCCCTGC CCAATTTTGC  
 6661 AGGGAGCATG GCTGTGAGGA TGGGGTGAAC TCACGCACAG CCAAGGACTC CAAATCACA  
 6721 ACAGCATTAC TGTTCTTATT TGCTGCCACA CCTGAGCCAG CCTGCTCCTT CCCAGGAGTG  
 6781 GAGGAGGCCT GGGGGCAGGG AGAGGAGTGA CTGAGCTTCC CTCCCGTGTG TTCTCCGTCC  
 6841 CTGCCCCAGC AAGACAACTT AGATCTCCAG GAGAACTGCC ATCCAGCTTT GGTGCAATGG  
 6901 CTGAGTGCAC AAGTGAGTTG TTGCCCTGGG TTTCTTTAAT CTATTGAGCT AGAACTTTGA  
 6961 AGGACAATTT CTTGCATTAA TAAAGGTTAA GCCCTGAGGG GTCCCTGATA ACAACCTGGA  
 7021 GACCAGGATT TTATGGCTCC CCTCACTGAT GGACAAGGAG GTCTGTGCCA AAGAAGAATC  
 7081 CAATAAGCAC ATATTGAGCA CTGCTGTAT ATGCAGTATT GAGCACTGTA GGCAAGAGGG  
 7141 AAGAAAGAGA AGGAGCCATC TCCATCTTGA AGGAACTCAA AGACTCAAGT GGGAACTGCT  
 7201 GGGCACTGCC ACCACCAGAA AGCTGTTTGA TGAGACGGTC GAGCAGGGTG CTGTGGGTGA  
 7261 TATGGACAGC AGAAGGGGGA GCCAGGTTCC AGCTCACCAA TACTATTGCA CACCACCTGT  
 7321 CCTGCCTC

## (2) INFORMATION FOR SEQ ID NO:2446:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2221 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2446:

1 CTGCAGAAA CAGCCTGAGC TCCACCTCGG CTTCTCCTTG CCCTGGCTGG TTGTCCTTAA  
 61 CCCCTGTCTC CTTCTGGACC AGTTTTTGTC CTTCCCTGTG GACCCCTGAGG GGTAACAGCC  
 121 TCTTTTCCAC TTTCTTTTCA CGCCGACATG CTCAATGTCA CCTTGCAAGG GCCCCTCTT  
 181 AACGGGACCT TTGCCCAGAG CAAATGCCCC CAAGTGGAGT GGCTGGGCTG GCTCAACACC  
 241 ATCCAGCCCC CTTCTCTCTG GGTGCTGTTT GTGCTGGCCA CCTAGAGAA CATCTTTGTC  
 301 CTCAGCGTCT TCTGCCTGCA CAAGAGCAGC TGCACGGTGG CAGAGATCTA CCTGGGGAAC  
 361 CTGGCCGCAG CAGACCTGAT CCTGGCCTGC GGGCTGCCCT TCTGGGCCAT CACCATCTCC  
 421 AACAACTTCG ACTGGCTCTT TGGGGAAGCG CTCTGCCGCG TGGTGAATGC CATTATCTCC  
 481 ATGAACCTGT ACAGCAGCAT CTGTTCTCTG ATGCTGGTGA GCATCGACCG CTACCTGGCC  
 541 CTGGTGAAAA CCATGTCCAT GGGCCGGATG CGCGGCGTGC GCTGGGCCAA GCTCTACAGC  
 601 TTGGTGATCT GGGGGTGTAC GCTGCTCCTG AGCTCACCCA TGCTGGTGTG CCGGACCATG  
 661 AAGGAGTACA GCGATGAGGG CCACAACGTC ACCGCTTGTG TCATCAGCTA CCCATCCCTC  
 721 ATCTGGGAAG TGTTACCAA CATGCTCCTG AATGTCGTGG GCTTCCTGCT GCCCCTGAGT  
 781 GTCATCACCT TCTGCACGAT GCAGATCATG CAGGTGCTGC GGAACAACGA GATGCAGAAG  
 841 TTCAAGGAGA TCCAGACGGA GAGGAGGGCC ACGGTGCTAG TCCTGGTTGT GCTGCTGCTA  
 901 TTATCATCTT GCTGGCTGCC CTTCCAGATC AGCACCTTCC TGGATACGCT GCATCGCCTC  
 961 GGCATCCTCT CCAGCTGCCA GGACGAGCGC ATCATCGATG TAATCACACA GATCGCCTCC  
 1021 TTCATGGCCT ACAGCAACAG CTGCCTCAAC CCACTGGTGT ACGTGATCGT GGCAAGCGC  
 1081 TTCCGAAAGA AGTCTTGGGA GGTGTACCAG GGAGTGTGCC AGAAAGGGGG CTGCAGGTCA  
 1141 GAACCCATTG AGATGGAGAA CTCCATGGGC AACTGCGGA CCTCCATCTC CGTGAACGC  
 1201 CAGATTACAA AACTGCAGGA CTGGGCAGGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT  
 1261 GCTGTGAATT TGTGTAAGGA TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC  
 1321 AAGGAGACAT CTATGCACGA CCTTGGGAAA TGAGTTGATG TCTCCGGTAA AACACCGGAG  
 1381 ACTAATTCCT GNCCTGCCCA ATTTTGCAAG GAGCATGGCT GTGAGGATGG GGTGAATCA  
 1441 CGCACAGCCA AGGACTCCAA AATCACAACA GCATTACTGT TCTTATTTGC TGCCACACCT  
 1501 GAGCCAGCCT GCTCCTTCCC AGGAGTGGAG GAGGCCTGGG GGCAGGGAGA GGAGTACTG  
 1561 AGCTTCCCTC CCGTGTGTTT TCCGTCCCTG CCCAGCAAG ACAACTTAGA TCTCCAGGAG  
 1621 AACTGCCATC CAGCTTTGGT GCAATGGCTG AGTGACAAAG TGAGTTGTTG CCCTGGGTTT  
 1681 CTTTAATCTA TTCAGCTAGA ACTTTGAAGG ACAATTTCTT GCATTAATAA AGGTTAAGCC  
 1741 CTGAGGGGTC CTTGATAACA ACCTGGAGAC CAGGATTTTA TGGCTCCCCT CACTGATGGA  
 1801 CAAGGGAGGT CTGTGCCAAA GAAGAATCCA ATAAGCACAT ATTGAGCACT TGCTGTATAT  
 1861 GCAGTATTGA GCACTGTAGG CAAGAGGGAA GAAAGAGAAG GAGCCATCTC CATCTTGAAG  
 1921 GAACTCAAAG ACTCAAGTGG GAACGACTGG CACTGCCACC ACCAGAAAGC TGTTCCAGCA  
 1981 GACGGTCGAG CAGGGTGCTG TGGGTGATAT GGACAGCAGA AGGGGGAGAC CAAGGTTCCA  
 2041 GCTCAACCAA TAACTATTGC ACRAACCCT GTCCCTGCCT CAGTTCCCTC TTCTGTAAAC  
 2101 TGAAGTCGTT GTGAGGGTTA AAGGCAGTAA CAGGTATAAA GTACTTAGAA AAGCAAAGGG  
 2161 TGCTACGTAC ATGTGAGGCA TCATTACGCA GACGTAACCT GGATATGTTT ACTATAAGGA  
 2221 AAAGACACTG AGGTCTAGA

## (2) INFORMATION FOR SEQ ID NO:2447:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2461 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2447:

1 TGATCCTATC ACAACCTGAG AGTAGTTTTT ACTCCATTTA CAGGTGAGGT CATTGTGGTT  
 61 CAAGGACGTT AAGTAACTTC CCCAGCTCAC ACGGCTTATA AGTAAGGCAG CCAGGATGTG

```

121 AAGCCAGTAG GACTATCTGG CTGCAAAGTC CCCACCTCC CTGCCATCT GTATCTCTCA
181 ATCATCTTCA GTGCTTTGCT GATAGAAGGT ACGGAAATAC GATGCCACAG ACTGTCCAGG
241 AAGACAGAAA CTAGGCAGAT GGGCTGGCCA TGGTCTCAA GCCAGACTGG AATCTCCAGG
301 TCTGGAATGA TATCATTTTT CTCTTTTAAT AAATTAAGTC ACCCACCACA CGGCTTTGAG
361 AGGCTCAAAG GTGACCAACT CCCTTGGGAG GGCCCGGTT GATAAGGAAG GAATGTGAAT
421 CCTCCCATCA CGGAAGCTTC AAGGAGGTCA AGGGTCCAAC ACTTGAGATT GTTAGTGCTG
481 TTGGTGGATA CTGCAGAATA TCCAGTGGAG CCTCAGATGA AGAACATGAG GCCCCGTTTA
541 GATCCAAGGA TCAGAGGGGG CTCTGTAAGA CCCAGGGGAG TCAGGTGCAC TGGAGCGCGG
601 GCTGCAGAAA ACAGCCTGAG CTCCACCTCG GCTTCTCCTT GCCCTGGCTG GTTGTCTTCA
661 ACCCTGTCT CTTCTGGAC CAGTTTTTGT CTTCCCTTG TGACCTGAGG GGTAAACAGCC
721 TCTTTTCCAC TTTCTTTCAG CGCCGACATG CTCAATGTCA CCTTGCAAGG GCCCCTCTT
781 AACGGGACCT TTGCCAGAG CAAATGCCCC CAAGTGGAGT GGCTGGGCTG GCTCAACACC
841 ATCCAGCCCC CCTTCCTCTG GGTGCTGTTT GTGCTGGCCA CCCTAGAGAA CATCTTTGTC
901 CTCAGCGTCT TCTGCCTGCA CAAGAGCAGC TGCACGGTGG CAGAGATCTA CCTGGGGAAC
961 CTGGCCGAG CAGACCTGAT CTGGCCCTGC GGGCTGCCCT TCTGGGCCAT CACCATCTCT
1021 AACAACTTCG ACTGGCTCTT TGGGGAGACG CTCTGCCGCG TGGTGAATGC CATTATCTCC
1081 ATGAACCTGT ACAGCAGCAT CTGTTTCTTG ATGCTGGTGA GCATCGACCG CTACCTGGCC
1141 CTGGTGAAAA CCATGTCCAT GGGCCGATG CGCGGCGTGC GCTGGGCCAA GCTCTACAGC
1201 TTGGTGATCT GGGGGTGTAC GCTGCTCCTG AGCTCACCCA TGCTGGTGT CCAGACCATG
1261 AAGGAGTACA GCGATGAGGG CCACAACGTC ACCGCTTGTG TCATCAGCTA CCCATCCCTC
1321 ATCTGGGAAG TGTTCACCAA CATGCTCCTG AATGTCGTGG GCTTCTGCT GCCCTGAGT
1381 GTCATCACCT TCTGCAGAT GCAGATCATG CAGGTGCTGC GGAACAACGA GATGCAGAAG
1441 TTCAAGGAGA TCCAGACGGA GAGGAGGGCC ACGGTGCTAG TCCTGGTTGT GCTGCTGCTA
1501 TTCATCATCT GCTGGCTGCC CTTCCAGATC AGCACCTTCC TGGATACGCT GCATCGCCTC
1561 GGCATCCTCT CCAGCTGCCA GGACGAGCGC ATCATCGATG TAATCACACA GATCGCCTCC
1621 TTATGGCCT ACAGCAACAG CTGCCTCAAC CCACTGGTGT ACGTGATCGT GGGCAAGCGC
1681 TTCCGAAAGA AGTCTTGGGA GGTGTACCAG GGAGTGTGCC AGAAAGGGGG CTGCAGGTCA
1741 GAACCCATTC AGATGGAGAA CTCCATGGGC AACTGCGGA CCTCCATCTC CGTGGAACGC
1801 CAGATTCACA AACTGCAGGA CTGGGCAGGG AGCAGACAGT GAGCAACGC CAGCAGGGCT
1861 GCTGTGAATT TGTGTAAGGA TTGAGGGACA GTTGCTTTT AGCATGGGCC CAGGAATGCC
1921 AAGGAGACAT CTATGCACGA CCTTGGGAAA TGAGTGTGTA TGTCTCCGGT AAAACACCGG
1981 AGACTAATTC CTGCCCTGCC CAATTTTCGA GGGAGCATGG CTGTGAGGAT GGGGTGAACT
2041 CACGCACAGC CAAGGACTCC AAAATCACAA CAGCATTACT GTTCTTATTT GCTGCCACAC
2101 CTGAGCCAGC CTGCTCCTTC CCAGGAGTGG AGGAGGCCTG GGGGAGGGAG AGGAGTGACT
2161 GAGCTTCCCT CCCGTGTGTT CTCCGTCCCT GCCCCAGCAA GACAACCTAG ATCTCCAGGA
2221 GAACTGCCAT CCACGTTTGG TGCAATGGCT GAGTGCACAA GTGAGTTGTT GCCCTGGGTT
2281 TCTTTAATCT ATCAGCTAGA ACTTTGAAGG ACAATTTCTT GCATTAATAA AGGTTAAGCC
2341 CTGAGGGGTC CCTTGATAAC AACCTGGAGA CCAGGATTTT ATGGCTCCCC TCACTGATGG
2401 ACAAGGAGGT CTGTGCCAAA GAAGAATCAA TAAGCACATA TGAGCACTTC TGTATATCAG
2461 TATTGAGCAC TGTAGGCA

```

## (2) INFORMATION FOR SEQ ID NO:2448:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2448:

```

1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGCTGTTT GTGAGGACTC CGTGCCACC
61 ACGGCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTGC AAGGGCCAC TCTTAACGGG
121 ACCTTTGCCC AGAGCAAATG CCCCAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG
181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAATCTT TGTCTCAGC
241 GTCTTCTGCC TGCACAAGAG CAGCTGCAG GTGGCAGAGA TCTACCTGGG GAACCTGGCC
301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC
361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC
421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG
481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG
541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG GTTCCGGAC CATGAAGGAG
601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG
661 GAAGTGTTC CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCTT GAGTGTCTATC
721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG
781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCTGCG TTGTGCTGCT GCTATTCTATC
841 ATCTGCTGGC TGCCCTTCCA GATCAGACCC TTCCTGGATA CGCTGCATCG CCTCGGCATC
901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG
961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA
1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC
1081 ATTGAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT
1141 CACAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG
1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT T

```

## (2) INFORMATION FOR SEQ ID NO:2449:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2449:

```

1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTC GTGAGGACTC CGTGCCCACC
61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG
121 ACCTTTGCCC AGAGCAAATG CCCCAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG
181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCTCAGC
241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC
301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC
361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC
421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG
481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG
541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCGGCA CAGTAAGGAG
601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG
661 GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCTT GAGTGTCTATC
721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG
781 GAGATCCAGA CGAGAGGAG GGCCACGGTG CTAGTCCCTG TGTGCTGCT GCTATTCTATC
841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC
901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG
961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA
1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC
1081 ATTGAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT
1141 CACAACTGCA AGGACTGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG
1201 AATTGTGTA AGGATTGAGG GACAGTTGCT T

```

## (2) INFORMATION FOR SEQ ID NO:2450:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2450:

```

1 GCCCTTCAAA GATGAGCTGT TCCCGCCGCC ACTCCAGCTC TGGCTTCTGG GCTCCGAGGA
61 GGGGTGGGGA CGGTGGGGAC ATCAGGCTGC CCCGAGTAC CAGGGAGCGA CTGAAGTGCC
121 CATGCCGCTT GCTCCGGAGA AGGTGGGTGC CGGGCAGGGG CTGCTCCAGC CGCCTCACCT
181 CTGCTGGGAG GACAACTGT CCCAGCACAG AGGGAGGGAG GGAGGGCAGG CAGCGGGGAG
241 AAGTTTCCCT GTGGTCGTGG GGAGTT

```

## (2) INFORMATION FOR SEQ ID NO:2451:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2451:

```

1 GCCCTTCAAA GATGAGCTGT TCCCGCCGCC ACTCCAGCTC TGGCTTCTGG GCTCCGAGGA
61 GGGGTGGGGA CGGTGGTGAC GGTGGGGACA TCAGGCTGCC CCGCAGTACC AGGGAGCGAC
121 TGAAGTGCCC ATGCCGCTTG CTCCGGAGAA GGTGGGTGCC GGGCAGGGGC TGCTCCAGCC
181 GCCTCACCTC TGCTGGGAGG ACAAAGTGT CCAGCACAGA GGGAGGGAGG GAGGGCAGGC
241 AGCGGGGAGA AGTTTCCCTG TGGTCGTGGG GAGTT

```

## (2) INFORMATION FOR SEQ ID NO:2452:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1441 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2452:

```

1 GAGCTCTTCA ATATTTAGT GAAAGCTATA GATGAGGCTC CATAGGGGAT AAAGCACAGA
61 CACACCTTTT CAGAGGGCTT GTGGACTCTG GGCAGCCTGT CCATAGACCT CTGTCCCCAA
121 CTGGCAAGTC AGGAACTCC AGATTAAGGA GCCCAATGT GGTGAACAG CCAGGTGCAC
181 AGATGAGTCA ACCACACAGC CAGGCCAGGG AGGGCCTTCA CTCAAGAGCC TACAGCCAGT
241 TCACAGCCAA GCCAGGGCTA GCGCCAGGCC ACCCATAAAC TGATCTGAGA CTCTGTTTCC
301 CTGTCTCCAT GATGATGGGA TCAGGCTTGA TTGCTGGTTT GTAGGCTTGT TATGAATCAA
361 GTCACAGGGA AGAGGAGCTG ATGGGCTGGG GGGACGTCCT CTGGCCCTCC TGTCTCTTCC

```

421 CCAGATCCAC TGGGCCCACT CTTATCTGTT CTCTTCTGAA GGAAGGGTTT TAAGGCTTCA  
481 AAAAAAATG TTTTGAAAGT CCCTGCCCTT TCCAGCTCCT ACCGTCTCAG CCCTGGGAGT  
541 GTAAAGTGCT GCAGATAGTT AGTAAGTCTT TGAGCAAAC TGAGAAAGCC AGCCTGAGCC  
601 TTGACATGGG AGAAACCTCC GCCATACATC TCCGAAGAAA CGGCCGCGTG TCTCAGGGGA  
661 GCGCAAACAC CCGTACCCAG GAAACAGGAC AGCTTCTGCC ACTGTGCGCC TTGGGAGCCG  
721 TACGTGGCAT GACAAAGAAA TCCAGGACT CCGCCTGCCC ACCTGGCCAC CCTCTGTTTA  
781 CACCTTCCGC GTAAACGCCC ACTGTTTACA TCCAAACTC AGACACAAAA TAACCACCTC  
841 AAGAAGATAA ATAATGATAA GAAATAAATG TTACGCGAGG CAAATTTATT CACATGGGGC  
901 TTCCAGGCC ACTTTGTGGT CAGCCGGGAG GGACGTTTTT GCCGTCCCAC GACTCCAACG  
961 GGCAGCCGGG CCTACGCAAA CATGGAAATC TTCCAAGAGC CTCCTGGCC CCCAGGGCTC  
1021 AGAGGGTGGC AGAGCGGAGA GCGAAGGTGG CCGCAGCCTT CCCGGCCCCA CAGCCAGCCT  
1081 GGCTCCAGCT GGGCAGGAGT GCAGAGCTCA GCTGGAGGCG AGGGGGAAGT GCCCAGGAGG  
1141 CTGATGACAT CACTACCCAG CCCTTCAAAG ATGAGCTGTT CCGCCGCCA CTCCAGCTCT  
1201 GGCTTCTGGG CTCCGAGGAG GGGTGGGGAC GGTGGTGACG GTGGGGACAT CAGGCTGCCC  
1261 CGCAGTACCA GGGAGCGACT GAAGTGCCCA TGCCGCTTGC TCCGGAGAAG GTGGGTGCCG  
1321 GGCAGGGGCT GCTCCAGCCG CCTCACCTCT GCTGGGAGGA CAAACTGTCC CAGCACAGAG  
1381 GGAGGGAGGG AGGGCAGGCA GCGGGGAGAA GTTTCCTGT GGTGCTGGGG AGTTGGGAAA  
1441 AGTTCCCTTC CTTCCGGAGG GAGG

## (2) INFORMATION FOR SEQ ID NO:2453:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2581 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO:2453:

1 CAGATTCACA AACTGCAGGA CTGGGCAGGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT  
61 GCTGTGAATT TGTGTAAGGA TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC  
121 AAGGAGACAT CTATGCACGA CCTTGGGAAA TGAGTTGATG TCTCCGGTAA AACACCGGAG  
181 ACTAATTCCT GCCCTGCCCA ATTTTGCAAG GAGCATGGCT GTGAGGATGG GGTGAATCA  
241 CGCACAGCCA AGGACTCCAA AATCACAACA GCATTACTGT TCTTATTTGC TGCCACACCT  
301 GAGCCAGCCT GTCCTTCCC AGGAGTGGAG GAGGCCTGGG GGGAGGGAGA GGAGTGAATG  
361 AGCTTCCCTC CCGTGTGTTT TCCGTCCCTG CCCCAGCAAG ACAACTTAGA TCTCCAGGAG  
421 AACTGCCATC CAGCTTTGGT GCAATGGCTG AGTGACAAAG TGAGTTGTTG CCCTGGGTTT  
481 CTTTAATCTA TTCAGCTAGA ACTTTGAAGG ACAATTTCTT GCATTAATAA AGGTTAAGCC  
541 CTGAGGGGTC CCTGATAACA ACCTGGAGAC CAGGATTTTA TGGCTCCCTT CACTGATGGA  
601 CAAGGAGGTC TGTGCCAAAG AAGAATCCAA TAAGCACATA TTGAGCACTT GCTGTATATG  
661 CAGTATTGAG CACTGTAGGC AAGACCCAAG AAAGAGAAGG AGCCATCTCC ATCTTGAAGG  
721 AACTCAAAGA CTCAAGTGGG AACGACTGGG CACTGCCACC ACCAGAAAGC TGTTCGACGA  
781 GACGGTCGAG CAGGGTGCTG TGGGTGATAT GGACAGCAGA AGGGGGAGAC CAAGGTTCCA  
841 CTTCAACCAA TAATATTGC ACAACCACCT GTCCCTGCCT CAGTTCCCTT TTATGTAACA  
901 TGAAGTCGTT GTGAGGGTTA AAGGCAGTAA CAGGTATAAA GACTTGAAGA AGGCAAGGG  
961 TGCTACGTAC ATGTGAGGCA TCATTACGCA GACGTAAGTG GGATATGTTT ACTATAAGGA  
1021 AAAGACACTG AGGTCTAGAA ATAGCTCCGT GGAGCAGAAT CAGTATTGGG AGCCGGTGGC  
1081 GGTGTGAAGC ACCAGTGTCT GGCACACAGT AGGTGCTCAT TGGCTCCCTT CCACCTGTCA  
1141 TTCCCAACAC CCTGAGGCC CAACCGCCAC ACACACAGGA GCATTTGGAG AGAAGGCCAT  
1201 GTCTTCAAAG TCTGATTTGT GATGAGGACG AGGAAGATAT TTCTAATCGG TCTTGCCAG  
1261 AGGATCACAG TGCTGAGACC CCCCACCACC AGCCGGTACC TGGGAAGGGG GAGAGTGCAG  
1321 GCCTGTCTAG GACTGTCTCC TGCTCAGCA ACCAAGGGAT TGTTCTGTG AATCAATGGT  
1381 TTATTGGAAG GTGGCCAGT ATGAGCCCTA GAAGAGTGTG AAAAGGAATG GCAATGGTGT  
1441 TCACCATCGG CAGTGCCAGG GCAGCACTCA TTCACCTGAT AAATGAATAT TTATTAGCTG  
1501 GTTGAGAGC TAGAACCTGG AGAGCTAGAA CCTGGAGAAC TAGAACCTGG AGGGCTAGAA  
1561 CCTGGAGAGG CTAGAACCAA GAAGGCTAG AACCTGGAGG GGCTAGAACC TAGAGAAGCT  
1621 AAAACCTGAG CTAGAAGCTG GAGGACTAGA ACCTGGAGGG CTGGAATCTG AAGGGCTAGA  
1681 ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG GAGGGCTAGA  
1741 CTTAGAAGG GCTAGAACCT GGAGGGCTGG AATCTGGAGA GCTAGAACCT GGAGGGCTAG  
1801 AACCTGGAGG GCTAGAACCT AGAAGGGCTA GAACCTGGAG GGCTAGAACC TGGCAGGTTA  
1861 GAACCTAGAA GGGCTAGAAC CTGGAGAGCC AGAACCTGGA GGGCTAGAAC CTGGAAGGGC  
1921 TAGAACCTGT AGAGCTAGAA CATGGAGAGC TAGAACCCGG CAGGCTAGAA CCTGGCAAGC  
1981 TAGAACCTGG AGGGAATGAA CCTGGAGGGC TAGAACCTGG AGAATGAGAA AAATTTACAT  
2041 GGCAAAGAGC CCATAAATCC TGACCAATCC AACTCTGAAT TTTAAAGCAA AAGCGTGAAA  
2101 AAAAAGATT CCTCCTTACC CCCAACCCAC TCTTTTTTCC CACCACCCAC TCTCCTCTGC  
2161 CTCAGTAAGT ATCTGGAGGA AGAAAAAGG TGAAAGAAGA AGTAAAAACC ATTTAGTATT  
2221 AGTATTAGAA TGAAGTCAA CATGTGCCACA CATGGTGAAT GAAAAAAGG AAGAAAGAGC  
2281 TGTGTTTTGT CACACAGGGC AGTCATTGAG CACCAGAGCA CGTGATGGTC TGAGACTCTC  
2341 TTAGGAGCAG AGCTCTGCCG CAATGGCCAT GTGGGGATCC ACACCTGGTC TGAGGGGCAA  
2401 CTGAGTCTGC GGGAGAAGAG CGGCCCTATG CATGGTGTAG ATGCCCTGAT AAAGAACATC  
2461 TGTCTGTGA AAGACTCAAT GAGCTGTTAT GTTGTAACA GGAAGCATTT CACATCCAAA  
2521 CGAGAAAATC ATGTAAACAT GTGCTTTTTC TGTAGAGCAT AATAAATGGA TGAGGTTTTT

2581 GCAAAAAAAA AAAAAAAAAA

## (2) INFORMATION FOR SEQ ID NO:2454:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7321 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2454:

1 AAATGATAGA CCGTCAATAA TTTGTTAAAT GCTTTTAAAT ATGAATGCTT TAAGCCGGGT  
61 GCAGTGCCTC ACATCTGTAA TCCCAGCACT TTGGAGCCGA GCGGGTGGAT TGTGTGAGGT  
121 CAGGAGTTCG AGACCAACCT GGCCAACATG GCAAAACCTC ACTCTCTACC AAAAATACAA  
181 AAATTAGCCA GGCATGGTGG CAGGCACCTG TGATCCAGC TACTCAGGAG GCTGAGACAG  
241 GAGAATCGCT TGAACCCGGG AGGCAAGGTT GCAGTGAGCC AAGATTACGC CATTGTACTC  
301 CAGCCTGGGT GACAGAGAGA GACTCCGTCT CAAAAAATAA AAAAAAATTAC  
361 GCTTCAAACA CATGATCTCT CACCAGTGT GAATTTTCTT TCTATGAGCC CAGGAGGGCC  
421 TCTCAGAGAG GAAAGCTCCT AGGTCTTCCT TTCCCTCTGC AAACCTCCCTG CCTTGAAGGT  
481 TCAGAAGGAC TGTGCGTGCT CGTGCATCC TTTGCAAGTG TCCAAACCTT GATCCAGCT  
541 GTGCTTAGGG GTTCTGCAA ACCTTTTCCA GGTGTAATT ACCTCCCACT TCATTTCTCTG  
601 TTTACCAACT CAGCTTTTGG TTTTAGTGTG TTTGAATTCC CTGAAGTAC CGTTGTCTGA  
661 TGTCCACCTC CCAACTGAAT TAGGGGAGCT GGGCTTCTGG AAACCCAGGT GCCGGGTGTT  
721 GCAGAGTGGC TGAAAGCTGG GATGTGGCAG ATCCGTGGCT ACATTCATGC ACACACACAC  
781 ACCCACATAC CCACACATGC ACACACACAC ACACACCCGC ACTCACACAC TTGGACATGC  
841 ATAGACCACA GCTTTCACA CCCTTCCTAG ACAGGGGTCA CTTGGTATCC TGGAGAGAGT  
901 GTGAAGTCTT GGAATGGAAA GAGGGGGGAT TAAGCCCCAC CTCTAGCCAT GGGACTGAGA  
961 CAAGTCACCA CCAACCCATC TGCGCCTTGT TTACCTCCTC TGTGAGGCAA GCACAGAGCC  
1021 CATGCCGTGCC CCCCTGGATG GGAGTGATGT GAAACTTGAA GGGCGGTGAG AGCAAGGGTC  
1081 GGAATGGAA GGCCTTGGG AAAAAAGGCC CTTCAACTA GGGGCACAGA GGAGGCCCTG  
1141 GGCTGAGAAC TTGACAGCAC CTTGTAATTG GTAAGCCAAG CCCGAAGGGA CTGGAATAC  
1201 TCAGATGTGT CTGTCTCCCT TATTAGGTTT AAAGTCCCTC AAGACCTGT CTCCATCACA  
1261 GTGCTCCAGT CCAGACCCCT CCTCTGAGCT CCAGACCCCTG CTGGACCCAA CCAGCCCTAT  
1321 GGGGTGCGAT CCCACCTGC CTGGAATTCT CCAAAGAACC TCCCCTTTAA CAGTTCCAGC  
1381 CTTTAACAGT TCCAGTCTAA ACACATGACC TTTCTCCTCT AAATCAGCCC CCCATCTCTG  
1441 CCTTTGCAGG AGATGGAAGC CATGACACCT GCCTCGCCCC TGCTCTCACC CCATCCATGT  
1501 CCAATCAAGC ACTAGGCATG TCAGGTTTAC CCTCTAACT CCTCTGGAAT CCAGTCTCTC  
1561 AGTCTCCATC ATCCCAGGTG GAAGCTAATG GGCTAAGTGG TCCTTGCTTC CACTCTACCC  
1621 CCACTGCAGT CCTGACTTCC TGAGCAGCAG CCAGGGCCTA ATCGATATTC ACACCAAGCG  
1681 CCAACCTGAC TGAGATATCC TCCTGCACCA TCATCCCTCC ACCCTGTTTA GTTCTGCTCA  
1741 CCCTCAGTGT TCTCATCAAT AATCCACTCC CCTCACAGGC GCGTTTGGGA CCCCATGTTC  
1801 TATGCTCTCA CAGGACCTTT TGCTTGATTT TCACTGTAC TTAGGTCACT TTGCAGTTAT  
1861 TAAGTGACTG AGCAATGTCT GGCTTCTCCA GTAGACTGTC AGCTCCTAGC CATTGTATAC  
1921 CTAGCACCGC TGTGTGGGAG CACGTGACAA ACGTCCAGTG AGTCAGGGAC TCAGCAGTCT  
1981 CCATTTCTCC GCCCTGCTGG AGAATGCGTG TATTTGGCAA TCCCCAGCCC CTGTGCCATC  
2041 TAACCATCTT TTCTTCTCTG TTCAGCCCAG GTGTGGCCTC ACTCACATCC CACTCTGAGT  
2101 CCAATGTTC TCTCCCTGGA AGATATCAAT GTTCTGTCT GTTCGTGAGG ACTCCGTGCC  
2161 CACCACGGCC TCTTTCAGGT GAGTCAAAGG GATTCCTCAG TTTCACTAGT AGGGGAGGTG  
2221 GGCAAGACAC CTGGAGAACT CCCTGGAAAG CTCAACTCTC ATGCCCCGGA CAACAGTTGA  
2281 AGGAACCATG GTGATGTTAA GCCCCAAGAC AAAACCTCTC AGGTGTCCAA GTCCCTGTTG  
2341 GAATCTTGGG AGCAGAGGGA ATGTTCTGTG GTCTAGAGGA AGAGGGGCTC AGGGAGGAGA  
2401 AGGGCAGATT CCTGGTTGTT ATATGTTTCT ATCTATCCCA GATGAAGTGT GAAGTGAAGG  
2461 GAAGAGAGTT AAACATTAAT GTAAATACCC AGTGGATCAG ACAGCAATGT GCCAGATTGC  
2521 CTTGGAAACA AAATATCTCC AACACATGGC TGACATTTGG TGGGAGATCA GAACACCCTA  
2581 AAGAGAGAAT TTAAGGGGAG GGGGAGGAGG ACCTGAGCCA GAGTAGAAGC AGAGGATAGG  
2641 GAGATCTGTT CTTGGGGACA GCATTTGCAA GAAACAAGGC TGAGGGGTCC ACTCCAACCT  
2701 CTCCACCCCTG CTGCAGGTGC TGCTATGAT GAAGATGAGC AGATGGCCAT CTCAGCTGGG  
2761 CACCAAGTGC ACTGGACCTA TAGTTTCCAA TTCCGCACTC AGCAGGCATC TTTCTGATGA  
2821 TCCGATGGCT TCTCAGAGCC AGGGATGGGC CAGGATCCAT CCCCTTGGCT ACTGTCTTGC  
2881 TGAGAAATTT ATAAGCAGCA TCTGGTGCTA TACTTTGGTC TCTAGTAGT TAGCTCATGA  
2941 AAGATGATAG ACTCTCCAAG CCAGGGGTAT GCAGGAAATG GGTTTTCTGT AGCTACAGAA  
3001 ATGGGGTTGA GGGTGGACC AAGGGACTAC CCAGGGGAAG TCTTACCTTC AGAGGACTCT  
3061 GGAAAGGAGG CTGCAAGTTT TCATGGGTCA AGAATTCAGA GCCCAGTAGA GACAGCTTAT  
3121 CTCTGTTCCA AGATGTCTGG GGCCTTGGTT GGAAGATTCA AAGGCTAGGA AACCAGGAGC  
3181 CACCAAAAGC GTAAGTGGG CCAGAGGATC CACTTTCAAG GTGGCAAGTT GGTTCCTCCC  
3241 ATGTGGCTGC TTGAGTATCC TCACATGGCG GCTCACATCC TTCCAAGTAA GCAATGCAAA  
3301 AGGCCAAGAA AGATGCTGCA AAGATGTTAT GACCTAGCCT CAGAAATCAC ACACATCCC  
3361 TGCCACCATT AGTAAGAAGT CCAGCCACG TCCAGGAGAA GAGGAAGCAG ATTCCTCCTT  
3421 TTGAAATGAA GAATATCAAG TAATTCGGGG GGCATATGAA AGCCACCACA CACCACAGGG  
3481 ATCTTTTATG AGCATACTTC TTATACCATC ACTGTAGTTC CTTAAGACTC AGGGGCAAG  
3541 CCTCACTTCC TTAGCACCCA GTGAAGACCA CGCTTACTCC CTCCTCAAC CTCTTGCTAC

3601 TTCCACCTC TCCTGTCCAA CATCTAGTGT CACTTTCCAG AACATACCAA CAGCTTCCCC  
3661 AGTTCTGTGC CTCTGCTCAG GCTGTTCCTC CTGCCTGGTC CACTTGTCTT CCTTCTTGTC  
3721 CGGTCAAAT GCTTCTTATC CTTCAAGACC CAGCTCTAGA GTCACCTCCA ACCCCTTACC  
3781 CACCAGCCCC CTCTCCAAGT CTGTGTCCCA CAACCCCTCT GCTCCCTCCA GGGCACCCTC  
3841 CACCCCTCTGG GCCACAGTTG TCAGGAGTCA GGCAGGGCAG GGGCCGGGTG GTGTCTTCTT  
3901 TGTATTCTTG CACTCAGGGC AGAGCTCAGC ACAGAGCAGA CGCTCAAAAA ACATTTAAAG  
3961 TAGAGAAGCA TTGATTTGTG GGTCCCCCAG TCTGGCTCCA GGATGCCAGC CAGCTGCTCC  
4021 TAGAAGCAAA CGGACTTTTC CTGGGAAATC CCAGAGGTGA TGATCAGTAA TCTCTCCGT  
4081 GACTCGTAGT TCAGCTCTTC CTCCATGAGC CTGACTATCA GTGGACCTTC CAGAAAGAGC  
4141 CCCTTTTCTT TCTCTCACC ACAGCACAGG GCACTGGGAA AATGCCCAAT GAGTCTGCTC  
4201 TCTGGGTGTG GCTTTGGACT TTTCTAGTGT TCTCGCATCC ACTCTTCAAC TTGAATGTTG  
4261 CAACAGCCAT GAAAAAGAA ATGCAAAGCG ATTCAAGATG AGAGCAATAC CCTACTCCAA  
4321 AGAAGGCAAC ATAGAAGTCA AGAGAGATCA AGCAATTGTC CCAAGACCAC ACAGCTAGGA  
4381 GTGGAACTCA TGGCTGTCCA AGCCCATGCT CTCTGCTGAA GGTAGAGATG AATTACAGCA  
4441 ACAAGTCTAG AAAGGTGCCT GCCCTATGGT CTGTGAGTCT TGCTAAGAA TGAAAGAGGA  
4501 GCCAGTGGGT TAAAGATGAG GTCACCAACA ACGGTGGTGT TGGAGTTTAC CACTGATAAT  
4561 AAGGGTGCAA AATGTAAATT ACTAATGTTT ATTGAGCCTA GTGCACTGCG TGGGGCATT  
4621 TGACATTGT CTCTGATCCC TATGACAACC CTGAGAGGTA GTGTTTTTAA CTGCCATGTT  
4681 ACAGGTGAGG TCATTGTGGT TCAAGGACGT TAAGTAACTT CCCAGCGTG ACACGGCTTA  
4741 TAAGTAAGGC AGCCAGGATG TGAACCCAGT AGGACTATCT GGCTGCAAAG TCCCCACCCC  
4801 CCTCGCCATC TGTATCTTCC AATCACTTCA GTGCTTTGCT GCATAGAAGG TAACGGAAAT  
4861 CACGATGCCA CAGACTGTCC AGGAAGACAG AAAGTGGCA GATGGGCTG CCATGGTCTC  
4921 CAAGCCAGAC TGAATCTCC AGGTCTGGAA TGATATCATT TTTCTCTTTT AATAAATTAA  
4981 CTCACCCACC ACACGGCTTT GAGAGGCTCA AAGTTGACCA ACTCCCTTGG GAGGGCCCCG  
5041 GTTGATAAGG AAGGAACGTG AATCCTCCCA TCACGGAAGC TTCAAGGAGG TCAAGGTCC  
5101 AACACTTGAG ATTGTTAGTG CTGTTGGTGG ATACTGGCCA AGGAAATATC CCAGTGAGGC  
5161 CTCGAGATGA AGAATCATGAG GCCCCGTTT AGAACCAAGG ATCAGAGGGG GCTCTGTAAG  
5221 ACCGAGGGA GTCAGGTGCA CTGGAGCGCG GGCATGCAGA AAACAGCCTG AGCTCCACCT  
5281 CGGCTTCTCC TTGTCTGGC TGGTTGCTCT TAACCCCTGT CTCTTCTGG ACCAGTTTTT  
5341 GTCCTTCCCT TGTGACCGCT GAGGGGTAAC AGCCTCTTTC CACTTTCTTT CAGCGCCGAC  
5401 ATGCTCAATG TCACCTTGCA AGGGCCACT CTTAACGGGA CCTTTGCCCA GAGCAAATGC  
5461 CCCCAAGTGG AGTGGCTGGG CTGGCTCAAC ACCATCCAGC CCCCTTCTCT CTGGGTGCTG  
5521 TTCGTGCTGG CCACCTAGA GAACATCTTT GTCCTCAGCG TCTTCTGCTT GCACAGAGC  
5581 AGCTGCACGG TGGCAGAGAT CTACCTGGGG AACCTGGCCG CAGCAGACCT GATCCTGGCC  
5641 TCGGGGCTGC CCTTCTGGGC CATCACCATC TCCAACAAT TCGACTGGCT CTTTGGGGAG  
5701 ACGCTCTGCC GCGTGGTGA TGCATTATC TCCATGAACC TGTACAGCAG CATCTGTTTC  
5761 CTGATGCTGG TGAGCATCGA CCGCTACCTG GCCCTGGTGA AAACCATGTC CATGGGCCGG  
5821 ATGCGCGGCG TCGCTGGGC CAAGCTCTAC AGCTTGGTGA TCTGGGGGTG TACGCTGCTC  
5881 CTGAGCTCAC CCATGCTGGT GTTCCGGACC ATGAAGGAGT ACAGCGATGA GGGCCACAAC  
5941 GTCACCGCTT GTGTATCAG CTACCCATCC CTCACTCTGG AAGTGTTCAC CAACATGCTC  
6001 CTGAATGTCG TGGGCTTCTT GCTGCCCCTG AGTGTCTATCA CCTTCTGCAC GATGCGATC  
6061 ATGAGGTGTC TCGGAACAA CGAGATGCAG AAGTTCAAG AGATCCAGC GGAGAGGAGG  
6121 GCCACGGTGC TAGTCTGGT TGTGCTGCTG CTATTCATCA TCTGCTGCTT CCCTTCCAG  
6181 ATCAGCACCT TCCTGGATAC GCTGCATCGC CTCGGCATCC TCTCCAGCTG CCAGGACGAG  
6241 CGCATCATCG ATGTAATCAC ACAGATCGCC TCCTTCATGG CCTACAGCAA CAGCTGCCTC  
6301 AACCACCTGG TGTACGTGAT CGTGGGCAAG CGCTTCCGAA AGAAGTCTTG GGAGGTGTAC  
6361 CAGGGAGTGT GCCAGAAAGG GGGCTGCAGG TCAGAACCCA TTCAGATGGA GAACTCCATG  
6421 GGCACACTGC GGACCTCCAT CTCCGTGGAA CGCCAGATTC ACAAATGCA GGAATGGGCA  
6481 GGGAGCAGAC AGTGAGCAA CGCCAGCAGG GCTGCTGTGA ATTTGTGTA GGATTGAGGG  
6541 ACAGTTGCTT TTCAGCATGG GCCAGGAAT GCCAAGGAGA CATCTATGCA CGACCTTGGG  
6601 AAATGAGTTG ATGTCTCCGG TAAAACACCG GAGACTAATT CCTGCCCTGC CCAATTTTGC  
6661 AGGGAGCATG GCTGTGAGGA TGGGGTGAAC TCACGCACAG CCAAGGACTC CAAAATCACA  
6721 ACAGCATTAC TGTCTTATT TGCTGCCACA CCTGAGCCAG CCTGCTCCTT CCCAGGAGTG  
6781 GAGGAGGCTT GGGGCGAGG AGAGGAGTGA CTGAGCTTCC CTCCCGTGTG TTCTCCGTCC  
6841 CTGCCCCAGC AAGACAATT AGATCTCCAG GAGAACTGCC ATCCAGCTTT GGTGCAATGG  
6901 CTGAGTGAC AAGTGAGTTG TTGCCCTGGG TTTCTTTAAT CTATTCAGCT AGAATTTGA  
6961 AGGACAATTT CTGCAATTAA TAAAGTTAA GCCCTGAGG GTCCCTGATA ACAACCTGGA  
7021 GACCAGGATT TTATGGCTCC CCTCACTGAT GGACAAGGAG GTCTGTGCCA AAGAAGAATC  
7081 CAATAAGCAC ATATTGAGCA CTTGCTGTAT ATGCAGTATT GAGCACTGTA GGCAAGAGGG  
7141 AAGAAAGAGA AGGAGCCATC TCCATCTTGA AGGAACTCAA AGACTCAAGT GGGAAAGACT  
7201 GGGCACTGCC ACCACCAGAA AGCTGTTTGA TGAGACGGTC GAGCAGGGTG CTGTGGGTGA  
7261 TATGGACAGC AGAAGGGGGA GCCAGGTTCC AGCTCACCAA TACTATTGCA CACCACCTGT  
7321 CCTGCCTC

## (2) INFORMATION FOR SEQ ID NO:2455:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2221 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2455:

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1 CTGCAGAAAA CAGCCTGAGC TCCACCTCGG CTTCTCCTTG CCCTGGCTGG TTGTCCTTAA
61 CCCCTGTCTC CTTCTGGACC AGTTTTTGTG CTTCCCTTGT GACCTGAGG GGTAACAGCC
121 TCTTTTCCAC TTTCTTTTCA CGCCGACATG CTCAATGTCA CCTTGCAAGG GCCACTCTT
181 AACGGGACCT TTGCCAGAG CAAATGCCCC CAAGTGGAGT GGCTGGGCTG GCTCAACACC
241 ATCCAGCCCC CTTCTCTCTG GGTGCTGTTC GTGCTGGCCA CCCTAGAGAA CATCTTTGTC
301 CTCAGCGTCT TCTGCCTGCA CAAGAGCAGC TGCACGGTGG CAGAGATCTA CCTGGGGAAC
361 CTGGCCGCGAG CAGACCTGAT CCTGGCCTGC GGGCTGCCCT TCTGGGCCAT CACCATCTCC
421 AACAACTTCG ACTGGCTCTT TGGGGAGACG CTCTGCCCGG TGGTGAATGC CATTATCTCC
481 ATGAACCTGT ACAGCAGCAT CTGTTTCTTG ATGCTGGTGA GCATCGACCG CTACCTGGCC
541 CTGGTGAAAA CCATGTCCAT GGGCCGGATG CGCGCGGTGC GCTGGGCCAA GCTCTACAGC
601 TTGGTGATCT GGGGGTGATC GCTGCTCCTG AGCTCACCCA TGCTGGTGTT CCGGACCATG
661 AAGGAGTACA GCGATGAGGG CCACAACGTC ACCGCTTGTG TCATCAGCTA CCCATCCCTC
721 ATCTGGGAAG TGTTCACCAA CATGCTCCTG AATGTCGTGG GCTTCCTGCT GCCCTGAGT
781 GTCATCACCT TCTGCACGAT GCAGATCATG CAGGTGCTGC GGAACAACGA GATGCGAAG
841 TTCAAGGAGA TCCAGACGGA GAGGAGGGCC ACGGTGCTAG TCCTGGTTGT GCTGCTGCTA
901 TTCATCATCT GCTGGCTGCC CTTCCAGATC AGCACCTTCC TGGATACGCT GCATCGCCTC
961 GGCATCCTCT CCAGCTGCCA GGACGAGCGC ATCATCGATG TAATCACACA GATCGCCTCC
1021 TTCATGGCCT ACAGCAACAG CTGCCTCAAC CCACTGGTGT ACGTGATCGT GGGCAAGCGC
1081 TTCCGAAAGA AGTCTTGGGA GGTGTACCAG GGAGTGTGCC AGAAAGGGGG CTGCAGGTCA
1141 GAACCCATTC AGATGGAGAA CTCCATGGGC AACTGCGGA CCTCCATCTC CGTGGAAACG
1201 CAGATTACCA AACTGCAGGA CTGGGACAGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT
1261 GCTGTGAATT TGTGTAAGGA TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC
1321 AAGGAGACAT CTATGCACGA CCTTGGGAAA TGAGTTGATG TCTCCGGTAA AACACCGGAG
1381 ACTAATTCCT GNCCTGCCCA ATTTTGAGG GAGCATGGCT GTGAGGATGG GGTGAACCTA
1441 CGCACAGCCA AGGACTCCAA AATCACAACA GCATTACTGT TCTTATTGTC TGCCACACCT
1501 GAGCCAGCCT GCTCCTTCCC AGGAGTGGAG GAGGCCTGGG GGCAGGGAGA GGAGTGACTG
1561 AGCTTCCCTC CCGTGTGTTT TCCGTCCCTG CCCAGCAAG ACAACTTAGA TCTCCAGGAG
1621 AACTGCCATC CAGCTTGGT GCAATGGCTG AGTGACAAAG TGAGTTGTTT CCCTGGGTTT
1681 CTTAATCTA TTCAGCTAGA ACTTTGAAGG ACAATTTCTT GCATTAATAA AGGTAAAGCC
1741 CTGAGGGGTC CCTGATAACA ACCTGGAGAC CAGGATTTTA TGCTCCCCCT CACTGATGGA
1801 CAAGGGAGGT CTGTGCCAAA GAAGAATCCA ATAAGCACAT ATTGAGCACT TGCTGTATAT
1861 GCAGTATTGA GCACTGTAGG CAAGAGGGAA GAAAGAGAAG GAGCCATCTC CATCTTGAAG
1921 GAACTCAAAG ACTCAAGTGG GAACGACTGG CACTGCCACC ACCAGAAAGC TGTTCGACGA
1981 GACGGTCGAG CAGGGTGTG TGGGTGATAT GGACAGCAGA AGGGGGAGAC CAAGGTTCGA
2041 GCTCAACCAA TAACATTATG ACAACCACT GTCCCTGCCT CAGTTCCCTC TTCTGTAACA
2101 TGAAGTCGTT GTGAGGGTTA AAGGCAGTAA CAGGTATAAA GTACTTAGAA AAGCAAAGGG
2161 TGCTACGTAC ATGTGAGGCA TCATTACGCA GACGTAACCT GGATATGTTT ACTATAAGGA
2221 AAAGACACTG AGGTCTAGA

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(2) INFORMATION FOR SEQ ID NO:2456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2461 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2456:

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1 TGATCCTATC ACAACCTGAG AGTAGTTTTT ACTCCATTTA CAGGTGAGGT CATGTGGTT
61 CAAGGACGTT AAGTAACTTC CCCAGCTCAC ACGGCTTATA AGTAAGGCAG CCAGGATGTG
121 AACCAGTAG GACTATCTGG CTGCAAAGTC CCCACCCTCC CTCGCCATCT GTATCCTCCA
181 ATCATCTTCA GTGCTTTGCT GATAGAAGGT ACGGAAATAC GATGCCACAG ACTGTCCAGG
241 AAGACAGAAA CTAGGCAGAT GGGCTGGCCA TGGTCTCCAA GCCAGACTGG AATCTCCAGG
301 TCTGGAATGA TATCATTTT CTCTTTTAAAT AAATTAATC ACCCACCACA CGGCTTTGAG
361 AGGCTCAAAG GTGACCAACT CCCTTGGGAG GGCCCGGTT GATAAGGAAG GAATGTGAAT
421 CCTCCCATCA CGGAAGCTTC AAGGAGGTCA AGGGTCCAAC ACTTGAGATT GTTAGTGCTG
481 TTGGTGGATA CTGCAGAATA TCCAGTGGAG CCTCAGATGA AGAACATGAG GCCCGTTTA
541 GATCCAAGGA TCAGAGGGGG CTCTGTAGA CCCAGGGGAG TCAGGTGCAC TGGAGCGCGG
601 GCTGCAGAAA ACAGCCTGAG CTCCACCTCG GCTTCTCCTT GCCCTGGCTG GTTGTCTTAA
661 ACCCTGTCT CTTCTGGAC CAGTTTTTGT CTTCCCTTG TGACCTGAGG GGTAACAGCC
721 TCTTTTCCAC TTTCTTTTCA CGCCGACATG CTCAATGTCA CCTTGCAAGG GCCACTCTT
781 AACGGGACCT TTGCCAGAG CAAATGCCCC CAAGTGGAGT GGCTGGGCTG GCTCAACACC
841 ATCCAGCCCC CTTCTCTCTG GGTGCTGTTC GTGCTGGCCA CCCTAGAGAA CATCTTTGTC
901 CTCAGCGTCT TCTGCCTGCA CAAGAGCAGC TGCACGGTGG CAGAGATCTA CCTGGGGAAC
961 CTGGCCGCGAG CAGACCTGAT CCTGGCCTGC GGGCTGCCCT TCTGGGCCAT CACCATCTCC
1021 AACAACTTCG ACTGGCTCTT TGGGGAGACG CTCTGCCCGG TGGTGAATGC CATTATCTCC
1081 ATGAACCTGT ACAGCAGCAT CTGTTTCTTG ATGCTGGTGA GCATCGACCG CTACCTGGCC
1141 CTGGTGAAAA CCATGTCCAT GGGCCGGATG CGCGCGGTGC GCTGGGCCAA GCTCTACAGC
1201 TTGGTGATCT GGGGGTGATC GCTGCTCCTG AGCTCACCCA TGCTGGTGTT CCGGACCATG

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1261 AAGGAGTACA GCGATGAGGG CCACAACGTC ACCGCTTG TG TCATCAGCTA CCCATCCCTC  
1321 ATCTGGGAAG TGTTACCAA CATGCTCTG AATGTCGTGG GCTTCCTGCT GCCCTGAGT  
1381 GTCATCACCT TCTGCACGAT GCAGATCATG CAGGTGCTGC GGAACAACGA GATGCAGAAG  
1441 TTCAAGGAGA TCCAGACGGA GAGGAGGGCC ACGGTGCTAG TCCTGGTTGT GCTGCTGCTA  
1501 TTCATCATCT GCTGGCTGCC CTTCCAGATC AGCACCTTCC TGGATACGCT GCATCGCCTC  
1561 GGCATCCTCT CCAGCTGCCA GGACGAGCGC ATCATCGATG TAATCACACA GATCGCCTCC  
1621 TTCATGGCCT ACAGCAACAG CTGCCTCAAC CCACTGGTGT ACGTGATCGT GGGCAAGCGC  
1681 TTCCGAAAGA AGTCTTGGGA GGTGTACCAG GGAGTGTGCC AGAAAGGGGG CTGCAGGTCA  
1741 GAACCCATTC AGATGGAGAA CTCCTAGGGC ACACTGCGGA CCTCCATCTC CGTGGAAACGC  
1801 CAGATTACAA AACTGCAGGA CTGGGCGAGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT  
1861 GCTGTGAATT TGTGAAGGA TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC  
1921 AAGGAGACAT CTATGCACGA CCTTGGGAAA TGAGTGTGA TGTCTCCGT AAAACACCGG  
1981 AGACTAATTC CTGCCCTGCC CAATTTTCGA GGGAGCATGG CTGTGAGGAT GGGGTGAAGT  
2041 CACGCACAGC CAAGGACTCC AAAATCACAA CAGCATTACT GTTCTTATTT GCTGCCACAC  
2101 CTGAGCCAGC CTGCTCCTTC CCAGGAGTGG AGGAGGCCCTG GGGGAGGGAG AGGAGTGACT  
2161 GAGCTTCCCT CCCGTGTGTT CTCCTGCCCT GCCCAGCAA GACAACCTAG ATCTCCAGGA  
2221 GAACTGCCAT CCACGTTTGG TGCAATGGCT GAGTGCACAA GTGAGTTGTT GCCCTGGGTT  
2281 TCTTTAATCT ATCAGCTAGA ACTTTGAAGG ACAATTTCTT GCATTAATAA AGGTTAAGCC  
2341 CTGAGGGGTC CCTTGATAAC AACCTGGAGA CCAGGATTTT ATGGCTCCCC TCACTGATGG  
2401 ACAAGGAGGT CTGTGCCAAA GAAGATCAA TAAGCACATA TGAGCACTTC TGTATATCAG  
2461 TATTGAGCAC TGTAGGCA

## (2) INFORMATION FOR SEQ ID NO:2457:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2457:

1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTT GTGAGGACTC CGTGCCCAAC  
61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTTAACGGG  
121 ACCTTTGCCC AGAGCAAATG CCCCAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG  
181 CCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCTCAGC  
241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC  
301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC  
361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC  
421 CTGTACAGCA GCATCTGTTT CTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG  
481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG  
541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCGGAC CATGAAGGAG  
601 TACAGCGATG AGGGCCACAA CGTACCCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG  
661 GAAGTGTTC CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCT GAGTGTCTATC  
721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG  
781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCTGG TTGTGCTGCT GCTATTCATC  
841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC  
901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG  
961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA  
1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC  
1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT  
1141 CACAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG  
1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT T

## (2) INFORMATION FOR SEQ ID NO:2458:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2458:

1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTT GTGAGGACTC CGTGCCCAAC  
61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTTAACGGG  
121 ACCTTTGCCC AGAGCAAATG CCCCAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG  
181 CCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCTCAGC  
241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC  
301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC  
361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC  
421 CTGTACAGCA GCATCTGTTT CTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG  
481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG  
541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCGGAC CATGAAGGAG  
601 TACAGCGATG AGGGCCACAA CGTACCCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG



661 GAAGTGTTC CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCT GAGTGTCTC  
 721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG  
 781 GAGATCCAGA CGGAGAGGAG GCCACCGTG CTAGTCCTGG TTGTGCTGCT GCTATTTCATC  
 841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC  
 901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG  
 961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA  
 1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC  
 1081 ATTCAGATGG AGAAGTCCAT GGGCACACTG CCGACCTCCA TCTCCGTGGA ACGCCAGATT  
 1141 CACAACTGC AGGACTGGG AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG  
 1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT T

## (2) INFORMATION FOR SEQ ID NO:2459:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2459:

1 GCCCTTCAA GATGAGCTGT TCCCGCCGCC ACTCCAGCTC TGGCTTCTGG GCTCCGAGGA  
 61 GGGGTGGGGA CGGTGGGGAC ATCAGGCTGC CCCGAGTAC CAGGGAGCGA CTGAAGTGCC  
 121 CATGCCGCTT GCTCCGAGA AGGTGGGTGC CGGGCAGGGG CTGCTCCAGC CGCCTCACCT  
 181 CTGCTGGGAG GACAACTGT CCCAGCACAG AGGGAGGGAG GGAGGGCAGG CAGCGGGGAG  
 241 AAGTTCCCT GTGGTCGTGG GGAGTT

## (2) INFORMATION FOR SEQ ID NO:2460:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2460:

1 GCCCTTCAA GATGAGCTGT TCCCGCCGCC ACTCCAGCTC TGGCTTCTGG GCTCCGAGGA  
 61 GGGGTGGGGA CGGTGGTGAC GGTGGGGACA TCAGGCTGCC CCGCAGTACC AGGGAGCGAC  
 121 TGAAGTGCCC ATGCCGCTTG CTCGGAGAAA GGTGGGTGCC GGGCAGGGG TGCTCCAGCC  
 181 GCCTCACCTC TGCTGGGAGG ACAAAGTGC CCAGCACAGA GGGAGGGAGG GAGGGCAGGC  
 241 AGCGGGGAGA AGTTTCCCTG TGTCGTGGG GAGTT

## (2) INFORMATION FOR SEQ ID NO:2461:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1441 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2461:

1 GAGCTCTTCA ATATTTAGT GAAAGCTATA GATGAGGCTC CATAGGGGAT AAAGCACAGA  
 61 CACACCTTTT CAGAGGGCTT GTGGACTCTG GGCAGCCTGT CCATAGACCT CTGTCCCCAA  
 121 CTGGCAAGTC AGGAACTCC AGATTAAGGA GCCCAATGT GGTGAACAG CCAGGTGCAC  
 181 AGATGAGTCA ACCACACAGC CAGGCCAGGG AGGGCCTTCA CTCAAGAGCC TACAGCCAGT  
 241 TCACAGCCAA GCCAGGGCTA GCGCCAGGCC ACCATAAAC TGATCTGAGA CTCTGTTTCC  
 301 CTGTCTCCAT GATGATGGA TCAGGCTTGA TTGCTGGTTT GTAGGCTTGT TATGAATCAA  
 361 GTCACAGGGA AGAGGAGCTG ATGGGCTGGG GGGACGTCTT CTGGCCCTCC TGTCTCTTCC  
 421 CCAGATCCAC TGGGCCCACT CTTATCTGTT CTCTTCTGAA GGAAGGGTTT TAAGGCTTCA  
 481 AAAAAAATG TTTTGAAGT CCCTGCCCTT TCCAGCTCCT ACCGTCTCAG CCCTGGGAGT  
 541 GTAAAGTGCT GCAGATAGTT AGTAAGTCTT TGAGCAAAAC TGAGAAAGCC AGCCTGAGCC  
 601 TTGACATGGG AGAAACCTCC GCCATACATC TCCGAAGAAA CGGCCGCGTG TCTCAGGGGA  
 661 GCGCAAACAC CCGTACCCAG GAAACAGGAC AGCTTCTGCC ACTGTCGCCC TTGGGAGCCG  
 721 TACGTGGCAT GACAAAGAAA TCCCAGGACT CCGCCTGCCC ACCTGGCCAC CCTCTGTTTA  
 781 CACCTTCCGC GTAAACGCCC ACTGTTTACA TCCAAACTC AGACACAAA TAACCACCTC  
 841 AAGAAGATAA ATAATGATAA GAAATAAATG TTACGCGAGG CAAATTTATT CACATGGGGC  
 901 TTCCAGGCC ACTTTGTGGT CAGCCGGGAG GGACGTTTTT GCCGTCCAC GACTCCAACG  
 961 GGCAGCCGGG CTTACGCAA CATGGAATC TTCCAAGAGC CTCCCTGGCC CCCAGGGCTC  
 1021 AGAGGGTGGC AGAGCGGAGA GCGAAGGTGG CCGCAGCCTT CCCGGCCCCA CAGCCAGCCT  
 1081 GGCTCCAGCT GGGCAGGAGT GCAGAGCTCA GCTGGAGGCG AGGGGGAAGT GCCCAGGAGG  
 1141 CTGATGACAT CACTACCCAG CCCTTCAAAG ATGAGCTGTT CCCGCCGCCA CTCCAGCTCT  
 1201 GGCTTCTGGG CTCCGAGGAG GGTGGGGGAC GGTGGTGACG GTGGGGACAT CAGGCTGCCC  
 1261 CGCAGTACCA GGGAGCGACT GAAGTGCCCA TGCCGCTTGC TCCGAGAAAG GTGGGTGCCC  
 1321 GGCAGGGGCT GCTCCAGCCG CCTCACCTCT GCTGGGAGGA CAACTGTCC CAGCACAGAG  
 1381 GGAGGGAGGG AGGGCAGGCA GCGGGGAGAA GTTCCCTGT GGTGCTGGGG AGTTGGGAAA  
 1441 AGTTCCTTC CTTCGGAGG GAGG

## (2) INFORMATION FOR SEQ ID NO:2462:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1381 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2462:

```
1 CTTTGTGAAG AAGGAATTGG CAACACTGAA ACCTCCAGAA CAAAGGCTGT CACTAAGGTC
61 CCGCTGCCTT GATGGATTAT ACACTTGACC TCAGTGTGAC AACAGTGACC GACTACTACT
121 ACCCTGATAT CTTCTCAAGC CCCTGTGATG CGGAACCTAT TCAGACAAAT GGCAAGTTGC
181 TCCTTGCTGT CTTTATTGTC CTCCTGTTTG TATTAGTCT TCTGGGAAAC AGCCTGGTCA
241 TCCTGGTCCT TGTGGTCTGC AAGAAGCTGA GGAGCATCAC AGATGTATAC CTCTTGAACC
301 TGGCCCTGTC TGACCTGCTT TTTGTCTTCT CCTTCCCCTT TCAGACCTAC TATCTGCTGG
361 ACCAGTGGGT GTTTGGGACT GTAATGTGCA AAGTGGTGTG TGGCTTTTAT TACATTGGCT
421 TCTACAGCAG CATGTTTTTC ATCACCCTCA TGAGTGTGGA CAGGTACCTG GCTGTTGTCC
481 ATGCCGTGTA TGCCCTAAAG GTGAGGACGA TCAGGATGGG CACAACGCTG TGCCTGGCAG
541 TATGGCTAAC CGCCATTATG GCTACCATCC CATTGCTAGT GTTTTACCAA GTGGCCTCTG
601 AAGATGGTGT TCTACAGTGT TATTCATTTT ACAATCAACA GACTTTGAAG TGAAGATCT
661 TCACCAACTT CAAAATGAAC ATTTTAGGCT TGTTGATCCC ATTCACCATC TTTATGTTCT
721 GCTACATTAA AATCCTGCAC CAGCTGAAGA GGTGTCAAAA CCACAACAAG ACCAAGGCCA
781 TCAGGTTGGT GCTCATTGTG GTCATTGCAT CTTTACTTTT CTGGGTCCCA TTCAACGTGG
841 TTCTTTTCTT CACTTCCTTG CACAGTATGC ACATCTTGA TGGATGTAGC ATAAGCCAAC
901 AGCTGACTTA TGCCACCCAT GTCACAGAAA TCATTTCCTT TACTCACTGC TGTGTGAACC
961 CTGTTATCTA TGCTTTTGTT GGGGAGAAGT TCAAGAAACA CCTCTCAGAA ATATTTTCAGA
1021 AAAGTTGCAG CCAAATCTTC AACTACCTAG GAAGACAAAT GCCTAGGGAG AGCTGTGAAA
1081 AGTCATCATC CTGCCAGCAG CACTCCTCCC GTTCTCCAG CGTAGACTAC ATTTTGTGAG
1141 GATCAATGAA GACTAAATAT AAAAAACATT TTCTTGAATG GCATGCTAGT AGCAGTGAGC
1201 AAAGGTGTGG GTGTGAAAGG TTTCCAAAAA AAGTTCAGCA TGAAGGATGC CGTGTGTGTT
1261 GTTGCCAAAC CTTGGAACAC AATGACTGGA GACATAGTTG TGCAATGCCTG GCACAACATC
1321 AAGCCTGTGA TTGTGTTTAT TGATGATGTT GAACAAGTGG TGGCTTTGAG GGATTCTGTA
1381 TGCCAAGTGG AAAAAAAGA TGTCTCCGGA ATTCGACAGG TTATCA
```

## (2) INFORMATION FOR SEQ ID NO:2463:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5161 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2463:

```
1 TTTTATCTCT CCGGGCTTAT TTGCTGGTTT CTCGGAATGC GGGCCTTGTC TGGTTCACGC
61 TGGATCCCCA ACGCCTAGAA CAGTGCCTGG CACGCAGTTC GTCCTTCTAT AAATATCGGA
121 CTAAATGCAT CTCTGTGATG GTAATACCCA CACGGTGTG TGAGATGAA TGAGTGATTC
181 TGTGCAAGTT CTAAGTGATC TGTTACAAA AGTACTGGTC GCTAAATTAC TCTTATAATA
241 AAGCATACTT TTAGGATAAT AAAGCACTAT TCGCGAATTG GTTACCGCTA TTATGAAATT
301 ACTGAGCAAT ACATATCTAC ATCTGATCAG TCTCCAGAA TATGCCAAAT CCTACCTTCT
361 TCTGAAAGTA TCTCCTAATT ATCTGCACCT GACCCTAGTG ATGCTGTGAA TGTGCAAGTA
421 TAGCTACATC CTCCGAAGGA AGGATCTTTA CTCCTTTTAC CTCCTGAAATG GGCTGCGTCT
481 GCTGAAAGCG CGGGGGAATG GCGGGTGGGA AGCTTGGCCC TACTTCCAGC ATTGCCGCCT
541 ACTGGTGGG TTAATCCAGC AAGTCACTCC CCTTCCCTGG GCCTCAGTGT CTCTACTGTA
601 GCATTCCCAG GTCTGGAATT CCATCCACTT TAGCAAGGAT GGACGCGCCA CAGAGAGACG
661 CGTTCCTAGC CCGCGCTTCC CACTGTCTT CAGGCGCATC CCGCTTCCCT CAACTTAGG
721 AAATGCCTCT GGGAGGTCCT GTCCGGCTCC GGACTCACTA CCGACCACCC GCAAACAGCA
781 GGGTCCCCTG GGCTTCCCAA GCCGCGCACC TCTCCGCCCC GCCCCTGCGC CCTCCTTCTT
841 CGCGTCTGCC CCTTCCCCC ACCCGCCTT CTCCTCCCC GCCCAGCGG CGCATGCGCC
901 GCGCTCGGAG CGTGTTTTAA TAAAAGTCCG GCCGCGGCCA GAAACTTCAG TTTGTTGGCT
961 GCGGCAGCAG GTAGCAAAGT GACGCGGAGG GCCTGAGTGC TCCAGTAGCC ACCGCATCTG
1021 GAGAACCAGC GGTACCATG GAGGGGATCA GTGTAAGTCC AGTTTCAACC TGCTTTGTCA
1081 TAAATGTACA AACGTTTGAA CTTAGAGCGC AGCCCTCTC CGAGCGGGCA GAAGCGGCCA
1141 GGACATTGGA GGTACCCGTA CTCCAAAAA GGGTCACCGA AAGGAGTTT CTTGACCATG
1201 CCTATATAGT GCGGGTGGGT GGGGGGGGAG CAGGATTGGA ATCTTTTCT CTGTGAGTCG
1261 AGGAGAAACG ACTGGAAGA GCGTTCCAGT GGCTGCATGT GTCTCCCCCT TGAGTCCCGC
1321 CGCGCGCGGC GGCTTGACAG CTGTTTGCAA ACGTAAGAAC ATTCTGTGCA CAAGTGCAGA
1381 GAAGGCGTGC GCGCTGCCTC GGGACTCAGA CCACCGGTCT CTTCTTGGG GAAGCGGGGA
1441 TGTCTTGGAG CGAGTTACAT TGTCTGAATT TAGAGGCGGA GGGCGGCGTG CCTGGGCTGA
1501 CTTCACAGGA GGAGATTGCG CCCGCTTTAA CTTGCGGGT AAGCGCCTG TGACTGTTCT
1561 TGACACTGGG TGCGTGTGTTG TTAAGTCTG TGCGCGCGAC GGAGCTGTGC CAGTCTCCCA
1621 GCACAGTAGG CAGAGGGCGG GAGAGGCGGG TGGACCCACC GCGCCGATCC TCTGAGGGGA
1681 TCGAGTGGTG GCAGCAGCTA GGAGTTGATC CGCCCGCGCG CTTTGGGTTT GAGGGGGAAA
1741 CCTTCCCGCC GTCCGAAGCG CGCTCTTCC CCACGGCCG GAGTGGGTCC TGCAGTTTCA
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1801 GAGTTTGGGG TCGTGCAGAG GTCAGCGGAG TGGTTTGACC TCCCCTTTGA CACCGCGCAG  
1861 CTGCCAGCCC TGAGATTTGC GCTCCGGGGA TAGGAGCGGG TACGGGGTGA GGGGCGGGGG  
1921 CGGTTAAGAC CGCACCTGGG CTGCCAGGTC GCCGCCCGGA AGACTGGCAG GTGCAAGTGG  
1981 GGAAACCGTT TGGCTCTCTC CGAGTCCAGT TGTGATGTTT AACCGTCGGT GGTTTCCAGA  
2041 AACCTTTTGA AACCTCTTG CTAGGGAGTT TTTGGTTTCC TGCAGCGGCG CGCAATTCAA  
2101 AGACGCTCGC GCGGAGCCG CCCAGTCGCT CCCAGCACC CTGTGGGACA GAGCCTGGCG  
2161 TGTCGCCAG CGGAGCCCCT GCAGCGCTGC TTGCGGGCGG TTGGCGTGGG TGTAGTGGGC  
2221 AGCCGCGGCG GCCCGGGGCT GGACGACCCG GCGGGGCGG TGCCACCGC CTGGAGGCTT  
2281 CCAGCTGCCC ACCTCCGGCC GGGTTAACTG GATCAGTGGC GGGGTAATGG GAAGCCACCC  
2341 GGGAGAGTGA GGAAATGAAA CTTGGGGCGA GGACCACGGG TGCAGACCCC GTTACCTTCT  
2401 CCACCCAGGA AAATGCCCGG CTCCTAACG TCCCAAACGC GCCAAGTGAT AAACACGAGG  
2461 ATGGCAAGAG ACCCACACAC CGGAGGAGCG CCCGCTTGGG GGAGGAGGTG CCGTTTGTTC  
2521 ATTTTCTGAC ACTCCGCGCC AATATACCCC AAGCACCGAA GGGCCTTCGT TTTAAGACCG  
2581 CATTCTCTTT ACCCACTACA AGTTGCTTGA AGCCCAGAAT GGTTCGTATT TAGGCAGGCG  
2641 TGGGAAAATT AAGTTTTTGC GCTTAGGAG AATGAGTCTT TGCAACGCCC CCGCCCTCCC  
2701 CCCGTGATCC TCCCTTCTCC CCTCTTCCCT CCCTGGGCGA AAAACTTCTT AAAAAAGTT  
2761 AATCACTGCC CCTCCTAGCA GCACCCACCC CACCCCCAC GCGCGCTGGG AGTGGCCTCT  
2821 TTGTGTGTAT TTTTTTTTTC CTCCTAAGGA AGGTTTTTTT TCTTCCCTCT AGTGGGCGGG  
2881 GCAGAGGAGT TAGCCAAGAT GTGACTTGA AACCTCAGC GTCTCAGTGC CCTTTTGTTC  
2941 TAAACAAAGA ATTTTGTAAAT TGGTTCTACC AAAGAAGGAT ATAATGAAGT CACTATGGGA  
3001 AAAGATGGGG AGGAGAGTTG TAGGATTCTA CATTAAATTCT CTTGTGCCCT TAGCCCACTA  
3061 CTTCAGAATT TCCTGAAGAA AGCAAGCCTG AATTGGTTTT TTAATGCT TTAATAATT  
3121 TTTTAACTG GGTAAATGCT TGCTGAATTG GAAGTGAATG TCCATTCTT TGCCCTCTTT  
3181 GCAGATATAC ACTTCAGATA ACTACACCGA GGAAATGGGC TCAGGGGACT ATGACTCCAT  
3241 GAAGGAACCC TGTTCCGTG AAGAAAATGC TAATTTCAAT AAAATCTTCC TGCCACCAT  
3301 CTACTCCATC ATCTTCTTAA CTGGCATTGT GGGCAATGGA TTGGTCATCC TGGTCATGGG  
3361 TTACCAGAAG AAAGTGAAG GCATGACGGA CAAGTACAGG CTGCACCTGT CAGTGGCCGA  
3421 CCTCCTCTT GTCATCAGC TTCCCTCTG GGCAGTTGAT GCCGTGGCAA ACTGGTACTT  
3481 TGGGAACCTC CTATGCAAGG CAGTCCATGT CATCTACACA GTCAACCTCT ACAGCAGTGT  
3541 CCTCATCTG GCCTTCATCA GTCTGGACCG CTACCTGGCC ATCGTCCACG CCACCAACAG  
3601 TCAGAGGCCA AGGAAGCTGT TGGTGAAAA GGTGGTCTAT GTTGGCGTCT GGATCCCTGC  
3661 CCTCCTGCTG ACTATTCCCG ACTTCATCTT TGCCAACGTC AGTGAGGCAG ATGACAGATA  
3721 TATCTGTGAC CGCTTCTACC CCAATGACTT GTGGGTGTT GTGTTCCAGT TTCAGCACAT  
3781 CATGGTTGGC CTTATCCTGC CTGGTATTGT CATCCTGTCC TGCTATTGCA TTATCATCTC  
3841 CAAGCTGTCA CACTCCAAGG GCCACCAGAA GCGCAAGGCC CTCAAGACCA CAGTCATCCT  
3901 CATCCTGGCT TTCTTCGCTT GTTGGCTGCC TTAATACATT GGGATCAGCA TCGACTCCTT  
3961 CATCCTCCTG GAAATCATCA AGCAAGGGTG TGAGTTGAG AACACTGTGC ACAAGTGGAT  
4021 TTCCATCACC GAGGCCCTAG CTTTCTTCCA CTGTTGCTG AACCCCATCC TCTATGCTTT  
4081 CCTTGGAGCC AAATTTAAAA CCTCTGCCA GCACGCACTC ACCTCTGTGA GCAGAGGGTC  
4141 CAGCCTCAAG ATCCTCTCCA AAGGAAAGCG AGGTGGACAT TCATCTGTTT CCACTGAGTC  
4201 TGAGTCTTCA AGTTTTCACT CCAGCTAACA CAGATGTAAA AGACTTTTTT TTATACGATA  
4261 AATAACTTTT TTTTAAGTTA CACATTTTTC AGATATAAAA GACTGACCAA TATTGTACAG  
4321 TTTTATTGCG TTGTTGGATT TTTGTCTTGT GTTTCTTTAG TTTTGTGAA GTTTAATTGA  
4381 CTTATTATTA TAAATTTTTT TTGTTTCATA TTGATGTGTG TCTAGGCAGG ACCTGTGGCC  
4441 AAGTCTTAG TTGCTGTATG TCTCGTGGTA GGAAGTGAAG AAAGGGAAGT GAACATTCCA  
4501 GAGCGTGTAG TGAATCAGT AAAGCTAGAA ATGATCCCCA GCTGTTTATG CATAGATAAT  
4561 CTCTCCATTC CCGTGGACG TTTTCTCTGT TCTTAAGACG TGATTTGCT GTAGAAGATG  
4621 GCACTTATAA CCAAAGCCCA AAGTGGTATA GAAATGCTGG TTTTTCAGTT TTAGGAGTG  
4681 GGTGATTTC AGCACCTACA GTGTACAGTC TTGTATTAAG TTGTTAATAA AAGTACATGT  
4741 TAACTTACT TAGTGTTATG TTCTGATTTC TGTGACATT CTTTGGCTA GTAGAAGACA  
4801 AAAGTAATAC ATTTATGGTA TGCAAAGCAC TATCCTAGGT ATTTTATTGT AATATTTTAC  
4861 TTACCCCTTA TCACAACTCT GATAGATTCT GCTTCTGTTA CTAATTACAT TTTATAGAAG  
4921 AGGAAACGGA GGCACAGAAA GCCTAAGTAA CTTGGTTAAA GGCATGTAGT AAGTATCAAA  
4981 TCCTGTATTT TAAACCAGGT AACATGACTT AACGAATCTG AAGCCTTCAC CACTTTAAAT  
5041 TCAATGGAA GTTTAGAAAT GGCCAGCCAG CACCTATTG TATGAAAGGT CATCTTTCAG  
5101 AGATAAGCA TGTATAAAGA AGAAAAGTA TGCAGTCGTG TTTGGATTTT ACTCCACCAT  
5161 C

## (2) INFORMATION FOR SEQ ID NO:2464:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 841 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2464:

1 AGGATGATGG TGATGGGGAA CTAAATGGGG AAATATGGAA GGTACAGGA AAAGTTAACA  
61 CAAGTTAGCA AAAAGTTAAC ATAACACAAA AAGTCTTGC AGGAAAAAAA AAAGAAAAGA  
121 AAAGAAAGAA AAAGTCTCCA AGAATGGTTT GGACAGCCAA AATGAATACT TATAGTCACG  
181 TATACCTGCT CACTCCTGAC GCTTCACTCA CACACAGCAC AGGATCTGGT GAGGCTATCA

241 CTAATGTGTC CACATTGTGG TTAAGTTTTC CCTGATTAAAC GAAATGCTCA CACTTCTAAA  
301 CTGAGGTCCT TACAGTAGAT TCCTTTTGCA AGATTGTTAC TGGCTTACAA CTTAAAAATA  
361 AAGGAAAATC ACAAGGAAAG AAAAGTGGGG AAAAAATCGG AGGAAACTTG CCCCTGCCCT  
421 GGCCACCGGC AAGGCTGCCA CAAAGGGGTT AAAAGTTAAG TGGAAAGTGA GCTTGAAGAA  
481 GTGGGATGGG GCCTCTCCAG GAAAGCTGAA CGAGGCATCT GGAGCCCGAA CAAACCTCCA  
541 CCTTTTGGG CCTCGACGGC GGCAACCCAG CCTCCCTCCT AACGCCCTCC GCCTTTGGGA  
601 CCAACCAGGG GAGCTCAAGT TAGTAGCAGC CAAGGAGAGG CGCTGCCTTG CCAAGACTAA  
661 AAAGGGAGGG GAGAAGAGAG GAAAAAGCA AGAATCCCCC ACCCTCTCC CGGGCGGAGG  
721 GGGCGGAAG AGCGCTCCTT GGCCAAGCCG AGTAGTGTCT TCCACTCGGT GCGTCTCTCT  
781 AGGAGCCGCG CGGGAAGGAT GCTGGTCCGC AGGGGCGCGC GCGCAGGGCC CAGGATGCCG  
841 CGGGGCTGGA CCGCGCTTG CTTGCTGAGT TTGCTGC

## (2) INFORMATION FOR SEQ ID NO:2465:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2581 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2465:

1 CCTTTTGGG CCTCGACGGC GGCAACCCAG CCTCCCTCCT AACGCCCTCC GCCTTTGGGA  
61 CCAACCAGGG GAGCTCAAGT TAGTAGCAGC CAAGGAGAGG CGCTGCCTTG CCAAGACTAA  
121 AAAGGGAGGG GAGAAGAGAG GAAAAAGCA AGAATCCCCC ACCCTCTCC CGGGCGGAGG  
181 GGGCGGAAG AGCGCTCCTT GGCCAAGCCG AGTAGTGTCT TCCACTCGGT GCGTCTCTCT  
241 AGGAGCCGCG CGGGAAGGAT GCTGGTCCGC AGGGGCGCGC GCGAGGGCCC AGGATGCCGC  
301 GGGGCTGGAC CGCGCTTGGC TTGCTGAGTT TGCTGCCTTC TGGGTTTCATG AGTCTTGACA  
361 ACAACGGTAC TGCTACCCCA GAGTTACCTA CCCAGGGAAC ATTTTCAAAT GTTCTACAA  
421 ATGTATCCTA CCAAGAACT ACAACACCTA GTACCCTTGG AAGTACCAGC CTGCACCTG  
481 TGTCTCAACA TGGCAATGAG GCCACAACAA ACATCAGAGA AACGACAGTC AAATTCACAT  
541 CTACCTCTGT GATAACCTCA GTTTATGGAA ACACAACTC TTCTGTCCAG TCACAGACCT  
601 CTGTAATCAG CACAGTGTTC ACCACCCAG CCAACGTTTC AACTCCAGAG ACAACCTGA  
661 AGCCTAGCCT GTCACCTGGA AATGTTTCAG ACCTTTCAC CACTAGCACT AGCCTTGCAA  
721 CATCTCCAC TAAACCTAT ACATCATCTT CTCCTATCCT AAGTGACATC AAGGCAGAAA  
781 TCAAATGTT AGGCATCAGA GAAGTGAAT TGACTCAGGG CATCTGCCTG GAGCAAAATA  
841 AGACCTCCAG CTGTGCGGAG TTTAAGAAGG ACAGGGGAGA GGGCCTGGCC CGAGTGCTGT  
901 TGGGGGAGGA GCAGGCTGAT GCTGATGCTG GGGCCAGGT ATGCTCCCTG CTCCTGCCC  
961 AGTCTGAGGT GAGGCCTCAG TGTCTACTGC TGGTCTTGGC CAACAGAACA GAAATTTCCA  
1021 GCAAACCTCA ACTTATGAAA AAGCACCAT CTGACCTGAA AAAGCTGGGG ATCCTAGATT  
1081 TCACTAGCA AGATGTTGCA AGCCACCAGA GCTATTCCCA AAAGACCCTG ATTGCACTGG  
1141 TCACCTCGGG AGCCCTGCTG GCTGTCTTGG GCATCACTGG CTATTTCCCTG ATGAATCGCC  
1201 GCAGCTGGAG CCCACAGGA GAAAGGCTGG GCGAAGACCC TTATTACAG GAAAACGGTG  
1261 GAGGCCAGGG CTATAGCTCA GGACCTGGGA CCTCCCTGA GGCTCAGGGA AAGGCCAGTG  
1321 TGAACCGAGG GGCTCAGAAA AACGGGACCG GCCAGGCCAC CTCCAGAAAC GGCCATTCAG  
1381 CAAGACAACA CGTGGTGGCT GATACCGAAT TGTGACTCGG CTAGGTGGGG CAAGGCTGGG  
1441 CAGTGTCCGA GAGAGCACC CTCTCTGCAT CTGACCAGT GCTACCCCA TGCTGGAGGT  
1501 GACATCTCTT ACGCCCAACC CTTCCTCACT GCACACACT CAGAGGCTGT TCTTGGGGCC  
1561 CTACACCTTG AGGAGGGGGC AGGTAACTC CTGTCTTTTA CACATTCGGC TCCCTGGAGC  
1621 CAGACTCTGG TCTTCTTGG GTAAACGTGT GACGGGGGAA AGCCAAGGTC TGGAGAAGCT  
1681 CCCAGGAACA ATCGATGGCC TTGCAGCACT CACACAGGAC CCCCTTCCCC TACCCCTCC  
1741 TCTCTGCCGC AATACAGGAA CCCCAGGGG AAAGATGAGC TTTTCTAGGC TACAATTTT  
1801 TCCAGGAAG CTTTGATTTT TACCGTTTCT TCCCTGTATT TTCTTTCTCT ACTTTGAGGA  
1861 AACCAAAGTA ACCTTTTGCA CCTGCTCTCT TGTAATGATA TAGCCAGAAA AACGTGTTGC  
1921 CTTGAACCAC TTCCCTCATC TCTCTCCAA GACTGTGG ACTTGGTCAC CAGCTCCTCC  
1981 CTTGTTCTCT AAGTTCACCT GAGCTCCATG TGCCCCCTCT ACCATTGCA GAGTCTGCA  
2041 CAGTTTTCTG GCTGGAGCCT AGAACAGGCC TCCCAAGTTT TAGGACAAAC AGCTCAGTTC  
2101 TAGTCTCTCT GGGGCCACAC AGAACTCTT TTTGGGCTCC TTTTCTCCC TCTGGATCAA  
2161 AGTAGGAGG ACCATGGGAC CAGGTCTTGG AGCTGAGCT CTCACCTGTA CTCTCCGAA  
2221 AAATCCTCTT CCTCTGAGGC TGGATCCTAG CTTATCCTC TGATCTCCAT GGCTTCTCC  
2281 TCCCTCCTGC CGACTCCTGG GTTGAGCTGT TGCCCTCAGT CCCCACAGA TGCTTTCTG  
2341 TCTCTGCCCT CCTCACCCTG AGCCCTTCC TTGCTCTGCA CCCCATATG GTCATAGCCC  
2401 AGATCAGCTC CTAACCTTA TCACCAGCTG CCTCTCTGT GGGTGACCA GGTCTTGTT  
2461 TGCTGTTGAT TTCTTTCCAG AGGGGTTGAG CAGGGATCCT GGTTCATG ACGGTTGGAA  
2521 ATAGAAATTT CCAGAGAAGA GAGTATTGGG TAGATATTTT TTCTGAATAC AAAGTGATGT  
2581 GTTTAAATAC TGCAATTAAA GTGATACTGA AACAC

## (2) INFORMATION FOR SEQ ID NO:2466:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3422 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2466:

AGGATGATGG TGATGGGGAA CTAAATGGGG AAATATGGAA GGTACACAGGA AAAGTTAACA CAAGTTAGCA AAAGTTAAC  
ATAACACAAA AAGGTCTTGC AGGAAAAAAA AAAGAAAAGA AAAGAAAGAA AAAGTCTCCA AGAATGGTTT  
GGACAGCCAA AATGAATACT TATAGTCACG TATACCTGCT CACTCCTGAC GCTTCACTCA CACACAGCAC  
AGGATCTGGT GAGGCTATCA TAAATGTGC CACATTGTGG TTAAGTTTTA CCTGATTAAC GAAATGCTCA CACTTCTAAA  
CTGAGGTCTT TACAGTAGAT TCCTTTTGCA AGATTGTTAC TGGCTTACAA CTTAAAAATA AAGGAAAAATC  
ACAAGGAAAG AAAAGTGGGG AAAAATCGG AGGAAACTTG CCCCTGCCCT GGCCACCGGC AAGGCTGCCA  
CAAAGGGGTT AAAAGTTAAG TGGAAGTGA GCTTGAAGAA GTGGGATGGG GCCTCTCCAG GAAAGCTGAA  
CGAGGCATCT GGAGCCCGAA CAAACCTCCA CCTTTTGGG CCTCGACGGC GGCAACCCAG CCTCTCTCTT  
AACGCCCTCC GCCTTTGGGA CCAACCAGGG GAGCTCAAGT TAGTAGCAGC CAAGGAGAGG CGTGTGCTTG  
CCAAGACTAA AAAGGGAGGG GAGAAGAGAG GAAAAAGCA AGAATCCCC ACCCTCTCC CGGGCGGAGG  
GGGCGGGAAG AGCGCTCCT GGCCAAGCCG AGTAGTGTCT TCCACTCGGT GCGTCTCTCT AGGAGCCGCG  
CGGGAAGGAT GCTGGTCCGC AGGGCGCGC GCGCAGGGCC CAGGATGCCG CGGGGCTGGA CCGCGCTTTG  
CTTGCTGAGT TTGCTGC CTTTGTGG CCTCGACGGC GGCAACCCAG CCTCCCTCCT AACGCCCTCC GCCTTTGGGA  
CCAACCGGG GAGCTCAAGT TAGTAGCAGC CAAGGAGAGG CGCTGCCTTG CCAAGACTAA AAAGGGAGGG  
GAGAAGAGAG GAAAAAGCA AGAATCCCC ACCCTCTCC CGGGCGGAGG GGCGGGAAG AGCGCTGCCA  
GGCCAAGCCG AGTAGTGTCT TCCACTCGGT GCGTCTCTCT AGGAGCCGCG CGGGAAGGAT GCTGTGCTCGC  
AGGGGCGCGC GCGAGGGCCC AGGATGCCGC GGGGCTGGAC CGCGCTTTGC TTGCTGAGTT TGCTGCCTTC  
TGGGTTCAATG AGTCTTGACA ACAACGGTAC TGCTACCCCA GAGTTACCTA CCCAGGGAAC ATTTTCAAAT  
GTTTCTACAA ATGTATCCTA CCAAGAACT ACAACACCTA GTACCTTGG AAGTACCAGC CTGACCCTG  
TGTCTCAACA TGGCAATGAG GCCACAACAA ACATCACAGA AACGACAGTC AAATTCACAT CTACCTCTGT  
GATAACCTCA GTTTATGGAA ACACAACTC TTCTGTCCAG TCACAGACCT CTGTAATCAG CACAGTGTTC  
ACCACCCAG CCAACGTTT AACTCCAGAG ACACCTTGA AGCCTAGCCT GTCACCTGGA AATGTTTCAG  
ACCTTTCAAC CACTAGCACT AGCCTTGCAA CATCTCCAC TAAACCTAT ACATCATCTT CTTGCTCTCT  
AAGTGACATC AAGGCAGAAA TCAAATGTT AGGCATCAGA GAAGTGAAT TGACTCAGGG CATCTGCCTG  
GAGCAAAATA AGACCTCCAG CTGTGCGGAG TTTAAGAAGG ACAGGGGAGA GGGCCTGGCC CGAGTGCTGT  
GTGGGGAGGA GCAGGCTGAT GCTGATGCTG GGGCCAGGT ATGCTCCCTG CTCTTGCCG AGTCTGAGGT  
GAGGCCCTCAG TGTCTACTGC TGGTCTTGGC CAACAGAACA GAAATTTCCA GCAAACCTCA ACTTATGAAA  
AAGACCAAT CTGACCTGAA AAAGCTGGGG ATCCTAGATT TCACTGAGCA AGATGTTGCA AGCCACCAGA  
GCTATTCCCA AAAGACCTG ATTGCACTGG TCACCTCGGG AGCCTGCTG GCTGTCTTGG GCATCACTGG  
CTATTTCCTG ATGAATCGCC GCAGCTGGAG CCCACAGGA GGAAGGCTGG CCTCCCCTGA GGCTCAGGGA  
GAAAACGGTG GAGGCCAGGG CTATAGCTCA GGACCTGGGA CCTCCCCTGA GGCTCAGGGA AAGGCCAGTG  
TGAACCGAGG GGCTCAGAAA AACGGGACCG GCCAGGCCAC CTCCAGAAAC GGCCATTTCAG CAAGACAACA  
CGTGGTGGCT GATACCGAAT TGTGACTCGG CTAGGTGGGG CAAGGCTGGG CAGTGTCCGA GAGAGCACCC  
CTCTCTGCAT CTGACCACGT GCTACCCCCA TGCTGGAGGT GACATCTCTT ACGCCCAACC CTTCCCCACT  
GCACACACCT CAGAGCTGT TCTTGGGGCC CTACACCTTG AGGAGGGGGC AGGTAAACTC CTGTCTTTA  
CACATTGCGC TCCCTGGAGC CAGACTCTGG TCTTCTTGG GTAAACGTGT GACGGGGGAA AGCCAAGGTC  
TGGAGAAGCT CCCAGGAACA ATCGATGGCC TTGCAGCACT CACACAGGAC CCCCTTCCC TACCCCTCC  
TCTCTGCCGC AATACAGGAA CCCCCAGGGG AAAGATGAGC TTTTCTAGGC TACAATTTTC TCCCAGGAAG  
CTTTGATTTT TACCGTTTCT TCCCTGTATT TTCTTTCTCT ACTTTGAGGA AACCAGTA ACCTTTTGCA  
CCTGCTCTCT TGTAATGATA TAGCCAGAAA AACGTGTTGC CTTGAACCAC TTCCCTCATC TCTCTCCAA  
GACACTGTGG ACTTGGTCAC CAGCTCCTCC CTTGTTCTCT AAGTTCCACT GAGCTCCATG TGCCCCCTCT  
ACCATTTGCA GAGTCTGCA CAGTTTTCTG GCTGGAGCCT AGAACAGGCC TCCCAAGTTT TAGGACAAAC  
AGCTCAGTTC TAGTCTCTCT GGGGCCACAC AGAAACTCTT TTTGGGCTCC TTTTCTCCC TCTGGATCAA  
AGTAGGCAGG ACCATGGGAC CAGGTCTTGG AGCTGAGCCT CTCACCTGTA CTCTTCCGAA AAATCCTCTT  
CCTCTGAGGC TGGATCCTAG CTTATCCTC TGATCTCCAT GGCTTCTCC TCCCTCCTGC CGACTCCTGG  
GTTGAGCTGT TGCCTCAGTC CCCCACAGA TGCTTTTCTG TCTCTGCCTC CCTCACCTG AGCCCTTCC  
TTGCTCTGCA CCCCATATG GTCATAGCCC AGATCAGCTC CTAACCTTA TCACCAGCTG CCTCTTCTGT  
GGGTGACCCA GGTCTTGTG TGCTGTTGAT TTCTTTCCAG AGGGGTTGAG CAGGGATCCT GGTTCATATG  
ACGTTTGAA ATAGAAATTT CCAGAGAAGA GAGTATTGGG TAGATATTTT TTCTGAATAC AAAGTGATGT  
GTTAAATATC TGCAATTAAA GTGATACTGA AACAC 3422

## (2) INFORMATION FOR SEQ ID NO:2467:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2467:

1 TCCCAGTTAA TACATAATCA ATATGCAATT TATTAATACA TCTCTCCATG TCCACTCCCC  
61 CTGTATCTTG CCATTCTTGA CCGTCAATTC CATCCTCCTT ACCTTCCCTA GAGGCCAACT  
121 CATTTTCTTT GAAAAACCTG GCATTTCCCA GAAAAAAG TGAAGGGCTG GGAGCTGTCC  
181 GTTGTCTTGA TTTGCTCCCT CTGGCCTTGC TTCCAAATGT GGTGGAAG AAGCACTATT  
241 GAAAAATCCC TAAACGCACC CCGTGCAGGT TGGCTCTACC CTGTAGCCAT GGACACATGC  
301 TGTGATACC ACCTGCCTCA TGAGTCTCAC ATAATTTGCC CTTTCACT ATCTACCCCA  
361 TCAGCCTTAC CAAAACATA CCGTGCATCT GGGCAGCATC TGCCCTTCAA GAGACTAAGG  
421 AATCTCCTTG CAACCAAGAA TGACTAGACC AATGAGACAC CTTTAAAGGC CCCAGCACAA  
481 TATAGAAATC CCACAATATG GTAATCCAG TAAGGAGCTA TCAAGCCATT GCAGGACCAT  
541 CTAGAATACA ACTAGAGTAT AGTTCTTTC AATCCAGGAA CTATACTCTA ACAGCTTGGC

601 TCACAGGAAC CAGAAGTGAA GATGATGAGG ATCAGGGCTG AGCCTGTGAG CACCAGCTCC  
661 ACCACTGACA CCAACCACAG ATTAACAAG CATCTTGTGG ACCCTGGGA TGGAAAGAAT  
721 AGTTGTTGCC TTATCAACCT CCCCACAGC CCACACAGAA AAGATAAAAT CATCATGGCT  
781 ACAGTGTTAC AGAAGATGAT GACCCAAGGA GTAGGCCTGC CTGAGTGAAT GCTGAGAGTG  
841 ATATGGGGAG CAGTAGCATC TCAGAGACTA CAGCAGAAAC CATCCACATA AAGAGCTTTG  
901 CCCAACTTA TGATAAAGGG CACCCTCAGA GACTCTCCCT ACTTTAATAT TAGCCCATTTG  
961 CAGAAATGGT GAGTGGAAAG AGAAATCTTA GGAAGAACCC CTTAAAAAAG CAAAATGCTT  
1021 TTTAGGTTTG TGCTGAAGAG CCTGGAAAG AAATAAGGAC ACACACGCTG AGAAATCTTC  
1081 CTCCTGCCCC AACACTGGGA TAATCTCCAA GGATCTCTCC ATATCTCATT CTCCTGGATA  
1141 CACTGTCCAC TCAGAAATAT TGTGCAGAGT GCAGTAATTC AAAAGTGAGC TATTGTGTTA  
1201 GGAGTGAAGG CAAGAGTATC GTAAAATAAA TCAAATTTGA AATGAATTCT CTTAAATTGC  
1261 TTTATAGATG TTTAATGTAA GCCAGCAGCT ATTAACGAT AAACCTTAA TTCGAGAAAA  
1321 ACTTGGTCAT TCAGAACTA TAGAAACAGG CAGGACTTAT TGCAGGGGCA AACACAGAGT  
1381 GAGCTCCAGC CTGCTTCAGG AAAATCTGCC AGTGCCATGA AGGATGTACT CTGTCTGCTC  
1441 CACTGCACTA CTGCTCAGTA TGAGCCCATG CCATCAGCTG TCCCTGACCC ACAGGAGTTC  
1501 TTTAGAAGAG ACTGGTCAAC AAAAGTTTCT AGGGTGT TTT ATACCTGCCA CTCGAGGGT  
1561 TAAACAAGT TGCATAGAAA TGCTCAATCA AGAAAGACAC AGTCATTACT CAGAGAATAA  
1621 TAAACAGCCT GGCAGCAGAT GAATGAATAG AAAAAGATG TTACATGCAA AGCATGAAAT  
1681 AACCAAATTC CATAACAGAT GTTAATCTGT AATGTGTTA GGAGAATTTA GAGGAAGTAT  
1741 AAGATTTATT CTTTCATCAA AAAAATTATA GCCAATGAGG ATATATCTAT CAATTATCCA  
1801 TCAAGTGGTG ATATGGCAGC ACAAGGTAAC ACACAAAGGA ATAAAACCAA CGTTTATTAA  
1861 GAACCAATCA TGTGGCATTT CACATTGAGC ATCATATTTA ATTCTGAAAA AAATCCTTGT  
1921 ACTGTATCAT TCTTCATATT TTATGGATGC AGTAACTAAG GCTGAGAAT TAAAAATTTT  
1981 TCCTAAGTTC AGACACATAG CTAAGTGGCA GAACCAAGAT TCAAACCTAC CCCATCTAAC  
2041 TGCAGAGCAA ACTGCATGCC TTAAATGTCA AAGTGAATAC TAGCACAGTT AATACAATGT  
2101 TTGGAAACTC AGAGAAGGAA TGATCCCTCT GCATTATAGT TACTAAGGAA TCATTGCCAT  
2161 TATTTAAATG CCAGTGCTTC TACATCAGGC CCAAATTTTC TGTCTACTA ACTGTGAATC  
2221 AAGACTTGAT TCAACCTCTA CTTGAGTATC TGCCGCAATG AGAAATCACT TACCTCCACT  
2281 AACCACATAT TTATTTTATA ACAACAGATT GTTAGTAAGT CCTTCTTAT ACATACTCAA  
2341 CAGCTGCTTC CCAAGATGCT GTAGGATTAT GTCTAGAGTC AAACCTAGCCA GAAGCAATGT  
2401 CCAAAATACA CCATAACACT GTGCAGCAA GGTCTACTA CCACTTGT TTT GGCCCAACA  
2461 TTCTAGGCAG CACTGGATAT CTGAATCATC AATTATTTCC ACAAACACTG ACCCCTCTAC  
2521 CAGTCACCCT CACTAGAAGA ATTAATTCCA CATGATAATA GCTCCCTCAT GTTACTCCCT  
2581 TCTAAGTCAA ATTGTACACC CCTTTATCTG ATTAACAGAG TCTAAGTCAC ATGACCTAAA  
2641 TGCAAGAGAA CTGGGAATGG ACGTTTGTGG ATTCTACCTT AGTAAGGCAA AGTTATCATT  
2701 GGGAAATCCT CTAATACAGG AAGGGTGTTC CAGAGACATT AAGGAGCCAT ATAAATGGAA  
2761 AATGTCCACT ACAATCCATC ACTTGGTTGC CCCACATCAA CATTCTTCT TTTGCCACAC  
2821 TTAAAGTTTC CAAGAACAAA AATTATCCCA CTGAACATAA TCTTTACTAT CTTTTATATA  
2881 AAGGAAAATT AGACTTGACT CAGCAGAACT GAAATAACCC AGCTCTAACA GTTACTGCTT  
2941 TTAACCTCAA GTACTGTGC TCTAGGTGAT ACCTGCTCCA ACAATAGTTT GGTCACATTT  
3001 TCAATTTGAT ATTCTCTAGT CTCCCAACTT GATAACTGTA CCCTAAACCA TAAAGTTCAC  
3061 TACCAACATG CTATATATAA AATAACCAA GGGGGAAGAA GAAAGAGAAA AAGGAAATCT  
3121 CTTAAAATAC ACAGGTATAC ATATGACAAA GCAAAGAAGG AAATGTGAGC AGATAGTGCA  
3181 GTCCTCGTTT CTGAAATTTG TCCCTGACT GGGGCTATAC CTATTCAT TCTCTACCCT  
3241 CAGCCAGGCA GGTGGAGCAA AAACCTAAGT CTTGGTGGAT CTGAATCTTG ATGCTGTGGA  
3301 GCTGTCTTAC TAGCCCCAGA CTACCTGCCT CTCAATTTCT AATTATATCA GTGAAAGCAA  
3361 ACAGCTTTGA TTTGTTTAAAG CCTCTGATTT TTTGGTCTAA CTGATGTAAG ACCACAAGGA  
3421 CAAGAGTTCT CCAGCTCCGG ATTCTCTTCT GTTCTGTAA TGGTGAATG CCCGAGAGAA  
3481 GAGTTGCCAA CTTTGGCAA TAAAAATAC AGGATTCCAG TTAAATTC AAATTTAGATAA  
3541 ACAACAATTT TTTAGTATTA GTGTGTCCCA TTCAATATTT GGACATACTT AACTAAAAAA  
3601 TGATTTGTTG TTCATCTGAA ATACAAATTT AACTGGGCAT TCTGAATATT CTCTGGCAAC  
3661 CCCCAGAGAG GTGAAGAAAG TGGTACAAGG AACTTAAGA AGACCAGATT TGAAAAGACA  
3721 TTACGGATGT GTTTAAATGT CTTATTCTAG AGAGAGTTAG AGCTGTAGGT AGAAGTTGGG  
3781 AAATTAAGTT AAAAGCAGAC ACAGAGACCT GGCCAATATA TACTAAGGAG TGGATCACTC  
3841 TGGTCACAAG CCCAACCTGA GACCAAGGGC ATAGTGAGAT GATTTGGGAA AGGCATTAT  
3901 AACTACTCA TCCCGTCTT TGAATAAAT GCCTTATAAA TCTCCAAGAG AAATGACAGT  
3961 CCACCATGTG GACTGCTTTC TGTAAGTCCA GGGAAATAA AAGCTATGTG CTTGAAACCC  
4021 ACTTCTGATA TTATAAGGTG TGTGATCTTT GTCATGTAA TGGGTCTGAG TATCAATTTT  
4081 ACAATTTGTA AGTGACAGTA ATGGTGTGTC CCCAGGTTGT TGTGGAAGC TGTGATTTTA  
4141 ATGCAACAGT AGGAAACCCC AGCCTCTCTG GAGCAACAC CTTTCTACAT CTTTACTTCC  
4201 CCTGCACATT GGCAGGACTC TATTCCTCTA TTTCTCTCTA GTGCTAGAGC AGAAAGGGAC  
4261 CTTGATTGTA TATCAGGAAA ATCTATTTCT GAACCATAAG CTATGATAGC TGATTTAAAA  
4321 AATTGACTAT CATGACATGA TAATGATCAT AATGGTAATA CATATTGATA GGGTGGCCGT  
4381 GAAAGTAATA ATATATCTAA GAGTTGTGAC AATATATGAT ACGCCTAGAC TCTCAGAAAA  
4441 TGCTAATTCC AATCCCAATT GCTCTTTGCA TAAAGTTCTG TCCTAGGGTC TGTCTTTTTC  
4501 CCACATCTAC CCTCCTTGA TCTCTTCTCT GTCTTTTCA TGTGGTTTCA AGGAGGAGAG  
4561 AGATCCAGGT CAATGTTTTT CAAATTACAA GGAATTATCA TTTAAATGGG GAAGAAGCTC  
4621 AAGTTTTGAC GTGTAGTGGA ATTGGAGTGG AGTGGAGTGG AATGGAAACT AACAGGAAGA

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4681 CACACAT GGTTAAGATA AAGATTGTTT CCTGAAACCT ATTGTG CTTACATACT
4741 CACACATACA TATGTGCATG CACTGGGACT CTGCAATATG CATTTCGAC TATGGAACAT
4801 AGCCATAAAA GTCTTTGCAC TGAACGTTCA GTGGGCCTTT CACAAGCTGC CCTAATTGGG
4861 AAAGAAAAAC ATGGTCCCTC CATTTCTGTC CCCCAACTCC AGAAAAGTCA CCATAGTTGA
4921 GGTACATCT GAGAAGCCAG CACTTGGGAG TTCAGGCTC AAGTTCCTTT CTAGAAAAAC
4981 ACTGGGTGAT TCTAGGGGAA CTTCCGATCA GAAACAGCCA ATTCAGAGTG AGAGAAGAAA
5041 ACGTGACCAT GCAGTTCCTG TGGTTACCAG CCTTGCCCTT CTCTGCCTT CTGGGAGTTA
5101 TAAAACCCAA GACTGGAAAG GAAAACCAGC ATTTGCTCAG GCAGCCTCTC TGGGAAGATG
5161 CTGCTTCTTC CTCTCCCCTT GCTGCTCTT CTCTTGTGCT CCAGAGCTGA AGCTGGTGAG
5221 TATCAGGGTT CTTCCCTCTG AAATCTGCAG TATCAGCTCC TGAACAAAG ATGTTTAGTC
5281 TGAAATAGCT GACTCCTAAA CAGGGTTCCA AGATCTCTCT TCAAGAGTCC CACAGAGGAA
5341 ATTTCCACTT GGGATGTGTG CCACCCACC CCCACCCCA CCCACTGCCA TTCTCTACAG
5401 CCTAGGACAC CCCAGGAAC AAGGAATTC ACCTCAATTG TAGAAAAGCC CAGAGCAAGT
5461 GGAAGAAAAA GGGGTATCCC CAGGAAAACA GACATGTCTT CTTAATCTT TGAGCATCAG
5521 GGCTACCCAT TACTTTGTGA CTTTCTCACT CTGTGACCAT GCTCAAGAGC TATGGAGAAA
5581 TCTAAAACAG GAACCTGGAC AGTGGGTCTT ACACAGAGAC AGAGGAGAGT GGGCCAGGGC
5641 AAGGTGGGAG TGGGAGAAGT CTGAGATGAA AACATCAGAA TGGAGCAGAG GCAAGAATGA
5701 GATTTACCTT GGGAGTTAT GGGTGGGGAA AGATACGAAA TACAGGAGAC AGGAGAGGGA
5761 AGATGGGCGG AACACAGGTG GAGAATGAGA TTCCAGGGAA GCCTAGCTCA GCTTTAACCC
5821 AATTTGTCCA TTCATTGGAG AGAGTATCTA TGGCCGTGTT CAAACCCTGG GGTGCTCTGT
5881 TCCAGGGGAG ATCATCGGGG GCACAGAATG CAAGCCACAT TCCCGCCCTT ACATGGCCTA
5941 CCTGGAAATT GTAACCTCCA ACGGTCCCTC AAAATTTTGT GGTGGTTTCC TTATAAGACG
6001 GAACTTTGTG CTGACGGCTG CTCATTGTGC AGGAAGGTGA GACAACAGGG TCTATTTATC
6061 TCCAAATGGG AGATGAACAA CCAGAGTAGC ATCCAGGAAT ACACCTGCAC TGGGGACTGA
6121 AGAGGGGGTC CTGGGTCTTG TCAACTTTCA GGAGAGGGAA GACTTTGGGC TGAAGACTT
6181 TAGTCTGTGT TTGAATAGTT CCTTGAGCCT CAGTCACTGA GCTAAGCTCC CTTCCGAGGA
6241 AAAGGAGGTC CTGTCCGAAG GTCCCTCTTG TTGCAGTAGC ACCCTCACC CCTACCCAAC
6301 TCAAGACACA CGGCTCACTT TTCAGGGCCC CACCCAGTCT CAGGGCCACT TCCTCTATGG
6361 CCTTTTCAAG AACACTGGCT CTAGTTCTCA GGGTCTGAA CCCATCATTT TATGGGAGCA
6421 GAGAACAGGT CTACATAAGA CCCCACCTT CCGTTTTTAA CTGATATCTC CTGCTTCAGG
6481 GGCTGGCCCT CATGCAGGT TCCCTGAATT AGGAAGTGTG AACCCTGTCC CCTGAGTCTT
6541 CCCTGGCCTG TTCAGTCCCC AGCAATTCCA GGGTCTGTAG AAATTGTGTC TGTTCTCTGA
6601 GAAAGCTCTT TCATGAGTTA AGCCTGAGCC CTCAAATGCC ACAAGTGGCC CATGAAAAGG
6661 GAGATGGGTA GAGTCCGGCN ACCCAGTGAC AGAGTTTAGT CCTCTTTTCT CAGAATGAGC
6721 TCACCTCAGA AGAAACCCCA AGCCATCACT GTCGCCTCCT TTTCTTCTCT TCTTCTCAC
6781 AGCAGGTCTA TAACAGTCAC CTTGGAGGCC CATAACATAA CAGAGGAAGA AGACACATGG
6841 CAGAAGCTTG AGGTTATAAA GCAATTCCGT CATCCAAAT ATAACACTTC TACTCTTCAC
6901 CACGATATCA TGTTACTAAA GGTGACAAAC CCTCTCTTCT CCCTTTCCAC TTCCCATTCT
6961 CCTAAGCTTC TCTTCAGGT CCTCATGCCC CTGAATTTT CTTAGGACTT GGCTATAACA
7021 TGAAGCTACT CACCCTGTCC CTCCCTGATC ACCTCCAAC GTCCAGAGCC CATTTGAGG
7081 ACTGACAGTC CTTATTCCC TTCACAGTTG AAGGAGAAAG CCAGCCTGAC CCTGGCTGTG
7141 GGGACACTCC CTTCCCCTC ACAATTCAAC TTTGTCCAC CTGGGAGAA GTGCCGGGTG
7201 GCTGGCTGGG GAAGAACAGC TGTGTTGAAG CCGGGCTCAG ACACCTGCA AGAGGTGAAG
7261 CTGAGACTCA TGGATCCCCA GGCCTGCAGC CACTTCAGAG ACTTTGACCA CAATCTTCAG
7321 CTGTGTGTGG GCAATCCAG GAAGACAAA TCTGCATTTA AGGTGATCCT CCAACTAGGT
7381 TTCTCTCCA AAACCTACTG TTCAGGAGCC TGAATGCTCT TAGAAGGAGA TGGGGTCAGC
7441 AGGTTGTGAG TCAGGTGACA GGGTGAAGC CACAGGAATT GCTGTCTCC CGTGGTCCAA
7501 GACAGCCTCT GACCATCCAT TCCAGTCTAC TGCAGTGGG GCATGGGGTG ACTGTGGAGA
7561 ATGTGATGA CGGTCCCAAG AAAGGAAGAA GGGGCATCAG AACTAGATGT ATAAGTGAGG
7621 AGCTCCACCT CTTGGGTCTG ACTTTAGGTC TCACTGTGAC TCCAAGCTGG CTGGCAGACA
7681 GGAGTGGAGG ACTTCCCGGG CTCACCTTCT TCTCTCTCTC CTCCCCCTAC AGGGAGACTC
7741 TGGGGGCCCT CTTCTGTGTG CTGGGGTGGC CCAGGGCATC GTATCCTATG GACGGTCGGA
7801 TGCAAAGCCC CCTGCTGTCT TCACCCGAAT CTCCCATAC CGGCCCTGGA TCAACCAGAT
7861 CCTGCAGGCA AATTAATCCT GGATCCTGAG CCAGCCTGAA GGGAGCTGG AACTGGACCT
7921 TAGCAGCAA GTGTGTGCAA CTCATTCTGG TTCTACCCTT GGTTCCTCA GCCACAACCC
7981 TAAGCCTCCA AGAGGTCTCC TACAGGTAAC AGAATTTCA ATAAACTTCA GTGAAGACAC
8041 AGCTTCTAGT CGTGAGTGTG TGTCCCTCTC TGCTGCTCTC TTCTCCTGCA CATGTGACCT
8101 GATTCACG CCAAGCACCA AGGA

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## (2) INFORMATION FOR SEQ ID NO:2468:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 661 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2468:

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1 ATCATCGGG GCACAGAATC CAAGCCACAT TCCCGCCCT ACATGGCCTA CCTGGAAATT
61 GTAACCTTCCA ACGTCCCTC AAAATTTTGT GGTGGTTTCC TTATAAGACG GAACTTTGTG
121 CTGACGGCTG CTCATTGTG AGGAAGGTCT ATAACAGTCA CCCTGGAGC CCATAACATA

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181 ACAGAGGAAG AAGACACATG GCAGAAGCTT GAGGTTATAA AGCAATTCCG TCATCCAAAA  
241 TATAACACTT CTACTCTTCA CCACGATATC ATGTTACTAA AGTTGAAGGA GAAAGCCAGC  
301 CTGACCCTGG CTGTGGGGAC ACTCCCCTTC CCATCACAAT TCAACTTTGT CCCACCTGGG  
361 AGAATGTGCC GGGTGGCTGG CTGGGGAAGA ACAGGTGTGT TGAAGCCGGG CTCAGACACT  
421 CTGCAAGAGG TGAAGCTGAG ACTCATGGAT CCCAGGCCT GCAGCCACTT CAGAGACTTT  
481 GACCACAATC TTCAGCTGTG TGTGGGCAAT CCCAGGAAGA CAAAATCTGC ATTTAAGGGA  
541 GACTCTGGGG GCCCTCTTCT GTGTGCTGGG GTGGCCAGG GCATCGTATC CTATGGACGG  
601 TCGGATGCAA AGCCCCCTGC TGTCTTCACC CGAATCTCCC ATTACCGGCC CTGGATCAAC  
661 CAGATCCTGC AGGCAATTA A

## (2) INFORMATION FOR SEQ ID NO:2469:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1261 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2469:

1 GCCACCATGG AAACCTTTG CCTCAGGGCA TCCTTTTGGC TGGCACTGGT TGGATGTGTA  
61 ATCAGTGATA ATCCTGAGAG ATACAGCACA AATCTAAGCA ATCATGTGGA TGATTTCCACC  
121 ACTTTTTCGTG GCACAGAGCT CAGCTTCCTG GTTACCACTC ATCAACCCAC TAATTTGGTC  
181 CTACCCAGCA ATGGCTCAAT GCACAACTAT TGCCACAGC AGACTAAAT TACTTCAGCT  
241 TTCAAATACA TTAACACTGT GATATCTTGT ACTATTTTCA TCGTGGGAAT GGTGGGGAAT  
301 GCAACTCTGC TCAGGATCAT TTACCAGAAC AAATGTATGA GGAATGGCCC CAACGCGCTG  
361 ATAGCCAGTC TTGCCCTTGG AGACCTTATC TATGTGGTCA TTGATCTCCC TATCAATGTA  
421 TTTAAGCTGC TGGCTGGGCG CTGGCCTTTT GATCACAATG ACTTTGGCGT ATTTCTTTGC  
481 AAGCTGTTCC CCTTTTTCGA GAAGTCCTCG GTGGGGATCA CCGTCTCAA CCTCTGCGCT  
541 CTTAGTGTG ACAGGTACAG AGCAGTTGCC TCCTGGAGTC GTGTTCAAGG AATTGGGATT  
601 CCTTTGGTAA CTGCCATTGA AATTGCCTCC ATCTGGATCC TGTCTTTTAT CCTGGCCATT  
661 CCTGAAGCGA TTGGCTTCGT CATGGTACCC TTTGAATATA GGGGTGGACA GCATAAAACC  
721 TGTATGCTCA ATGCCACATC AAAATTCATG GAGTTCTACC AAGATGTAAA GGACTGGTGG  
781 CTCTTCGGGT TCTATTCTG TATGCCCTTG GTGTGCACTG CGATCTTCTA CACCCTCATG  
841 ACTGGTGAGA TGTTGAACAG AAGGAATGGC AGCTTGAGAA TTGCCCTCAG TGAACATCTT  
901 AAGCAGCGTC GAGAAGTGGC AAAACAGATT TTCTGCTTGG TTGTAATTTT TGCTCTTTGC  
961 TGGTTCCTC TTCAATTAAG CCGTATATTG AAGAAAACCTG TGTATAACGA GATGGACAAG  
1021 AACCGATGTG AATTACTTAG TTTCTTACTG CTCATGGATT ACATCGGTAT TAACCTGGCA  
1081 ACCATGAATT CATGTATAAA CCCCATAGCT CTGTATTTTG TGAGCAAGAA ATTTAAAAAT  
1141 TGTTTCCAGT CATGCCTCTG CTGCTGCTGT TACCAGTCCA AAAGTCTGAT GACCTCGGTC  
1201 CCCATGAACG GAACAAGCAT CCAGTGAAG AACACGATC AAAACAACCA CAACACAGAC  
1261 CGGAGCAGCC ATAAGGACAG CATGAACTGA CCACCCTTAG AAGCACTCCT

## (2) INFORMATION FOR SEQ ID NO:2470:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1861 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2470:

1 GAATTCGGGA AAAAGTGAAG GTGTAAAAGC AGCACAAGTG CAATAAGAGA TATTTCTCTCA  
61 AATTTGCCCTC AAGATGGAAA CCCTTTGCCT CAGGGCATCC TTTTGGCTGG CACTGGTTGG  
121 ATGTGTAATC AGTGATAATC CTGAGAGATA CAGCACAAT CTAAGCAATC ATGTGGATGA  
181 TTTCAACACT TTTCTGGGCA CAGAGCTCAG CTTCTGCTT ACCACTCATC AACCCTACTAA  
241 TTTGGTCTCA CCCAGCAATG GCTCAATGCA CAACTATTGC CCACAGCAGA CTAAAATTAC  
301 TTCAGCTTTC AAATACATTA ACACTGTGAT ATCTTGTACT ATTTTCATCG TGGGAATGGT  
361 GGGGAATGCA ACTCTGCTCA GGATCATTTA CCAGAACAAA TGTATGAGGA ATGGCCCCAA  
421 CGCGCTGATA GCCAGTCTTG CCCTTGGAGA CCTTATCTAT GTGGTCATTG ATCTCCCTAT  
481 CAATGTATTT AAGCTGCTGG CTGGGCGCTG GCCTTTTGAT CACAATGACT TTGGCGTATT  
541 TCTTTGCAAG CTGTTCCCCT TTTTGAGAAA GTCCTCGGTG GGGATCACCG TCCTCAACCT  
601 CTGCGCTCTT AGTGTGACA GGTACAGAGC AGTTGCCTCC TGGAGTCTGT TTCAGGGAAT  
661 TGGGATTCTT TTGGTAACTG CCATTGAAAT TGTCTCCATC TGGATCCTGT CCTTTATCCT  
721 GGCCATTCTT GAAGCGATTG GCTTCGTCTG GGTACCCCTT GAATATAGGG GTGAACAGCA  
781 TAAACCTGT ATGCTCAATG CCACATCAA ATTCTAGGAG TTCTACCAAG ATGTAAAGGA  
841 CTGGTGCTC TTCGGGTTCT ATTTCTGTAT GCCCTTGGTG TGCAGTGGCA TCTTCTACAC  
901 CCTCATGACT TGTGAGATGT TGAACAGAG GAATGGCAGC TTGAGAATTG CCCTCAGTGA  
961 ACATCTTAAG CAGCGTCGAG AAGTGGCAAA AACAGTTTTC TGCTTGGTTG TAATTTTTCG  
1021 TCTTTGCTGG TTCCCTCTTC ATTTAAGCCG TATATTGAAG AAAACTGTGT ATAACGAGAT  
1081 GGACAAGAAC CGATGTGAAT TACTTAGTTT CTTACTGCTC ATGGATTACA TCGGTATTAA  
1141 CTTGGCAACC ATGAATTCAT GTATAAACCC CATAGCTCTG TATTTTGTGA GCAAGAAATT  
1201 TAAAAATTGT TTCCAGTCAT GCCTCTGCTG CTGCTGTTAC CAGTCCAAAA GTCTGATGAC  
1261 CTCGGTCCCC ATGAACGGAA CAAGCATCCA GTGGAAGAAC CAGCATCAA ACAACCACAA



1321 CACACCGG AGCAGCCATA AGGACAGCAT GAACTGACCA CCGTTAGAAG CACTCCTCGG  
 1381 TACTCCATA ATCTCTCGG AGAAAAAAT CACAAGGCAA CTGTGAGTCC GGGAACTCTCT  
 1441 TCTCTGATCC TTCTTCTTA ATTCATCCC ACACCCAAGA AGAAATGCTT TCCAAAACCG  
 1501 CAAGGGTAGA CTGGTTTATC CACCCACAAC ATCTACGAAT CGTACTTCTT TAATTGATCT  
 1561 AATTTACATA TTCTGCGTGT TGTATTACAG ACTAAAAAT GGTGGGAGCT GGGGGAGAAT  
 1621 GAAGACTGTT AATGAAACC AGAAGGATAT TTACTACTTT TGCATGAAAA TAGAGCTTTC  
 1681 AAGTACATGG CTAGCTTTTA TGGCAGTTCT GGTGAATGTT CAATGGGAAC TGGTCACCAT  
 1741 GAACTTTAG AGATTAACGA CAAGATTTTC TACTTTTTTT AAGTGATTTT TTTGTCCTTC  
 1801 AGCCAAACAC AATATGGGCT CAAGTCACTT TTATTGAAA TGTCATTTGG TGCCAGTATC  
 1861 CCGAATTC

## (2) INFORMATION FOR SEQ ID NO:2471:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2581 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2471:

TACCACTCCA	AAAGTCTGAT	GACCTCGGTC	CCCATGAACG	GAACAAGCAT	CCAGTGGGAAG	AACCACGATC
AAAACAACCA	CAACACAGAC	CGGAGCAGCC	ATAAGGACAG	CATGAAGTGA	CCACCCCTAG	AAGCACTCCT
GAATTCGGGA	AAAAGTGAAG	GTGTAAAAGC	AGCACAAGTG	CAATAAGAGA	TATTTCTCTA	AATTTGCCCTC
AAGATGGAAA	CCCTTTGCCT	CAGGGCATCC	TTTTGGCTGG	CACTGGTTGG	ATGTGTAATC	AGTGATAATC
CTGAGAGATA	CAGCACAAT	CTAAGCAATC	ATGTGGATGA	TTTCACCACT	TTTCGTGGCA	CAGAGCTCAG
CTTCCTGGTT	ACCACTCATC	AACCCACTAA	TTTGGTCCTA	CCCAGCAATG	GCTCAATGCA	CAACTATTGC
CCACAGCAGA	CTAAATATAC	TTCAGCTTTC	AAATACATTA	ACACTGTGAT	ATCTTGTAAT	ATTTTCATCG
TGGGAATGGT	GGGGAATGCA	ACTCTGCTCA	GGATCATTTA	CCAGAACAAA	TGTATGAGGA	ATGGCCCCAA
CGCGCTGATA	GCCAGTCTTG	CCCTTGAGAG	CCTTATCTAT	GTGGTCATTG	ATCTCCCTAT	CAATGTATTT
AAGCTGCTGG	CTGGGCGCTG	GCCTTTTGAT	CACAATGACT	TTGGCGTATT	TCTTGGCAAG	CTGTTCCCTC
TTTTGCAGAA	GTCCTCGGTG	GGGATCACCG	TCCTCAACCT	CTGCGCTCTT	AGTGTGACA	GGTACAGAGC
AGTTGCCTCC	TGGAGTCGTG	TTCAGGGAAT	TGGGATTCCT	TTGGTAACTG	CCATTGAAAT	TGTCTCCATC
TGGATCCTGT	CCTTTATCCT	GGCCATTCTT	GAAGCGATTG	GCTTCGTCAT	GGTACCCTTT	GAATATAGGG
GTGAACAGCA	TAAACCTGT	ATGCTCAATG	CCACATCAAA	ATTCATGGAG	TTCTACCAAG	ATGTAAAGGA
CTGGTGGCTC	TTGCGGTTCT	ATTTCTGTAT	GCCCTTGGTG	TGCACTGCGA	TCTTCTACAC	CCTCATGACT
TGTGAGATGT	TGAACAGAAG	GAATGGCAGC	TTGAGAATTG	CCCTCAGTGA	ACATCTTAAG	CAGCGTCGAG
AAGTGGCAAA	AACAGTTTTT	TGCTTGGTTG	TAATTTTTGC	TCTTGCTGG	TCTTCTCTTC	ATTTAAGCCG
TATATTGAAG	AAACTGTGT	ATAACGAGAT	GGACAAGAAC	CGATGTGAAT	TACTTAGTTT	CTTACTGCTC
ATGGATTACA	TCCGTATTAA	CTTGCCAACC	ATGAATTCAT	GTATAAACCC	CATAGCTCTG	TATTTTGTGA
GCAAGAAATT	TAAAAATTGT	TTCCAGTCAT	GCCTCTGCTG	CTGCTGTTAC	CAGTCCAAAA	GTCTGATGAC
CTCGGTCCCC	ATGAACGGAA	CAAGCATCCA	GTGGAAGAAC	CACGATCAAA	ACAACCACAA	CACAGACCCG
AGCAGCCATA	AGGACAGCAT	GAACTGACCA	CCCTTAGAAG	CACCTCTCGG	TACTCCCTA	ATCCTCTCGG
AGAAAAAAT	CACAAGGCAA	CTGTGAGTCC	GGGAATCTCT	TCTCTGATCC	TTCTTCTTCA	ATTCACCTCC
ACACCCAAGA	AGAAATGCTT	TCCAAAACCG	CAAGGGTAGA	CTGGTTTATC	CACCCACAAC	ATCTACGAAT
CGTACTTCTT	TAATTGATCT	AATTTACATA	TTCTGCGTGT	TGTATTCAGC	ACTAAAAAAT	GGTGGGAGCT
GGGGGAGAAT	GAAGACTGTT	AAATGAAACC	AGAAGGATAT	TTACTACTTT	TGCATGAAAA	TAGAGCTTTC
AAGTACATGG	CTAGCTTTTA	TGGCAGTTCT	GGTGAATGTT	CAATGGGAAC	TGGTCACCAT	GAAACTTTAG
AGATTAACGA	CAAGATTTTC	TACTTTTTTT	AAGTGATTTT	TTTGCCTTC	AGCCAAACAC	AATATGGGCT
CAAGTCACTT	TTATTGAAA	TGTCATTTGG	TGCCAGTATC	CCGAATTC		

## (2) INFORMATION FOR SEQ ID NO:2472:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2472:

1 GCTCAGCCTC CAAAGGAGCC AGCCTCTCCC CAGTTCCTGA AATCCTGAGT GTTGCCTGCC  
 61 AGTCGCCATG AGAACTTCTT ACCTTCTGCT GTTTACTCTC TGCTTACTTT TGTCTGAGAT  
 121 GGCCTCAGGT GGTAACCTTC TCACAGGCCT TGGCCACAGA TCTGATCATT ACAATTGCGT  
 181 CAGCAGTGGG GGGCAATGTC TCTATTCTGC CTGCCGATC TTTACCAAAA TTCAAGGCAC  
 241 CTGTTACAGA GGGGAAGCCA AGTGCTGCAA GTGAGCTGGG AGTGACCAGA AGAAATGACG  
 301 CAGAAGTGAA ATGAACCTTT TATAAGCATT CTTTAAATAA AGGAAAATTG CTTTGAAGT  
 361 AT

## (2) INFORMATION FOR SEQ ID NO:2473:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4621 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2473:

1 ATCCTTTAAG TCAATGGACT TTGCATCAGT CACACCATCT TTTGTTACTT TGGACTTCCC  
61 CAGCTATGTT CAATAATTAC TGTTCTTCCC TTGGGCCCCA TTGTAATGGC TACAGCCTCG  
121 ACAAAAAGTC TACACTTTGA AGCATTAAAG CTCGGACATC AGCACCAAAT TTTACATCTT  
181 TACCATCACT TCAAGTGAGG TGAGGAGCCA GTAGCCTGGA CACTGGTCTC ATCTGGTGAA  
241 AGACTGTGGG TAATGGAAGC ATTTCTGTGG GGTGCTGGCA GGACATGTGC ATGGCGAGGC  
301 AGGTCATCAG CAGCAAGTGA GAGCTGCCTC TTACTTTCTA AAGGTGACAT AGCAAATATA  
361 CAAAAAATAA TAAATAAATT ATTAATTTAG GTAGAGCACA TAAAGGCTTT ATTTTCATATT  
421 CCATTCTCTT GTATGCTTTC TTCACCAGGA AGAAATAGTT TTAGTGTGAG GAATGAATGA  
481 GTCTGCCCTT CAATTCCAGC CTGCTCAACA CACAAGGAAA CAAAGCCCTG ACAATCAGAG  
541 TGAATCCCTG GTGACTAAGC TCCCAGTCTT GGATGCATAT TTGTTTAGCA GTTCTGACAG  
601 CATTGACCC AGCCCTCTCT CTGCATATCC CATCAGAAC TTTCTTTTTT TTTTTTCTT  
661 TGAGACTGAG TCTTGCTCTG TCGGAAGCGA CTCCTGTGCC TCAGCCTCCC AAATACCTGG  
721 AATTATAGGC GTAAGCCATC ATGCTTGGCT AATTTTTGTA TTTTTCATGG AGATGGGGTT  
781 TTGCCATGTT GGTCAAATTG GTCTCACACT CCTGACCTCA TGTGATCCAC CTGCCTCAGC  
841 CTCCCAAACCT GCTGGGATGA CAGGTGTAAG CCACCATGCT AGGCTCAGAA ATTTCTTTT  
901 ATAAAAATGT CATTAAGGAT CTTGGCTGCA CAATATCGTT ACCAGCTTCC TTTAAATCCA  
961 CTTCTGGCCT GCCAGGAATC AGGTCTTCA GAACCTGACA TTTTAAATGA AGAGGTCAGG  
1021 CAGTTCATGA GGAAAGCCTC ATTGTCCCA TGTCTGTGTC ACTGCTGCAC CCCTGAGACA  
1081 TCACAGACAT GGACACTGGG GCCTGCTTGT TTCTCAAAC GCCCTTAGAT CGAAAGAGGG  
1141 AGGAACCAGG ATGAATGCCA CTCATTTTCC CAAGAAAGGC CCTCTCCTGA GTGCCCCGGA  
1201 TGGGGCTCTG TCCATTGCCT GGGGCCGCCA ATTGCTACTC TGGGTTACGG AGGAAGGACA  
1261 GGGTCTGAG AGACACCAGA GACCTCACAC AGCCCTGAAA ACATGGGGCT CCTTCATAAG  
1321 TGTTTCCCAT CACCAACAGG GAGACCACGT GGAGGCCCTT CAGCCCCACT CGGTGCTTCT  
1381 CCACCAAATC CCAAGGGCAG TGACGCTGAC GTCTGTGGAA AGCAGAGAAA GCCCTGGCTC  
1441 CCAAGGCCCT GAAGTCCCTG TGGAGCTGAC ATTCCCTGAG TGACGGTGTG AATGGAAGGA  
1501 ACTCAAGTGC GGGTGGTAGG CCACCTCCTG GCCCAGGCCCT GGGTGAATC TGAGGGGACA  
1561 CATGTAGTCA CAATCCCATC CTCCCATTCT CCTTCTCAGA GGAAGGAAGT GGGCATCCAT  
1621 CTGCCCTCAT TCTCTCCCGT GGGGAAGATG GGGAGTTTCA GGGGAACCTT CACATAAATT  
1681 TCACCAAGCT AGATCTCCTG TGAGGATGGG GCCCACCATG CTCCCGGTGC TGCCAGAGGC  
1741 CCTGAGCCCC TCCCAGGGTC CCTGGGTTTG AGCCAGCCCT GTATCATCCC CAGGAGCTGA  
1801 ATGTCAGAGC AATGGATAGA ATTAGATGGA AAGAGCTCTC AATTTGACCT GAGACTGTCC  
1861 CCAGATACTC AGGAAAAACA GGACGTCGCA CAGAGTGGGC AGCAGGTGAG TGGCAGGTTA  
1921 TAGGTCCCTGA GTTTGAGTTT GTTCTCACGT GAGACAGACC CAGCCCCTCA CTCCATTAC  
1981 ACATGGGTTT TTAATGGTG CAAGATAGGA GCAATTTTCT GGTCCCAAGA GCAGGAGGAA  
2041 GGGATTTTCT GGGGTTTCTT GAGTCCAGAT TTGCATAAGA TCTCCTGAGT GTGCATTGTT  
2101 CTTTGAGGAC CATTCTCTGA CTCACCAGT AAGTGGCTGA ATTCTAACCT CTGTAATGAG  
2161 CATTGCACCC AATACCAGTT CTGAACCTTA CCTGGTGACC AGGGACCAGG ACCTTTATAA  
2221 GGTGGAAGGC TTGATGTCTT CCCCAGACTC AGCTCCTGGT GAAGCTCCCA GCCATCAGCC  
2281 ATGAGGGTCT TGTATCTCCT CTCTCGTTC CTCTTCATAT TCCTGATGCC TCTTCCAGGT  
2341 GAGATGGGCC AGGGAAATAG GAGGGTTGGC CAAATGGAAG AATGGCGTAG AAGTCTCTG  
2401 TCTCCTCTCA TTCCCCTCCA CCTATCTCTC CCTCATCCCT CTCTCTCCTT CCTCTCTCTG  
2461 TGTGTCCCCT CCATCCTTTT CTCCTGCTTC TCTCTCTTCT TCCCTCTCTC TCTTTTTTCT  
2521 GTCTTTCTTT TTCTCTCTC CCTAGAGCAT GTCTTTCTTT CTTTCTCTTT CTTTCTTCT  
2581 ACCCACACTT TTAGACTGAA TGCCCTATT TAAATGAACAA AGCATTGTCT CTTCAATAG  
2641 AAAAGGAGTT TGAGAACCCA ATGGACACCT CACTCGTTCT TCTAAGCCAA TATGAAGGAG  
2701 CCCAGTAGCT TGTAATATC ATCTCTTAC TGCTTTCCAT GCTACAACCT CTGAGACTAT  
2761 GGTTGAAACC TGTTAGGTGA CTTTTTAAAT AAAAGGCAGA AATTTTGATT TTATCTAAAG  
2821 AAAGTAGTAT AGAATGTCAT TTTCTAAAT TTTATATTTA AAGGGTAGAT ACTGCAACCT  
2881 AGAGAAATCC AGATAATCTT AAGGCCCAGC CTATACTGTG AGAACTACTG CAGCAAGACA  
2941 CTCTGCCCTC AGGACTTTTC TGATCAGAGG CCCTGAGAAC AGTCCCTGCC ACTAGGCCAC  
3001 TGCAGGTTCA CAGGACAGGG TACAGCCCAT TGAAACCTAC TTTTAAACCT GGATGCCTAA  
3061 CCTTCATTTT CTCTTGATA TTATGAAAAT AAAATAAAAA CCATGAAAGG ATAAAAGAGG  
3121 GAGAGTGGA GGAAGGATG GAGAAAGGGA AAAAGAAAAT TTGAGAGTAA ATCCTAAAAC  
3181 AATTAATCTA ATAGATATCA TCTTGTAAG TCTCATTTT ACCAATCTTA TTTATGAGTC  
3241 CTGGGTTTTG TGAGAACAAAT GGGGTTCTGA GAGGCACCAG AGACCTCATG TTTTCCAAAA  
3301 CCTAGAACAG TATAATGAAG GAAGGCGGGG AGGCAGGGAG GCAGGGAGGC AGGGAGGCAG  
3361 GGAGGCGGGC AGGTGGGGAG GGAGGGACGG AAGGAGGGAG GGAGGGAGGG AGGGAGGGAG  
3421 GGAGGGATAA AAAAAGAAGA ATGAGTTGA AACCAGGACT TAGATATTAG AAACAAGCCA  
3481 TTACAAAATT TATTTCTATG GTTAATTGTG GTTTTCAACT GTAAGTTACT TGGTGTAAAT  
3541 TTTCTATTAA ACAATTTTCA TAAGTTGCAT CTTTTTATCC CATCTCAGGT CAAATACTTA  
3601 ACAGACTAAA TGATTTGAAA AAGCAAAAGT TTACTGGCTT GTGTGTGTTA AAATGGAGGT  
3661 ATGGTGGCTT TGATATTATC TTCTTGTTGT GGAGCTGAAT TCACAAGAGA TCGTTGCTGA  
3721 GCTCCTACCA GACCCACCTT GGAGGCCCCA GTCATCAGG AGAGATCAGG GTCTTTTACA  
3781 ATCAGGTTCT AAAAAATAA ACATCCCCC AACCACAGCA GTGCCAGTTT CCATGTCAGA  
3841 AACTTAGATC CAAATGACTG ACTCGCTCT CATTATCATG ATGGAAAAGC CCAGGCTTGA  
3901 GAAAGAAGCC CGCTGCGGAT TTAATCAAGG CGATACTGAC ACAGGGTTTG TGTTTTTCCA  
3961 ACATGAGTTT TGAGTTCTTA CACGCTGTTT GCTTTTTTGT TGTGTTTTTT CCTGTTAGG  
4021 TGTTTTTGGT GGTATAGGCG ATCCTGTTAC CTGCCTTAAG AGTGGAGCCA TATGTCATCC

4081 AGTCCTTGC CCTAGAAGGT ATAAACAAAT TGGCACCTGT GCTCTCCCTG GAACAAAATG  
 4141 CTGCAAAAAG CCATGAGGAG GCCAAGAAGC TGCTGTGGCT GATGCGGATT CAGAAAGGGC  
 4201 TCCCTCATCA GAGACGTGCG ACATGTAAAC CAAATTAAAC TATGGTGTCC AAAGATACGC  
 4261 AATCTTTATC CTAGTAATTG TGGTCATTGG GTGATGTTGG TTTGGGCAGG CCATCTCTAA  
 4321 TATCCTTGAA ACACCTTTTT CTGCTCTCCA GGAAGGGGTC AGGGCTGCCA CAGCGGGGCT  
 4381 TGGAGTGCTT TCCAGGGTCA CAGGCATCTG TATTCTTTGG ATTCTTTGAC CTTCCTTATT  
 4441 TATCCCGGC ATTTCCTTAA AACGTGTGCT TTGCTCCTCC TGCATCTCC CCTTGCATGC  
 4501 CCTCACCTAC CCCACATCTT CCTAAAAAAG AGCAAGCCCA ACTCAAAGAC CAGTTCCCTC  
 4561 ATGGAATCAT AGTGGATCTG CCAAGGGAGG GGATGCCAG TCCTCTGTTC TTCACAAGAC  
 4621 TCCCTTCTTC TGGCTAAGGT TTCTTATGCA ATTAT

## (2) INFORMATION FOR SEQ ID NO:2474:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1981 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2474:

1 CTGCAGTGGT AAAAAGATTCTATATCTGCT GTTTGATGAA TGCAGCACCC ACTAGCCACA  
 61 TAGTGCTCGT GAGCACTTGC AATGCGGCTA GGGTGATTTC AATTAACCTA AAAGAGAACA  
 121 GCCACAGGGA GCATGTGGCT GCCATATTGG ATGGTGTGCT TTTGAGAACA AAATGAGAGA  
 181 AATGAAGCCT CTATTTACCT TGGTTGGCGG AACACATTGA AGGGACTCTG TATTGATACC  
 241 AGGCTTCAAA CTTTGGGAAG TGTACTGGCC AACTTAAACA CATCCACAGG AGAATGAAGA  
 301 GGTTTGGGAA GGGACCAGAA ACCAGGCATT GAGGACAATG AGAAGAGTTT TTCAAAGTG  
 361 GAATTACTGC AAAAAGTGGG AAAATAGCCT TTGGATGGAA GTTACTGATG AGACAATTTC  
 421 CATCGGTGTG AAAGCCATCT TTCCAACAGA GATCTGCAAC ATGAGAATGT ACTGTCTCCT  
 481 AGGGTAGCGA TGGCCTCTTG TATTAGTCCG CTCAGGCTAC CAGATTTATC GTTTAACTG  
 541 CCCATAAACA GACCAGGCAG TTTAAACAAC AGAAATTTAT TTCCTCGCAG TCCTGGAGGC  
 601 AGGAAGTCTG CGATCAAGGT GGAAGCAGGG TTGGCTTCTT CTCAGGTGTC TGTCTTGGC  
 661 TGGTAGATGA CCGCCGCCTC CCTGGGTCCT CACATGGTCT TTCCTCTGTG TGTGTCTGTC  
 721 CCAATCTCTT CTTATAAGGA TGCAAGTCTT ATGGATCAGA GCACACCCCA ATGACCGTGT  
 781 TTAACCTGAA TCACCTCTTT AAAGTTTCTC TCTCAAATA CAATCACCTC CTGAGGCACT  
 841 GTTAGGGCTT CGACACAGGA ATTCTTTTCC TAGGGGATTC AGTTCAGTCC AAAACGCCTA  
 901 CCAGTGGAGA CTTGCAACAT GCGCGCCTGC TGGTCCCTCG CCAGGAATAT CACAGGCGAC  
 961 TGTTCCTGTG TGCATGGAAT AGAAGGCTAT TCCAGAGTAC TGTCTCTATT TATCAGATCT  
 1021 GGGATACTGG GAGAAGGCA AAATAAAGTC CAAGTAGAAA AAAAAACTAT GAAAGTTTAA  
 1081 GAGAGTAACC ATAATTTCAG CCCGATGTGA AACGATCCTA GATTTAGCTT GAAATAGTGA  
 1141 TGTGGGAAGT GAGGGGGCCG GGATTCAAGG CAGAGGGAAC AGCGTAACTG AAGGCATGGA  
 1201 AGGAGGGAAG TGTAGGCTGT GTTTGAAGAG TGGCAGCTGC TTCCACATTT CTAAACACA  
 1261 GGATGTGATT TTGGGGTGTG TTGAGACAAG GCAGAAACT TGTTTGAAA AATAACTTGA  
 1321 ATTCCCTGCA CATTAAAAAT CTCTCAGCAG AAGAAAACCC CACTCAGAAC CCCACTGTTC  
 1381 ATTCTTGGC TTGTATTGG SCACAGCTGG CATAGCCCA GACTGAGTAA GCTCTTCAGA  
 1441 CACCTCATTT CATGAGTAGC CCCAAAGATC AATCATGGGC CAATTTCTTG GAAGAGAAGA  
 1501 CTCTCCGGTG TTTTGCAGTT ATTTGTTCTG CTTTCGCGAG ATGTTCTCAA ATCGTTGCAG  
 1561 CTACAAGCCA TGAGTCTGAA GTTTTGTGT TCCCTCCTTA CAGGTGGTAA CTTTCTCACA  
 1621 GGCTTGGCC ACAGATCTGA TCATTACAAT TGCCTCAGCA GTGGAGGGCA ATGTCTCTAT  
 1681 TCTGCCTGCC CGATCTTTAC CAAAATTCAA GGCACCTGTT ACAGAGGGAA GGCCAAGTGC  
 1741 TGCAAGTGAG CTGAGAGTGA CCAGAAGAAA TGACGCAGAA GTGAAATGAA CTTTTTATAA  
 1801 GCATTCTTTT AATAAAGGAA AATTGCTTTT GAAGTATACC TCCTTTGGGC CAAAATGAAT  
 1861 CTTGTGTCTC AATTGGAAGA GGTAAAGAAG TAGGGGGTTA GGGTGCATGG GTTGGAACGT  
 1921 GAGACAGGTC GAACCACAAA GCCTGCCTGG AAAAGGGGAG TGACGTCCTA GGCTTCAGTG  
 1981 ATGTCACCTC CACTTTGTTT GATCCACAAA CCAACAGGTG ACTGATTTTG

## (2) INFORMATION FOR SEQ ID NO:2475:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2475:

1 GTCAGCTCAG CCTCCAAAGG AGCCAGCCTC TCCCCAGTTC CTGAAATCCT GAGTGTGCG  
 61 TGCCAGTCGC CATGAGAACT TCCTACCTTC TGCTGTTTAC TCTCTGCTTA CTTTGTGCTG  
 121 AGATGGCCTC AGGTGTAAC TTTCTCAGC GCCTTGCCCA CAGATCTGAT CATTACAATT  
 181 GCGTCAGCAG TGGAGGGCAA TGTCTCTATT CTGCCCTGCC GATCTTTACC AAAATTCAG  
 241 GCACCTGTTA CAGAGGGAAG GCCAAGTGCT GCAAGTGAGC TGGGAGTGAC CAGAAGAAAT  
 301 GACGCAGAAG TGAAATGAAC TT

## (2) INFORMATION FOR SEQ ID NO:2476:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4741 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2476:

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1 GAATTCACAT TTCTCACCTT TTGATGTATT AAGAAAGTAT GGAGAAATAT ATCCTCTATC
61 AAATTTTCAT GCCTTCAATA ATTTCTAATT CATCAGTCAG TGTTTTCCCA TCCTTTACTG
121 TGATGATGCC CTTTCTTCCA AACTTTTTCA TTGCATCAGA GATGATGTTA CCAATTTCTT
181 TGTCTCCATT TGCAGAAATT GTAGCAACCT GTGCAATTC TTCAGGTTTG GTCACAGGTT
241 TAGACTGCTT TTTAAGTTCA GCAATTACAG CATCAACAGC TAACATCACA CCTCTCTTGA
301 TTTCCACTGG ATTAGCACCT TTGCTAACCT TCTGGAAGGC TTATTTGGAA ATAGAGCATA
361 CCAGTACAGC AGCAGTGATA GTGCCATCCC CCAGTCTCTC CATTTGTGTT ATTGGCAACA
421 TCTTGGACAA GTTAGCTCC AATGCTTTTA TATTTATCCT TTAAGTCAAT TGACTTTGCA
481 TCAGTCACAC CATCTTTTGT TACTTTGGGA CTTCCTCCAGC TATGTTCAAT AATTACTGTT
541 CTTCCCTTTG GCCCATTGT AATGGCTACA GCATCGACAA AAAGTCTACA CTTTGAAGCA
601 TTAAGGCTCA GACATCAGCA CCAAATTTTA CATCTTTACC ATCACTTCAA GTGAGGTGAG
661 GAGCCAGTAG CCTGGACACT GGTCTCATCT GGTGAAAGAC TGTGGGTAAT GGAAGCATTT
721 CTGTGGGGTG GTGGCAGGAC ATGTGCATGG TGAGGCAGGT CATCAGCAGC AAGTGAGAGC
781 TGCCTCTTAC TTTCTAAAGG TGACATAGCA AGTATACAAA AAAAAATAAA ATATTAATTT
841 AGGCAGAGCA CATAAAGGCT TTATTCATA TTCCATTCT CTGTATGCTT TCTTCACCAG
901 GAAGAAATAG TTTTAGTGTC AGGAATGAAT GAGTCTGCCC CTCAATTCCA GCCTGCTCAG
961 CACACAAGGA AACAAAGCCC TGACAATCAG AGTGAATCCC TGGTGACTAA GCTCCAGTCC
1021 TGGATGCATA TTTGTTTAGC AGTCTGACA GCATCTGACC CAGCCCTCTC TTTGCATACC
1081 CCACCAGAAC CTTCTTTTTT TTTTTCCTT TTTGAGACTG AGTCTTGCTC TGTCCGAAGC
1141 GATTCCCCTG CCTCAGCCTC CCAAATACCT GGAATTATAG GCGTAAGCCA TCATGCCTGG
1201 CTAATTTTTG TATTTTTCAT GGAGATGGGG TTTTGCCATG TTGGTCAAAT TGGTCTCACA
1261 CTCCTGACCT CATGTGATCC ACCTGCCTCA GCCTCCCAA GTGCTGGGAT GACAGGTGTA
1321 AGCCACCATG CTAGGCTCAG AAATTTCTT TTATAAAAT GTCATTAAGG ATCTTGGCTG
1381 CACAATATCG TTACCAGCTT CCTTTAAATC CACCTCTGGC CTGCCAGGAA TCAGGGTTCT
1441 TCAGAACCTG ACATTTTAAA TGAAGAGGTC AGGCAGGTCA TGAGGAAAGC CTCATTGTCC
1501 CCATGTCTCT GTCAGTCTG CACCCTGAG ACATCACAGA CATGGACACT GGGGCTGCT
1561 TGTTTCTCAA ACTGCCCTTA GATCGAAAGA GGGAGGAACC AGGATGAATG CCACTCATTT
1621 TCCCAAGAAA GGCCCTCTCC TGAGTGCCCG GGATGGGGCT CTGTCCATTG CCTGGGGCCG
1681 CCAATTGCTA CTCTGGGTTA CGGAAGAAGG ACAGGGTCTT GAGAGACACC AGAGACCTCA
1741 CACAGCCCTG AAAACATGGG GCTCCTTCAT AAGTGTTCAT CATCACCAAC AGGGAGACCA
1801 CGTGGAGGCC TTGCAGCCCT ACTCGGTGCT TCTCCACCAA ATCCCAAGGG CAGTGACGCT
1861 GACGTCTGTG GAAAGCAGAG AAAGCCCTGG CTCCCAAAGC CCTGAAGTCC TGTGGAGCTG
1921 ACATTCCTCT AGTGACGGTG TGAATGGAAG GAACTCAAGT GCGGGTGGTA GGCCACCTCC
1981 TGGCCCAGGC CTGGGTGAAC TCTGAGGGGA CACATGTAGT CACAATCCCA TCCTCCCAT
2041 CTCCTTCTCA GAGGAAGGAA GTGGGCATCC ATCTGCCTCA TCTCTCTCCC GTGGGGAAGA
2101 TGGGGAGTTT CAGGGGAATC TTCACATAAA TTTACCAGC TCAGATCTCC TGTGAGGATG
2161 GGGCCACCA TGCTCCCGGT GCTGCCAGAG GCCCTGAGCC CCTCCAGGGT CCCTGGGTTT
2221 GAGCCAGCCC TGTATCATCC CCAGGAGCTG AATGTCCGAA CAATGGATAG AATTAGATGG
2281 AAAGAGCTCT CAATTTGGCC TGAGACTGTC CCCAGATACT CAGGAAAAAC AGGACGTCC
2341 ACAGAGTGGG CAGCAGGTGA GTGGCAGGTT ATAGGTCCTG AGTTTGAGTT TGTCTCACG
2401 TGAGACAGAC CCAGCCCCTC ACTCCATTCA CACTGAGGT TTTAATGGT GCAAGATAGG
2461 AGGAATTTT TGGTCCCAAG AGCAGGAGGA AGGGATTTTC TGGGGTTTCC TGAGTCCAGA
2521 TTTGCATAAG ATCTCCTGAG TGTGCATTGT TCTTTGAGGA CCATTCTCTG ACTCACCAGG
2581 TAAGTGGCTG AATTCTAACC TCTGTAATGA GCATTGCACC CAATACCAGT TCTGAATCT
2641 ACCTGGTGAC CAGGGACCAG GACCTTTATA AGGTGGAAGG CTTGATGTCC TCCCAGACT
2701 CAGTCTCTGG TGAAGCTCCC AGCCATCAGC CATGAGGGTC TTGTATCTCC TCTTCTCGTT
2761 CCTCTTCATA TTCCTGATGC CTCTTCAGG TGAGATGGGC CAGGGAAATA GGAGGGTTGG
2821 CCAAATGGAA GAATGGCGTA GAAGTCTCT GTCTCCTCTC ATTCCTCTCC ACCTATCTCT
2881 CCCTCATCCC TCTCTCTCCT TCCTCTCTCT CTCTTTTCTT CTGTCTTCTT TTTTCTCTC TCCCTAGAGC
2941 CTCTCTCTT TCCCTCTCT CTCTTTTCTT CTACCCACAC TTTTAGACTG AGTAGACTGA
3001 ATGTCTTTCT TCTTTTCTT TTCCCTTCTT TCCTTCAATA GAAAAGGAGT TTGAGAACCC
3061 ATGCCCTATT TAATTGAACC AAGCATTGCT TCCTTCAATA GAAAAGGAGT TTGAGAACCC
3121 AATGGACAAC TCACTCGTTC TTCTAAGCCA ATATGAAGGA GCCCAGTAGT TTGTAAATAT
3181 CATCTCTTCA CTGCTTTCCA TGCTACAAC GCTGAGACTA TGGTTGAAAC CTGTTAGGTG
3241 ACTTTTTTAA TAAAAGGCAG AAATTTTGAT TTTATCTAAA GAAAGTAGTA TAGAATGTCA
3301 TTTTCTAAAT TTTTATATT AAAGAGTAGA TACTGCAACC TAGAGAATTC CAGATAATCT
3361 TAAGGCCAG CCTATACTGT GAGAACTACT GCAGCAGACA CTCTGCCCCC AGGACTTTTC
3421 TGATCAGAGG CCTGAGAAC AGTCCCTGCC ACTAGGCCAC TGCAGGTTCA CAGGACAGGG
3481 ACAGCCCAT GAAACCAACT TTTAAACCTG GATGCCAAT CTTCATTTT TCCTTGATAT
3541 TATGAAAATA AAATAAAAC CATGAAAGGA TAAAAGAGGG AGAGTGGAAG GGAAGGATGG
3601 AGAAAGGGAA AAAGAAATTT TGAGAGTAAA TCCTAAAACA ATTAATCTAA TAGATATCAT
3661 CTGTGAAAT CCTCATTTTA CCAATCTTAT TTATGAGTCC TGGGTTTTGT GAGAACAATG
3721 GGGTTCTGAG AGGCACCAGA GACCTCATAT TTTCCAAAAC CTAGAACAGT ATAATGAAGG
3781 AAGGAGGGAA GGAGGGAGGG AGGGAGGGAA GGAGGGAGG AGGGAGGGAG GGAGGGAAAC
3841 AAAAGAAGA ATGAGGTTGA AACCAGGACT TAGATATTAG AAACAAGCCA TTACAAAATT
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3901 TATTTCATATG GTTAATTGTG GTTTTCAACT GTAAGTTACT TGGTGTAAAT TTCCTATTAA  
3961 ACAATTTTCAG TAAGTTGCAT CTTTTTATC CCATCTCAGA TCAAATACCT AACAGACTAA  
4021 ATGATTTGAA AAAGCAAAAG TTTACTGGCT TGTGTGTGTT AAAATGGAGG TATGGTGGCT  
4081 TTGATATTAT CTTCTTGTGG TGGAGCTGAA TTCACAAGAG ATCGTTGCTG AGCTCCTGCC  
4141 AGACCCACC TGGAGGCCCC AGTCACTCAG GAGAGATCAG GGTCTTTCAC AATCAGGTTT  
4201 TACAAAAATA AACATCCCCC AAACCACAGC AGTGCCAGTT TCCATGTCAG AAACCTAGAT  
4261 CCAAATGACT GACTCGCGTC TCATTATCAT GATGGAAAAG CCCAGGCTTG AGAAGAAGC  
4321 CCGCTGCGGA TTTACTCAAG GCGATACTGA CACAGGGTTT GTGTTTTTCC AACATGAGTT  
4381 TTGAGTTCTT ACACGCTGTT TGCTCTTTT GTGTGTTTT TCCCTGTTAG GTGTTTTTGG  
4441 TGGTATAGGC GATCCTGTTA CCTGCCTTAA GAGTGGAGCC ATATGTCATC CAGTCTTTTG  
4501 CCCTAGAAGG TATAAACAAA TTGGCACCTG TGGTCTCCCT GGAACAAAAT GCTGCAAAAA  
4561 GCCATGAGGA GGCCAAGAAG CTGCTGTGGC TGATGCGGAT TCAGAAAGGG CTCCTCATC  
4621 AGAGACGTGC GACATGTAAA CCAAATTAAT CTATGGTGT CAAAGATACG CAATCTTTAT  
4681 CCTAGTAATT GTGGTCATTG GGTGATGTTG GTTTGGGCAG GCCATCTCTA ATATCCTTGA  
4741 AACACCTTTT TCTGCTCTCC AGGAAGGGGT CAGGGCTGCC ACAGCGGGG TTGGAGTGC

## (2) INFORMATION FOR SEQ ID NO:2477:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3661 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2477:

1 GAATTCCTG TAAGCCCTGT TACAGGGGCT GCACCCAGA TACAACCTGA CCTGTGTCCA  
61 AGGCGGGCAA CTCAACCCTT AGATATTGAA TGGGTCCCAT GGCACCAATG CTTAAACACC  
121 AGCAGCCCTC ACAACCACAG ATCGTGTTTT AAGGATGAGG AGGTAGTTCT CTGGATGCAC  
181 AGGCTTCAAT CCAAATGGGC TCATGACGCC GCAGCACACA CCCAGTCTGC AGCCTGAAGA  
241 GTTGGAGCAT TGCATTACA GAAAGCATCC AGACATGATC ATGGGCTCAG GGATACACCT  
301 GTTCTCCGAT GTGTACCAGT GAAGGATGGA AACTCCTATG CCTCCAGAA AGCACCCTC  
361 AAGCTTTTGC TGAATGCTTC TCTGAAGGCC CACAAGGCTG AGAGGCTGTG CAACACCAGC  
421 AGTAAAGTGA ATGCCAGAC TCCACCTCC TTTCTGGGT GGCCATCTGG AAAGGCCACT  
481 CCCACCTGA TGCTAATGC CTCAGACCAG TTCTTGGCC AGATGATCCT AGACAATTGT  
541 TTAAGCTTAA ACTGTTTATT GGCCAAGCAA ACAGGTGATA GTACCTCTGG GGAACCACAT  
601 GCCGCGTGA CATCCAGATC TCAGGAGAAC CCAAAATGT CTGTTCCACA TAGCAACAGA  
661 AGCCAGGTA GCACTCAGTC TCACCTGGGT GTTCTCCAAC ATCCAGCTC AGCCAAATGG  
721 CTTTCATTAG TTTTATGGT TAGACCCAG GTCCTCGGA CACTGCTTTA GAAACACATT  
781 CCAAATCCTC CTCTGTGTGC AGGTGGCATT CCTATCCCA TCTCTTTGCA GGGCGTATAC  
841 TGTGATACGC AGCCAGGCTG TCCAGAGGC CTTAAATATT CCCTTGGTGC AGGTAGTTCA  
901 GCTTAGCCAC AGCCAATGCA TCACAGGGTC AACTGTGTTA GGAGCCATTG AGAATCCATA  
961 GTTGGTTGCT GCCTGGGCCT GGCCAGGGCT GACCAAGGTA GATGAGAGGT TCCTCTGTGG  
1021 AGTTCTACTT TAACCTCACC TTCCACCAA ATTTCTCAAC TGTCCTTGCC ACCACAATTA  
1081 TTTAATGGAC CCAACAGAAA GTAACCCCGG AAATTAGGAC ACCTCATCCC AAAAGACCTT  
1141 TAAATAGGGG AAGTCCACTT GTGCACGGCT GCTCCTTGCT ATAGAAGACC TGGGACAGAG  
1201 GACTGCTGTC TGCCCTCTCT GGTACCCCTG CCTAGCTAGA GGATCTGTAA GTACTACAAA  
1261 ACTTAAACTT TACACTGAGT TTTTCATCATT GAAGCTATGC CTCCAATCTG ACCTCTGACT  
1321 GTGGGGCCGC CCCAGAGGGA CCCAGCGGGT GAATCCCTGC TAGGAACGTC TGTCCGGACC  
1381 TCTGGTGACT GCTGGGACG ATGGCTTCCA GCTAACTTAA TAGAGAACT CAAGCAGTTT  
1441 CCTTCTAAAT ACACATGTCA CATGTCCTGG TTGACATGTC CAGTAAGAAG ACTATCACAG  
1501 GTCTTTGGAA CATTCTTTTG AGAGAAACCT ATTTAGGTCC TTGGTCTGTT TTTCAATCAG  
1561 GTTGTGTTGAT TTTTGCTATT GAGTTGTTGG AATTCCTTAT GTATTGAGT ATTTGCCCTT  
1621 TCTGCCATGT AGGTTTGGCA AATATTTTCT CTCATTTTCT GGGTTATCTT TTCACTCGGT  
1681 TGATTGTTTC CTTTCTGTG CAGATGCTTT AGCGTTAAAT GAAGCCACAC TTGTCTATTT  
1741 TCCCTTTTAT TGCTGTGCC TTTGGTGTCA TAGCCAAGAA ATCATTACCT ACATCAATGT  
1801 CAAAAGCTTT ATCCTTCTAT AACTTCTAG TAGTTTATGG TTTCACTTGT TACATTAGG  
1861 TTTTCAATTC ATTCTGAGTT GATGTTCTTA CATGGTGTGA GATAAAGATT TAAATACATA  
1921 CATATATAAA ATCATGAGGT AGTGTAACAT ATAAATATAC AATTGTTAAT TGTACTCAA  
1981 GTCTAAGTAG AGGTGGAAT AATAAATTT CTTTTTTTA CTTAAACCAC TCTGTGTCAC  
2041 TGAGCTGATT TCACCTTTAG CCTGATAAAA TCATTGCTCT CTCCACCCTG ATTCCTACAG  
2101 GAGACTACTC ACCCCATAAC CTCAAAACC TCTTCATGAG GATGGTAAGT CACCTGAATC  
2161 CTGAAGTGAA TTAATCGCTA TTCCATTGGA ACTCATATAG GACACCAGAA TCTAGACCTC  
2221 CAGAGAACAG CAGGACCCAT CTTGAGAAA TAAGAAGCAT TTGTCCCTG AGCCTGTTGA  
2281 ATCAAAGTGC AATTTCTATT CTTTTTGGAA TGTTAAAAAG TGAATCATAA TATTTAAGCA  
2341 GGTGAACCCA CGAGTAACAT AGCAGGGTCT TTCTGTGCT TATTAGCTCC AACCTAGCAC  
2401 AGACATTAAA GGTACAGATG TATACTAGCA TGAAACTGGG AGAACAGGAG CATTGAGCA  
2461 ACCTTGAGAC CAATGGGCCT CTCTTATAAA ATGCACACCT CCTCTACTG AGATTGAGGA  
2521 AGGTTTCTTG TCTCCGAGCC TTCTCCAGT AGAGCTATAA ATCCAGGCTG GCTCCTCCCT  
2581 CCCACACAG CTGCTCCTGC TCTCCCTCCT CCAGGTGACC CCAGCCATGA GGACCTCGC  
2641 CATCCTTGCT GCCATTCTCC TGGTGGCCCT GCAGGCCAG GCTGAGCCAC TCCAGGCAAG  
2701 AGCTGATGAG GTTGTGCGAC CCCCAGGCA GATTGCAGC GACATCCAG AAGTGGTTGT

2761 TTCCCTTGCA TGGGACGAAA GCTTGGCTCC AAAGCATCCA GGTGAGAGAG GCAGGCATGC  
2821 AGAGCTGCTA AGTCTAGAGG GAAGGACGGG AGAGAGGTTT CAGAGTTGGG TCTCAGCAGT  
2881 CTATGTCACT GAGGTGGCTT CACTTAGAAT CTCTGGGCAT TGATTTTCTC ATCTAGAAAT  
2941 TGAACAGAGA GCCAAATAAA CCTGAGAAAC TTTATTTCTC CAAAGACTTG ATTCCAAGAA  
3001 ACATCTGTGA AATTCACTAA GTTTAAGATA TGAAGAGACA GACTAGTTAT TTCTGGATCT  
3061 AAACAAGTAG ACTTAGTTGT AAAGAGAAACA TTTTACTCTA TCTACAGAAG AGCTTTTAAA  
3121 AACTGCAGCC AAGCCTGAGG GTAAGTTCAG GTGTGTGTGT GATGGGGCAG GAATGCAAAA  
3181 ATGAGAGCAA AGGAGAATGA GTCTCAAATT CTGTGTGACA AGCACTGCTC TGCCTGTTTA  
3241 TTCCTATCGA CTGAGGTTGT TCGTGCTACC GGCTGCAATG CAGCCAGCAT CACCTGTCTG  
3301 CTAGCATGTG ACTTCCCCGA GATTCTTTTT CTTACCCACT GCTAACTCCA TACTCAATTT  
3361 CTCATGCTCT CCCTGTCCCA GGCTCAAGGA AAAACATGGA CTGCTATTGC AGAATACCAG  
3421 CGTGCAATGC AGGAGAACGT CGCTATGGAA CCTGCATCTA CCAGGGAAGA CTCTGGGCAT  
3481 TCTGTGCTG AGCTTGCAGA AAAAGAAAAA TGAGCTCAAA ATTTGCTTTG AGAGCTACAG  
3541 GGAATTGCTA TTAATCTGT ACCTTCTGCT CAATTTCTT TCCTCATCTC AAATAAATGC  
3601 CTTGTTACAA GATTTCTGTG TTTCCACCTC TTTAATGTGT GATATGTGTC TGTGTCAAGA  
3661 CACTTGGGAT ACACGTACCA AAACGCAAAA TCAAATTTTT GAACAATATA

## (2) INFORMATION FOR SEQ ID NO:2478:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2478:

1 CCTACCTTGC TATAGAAGAC CTGGGACAGA GGACTGCTGT CTGCCCTCTC TGGTCACCCT  
61 GCCTAGCTAG AGGATCTGTG ACCCCAGCCA TGAGGACCCT CGCCATCCTT GCTGCCATTC  
121 TCCTGGTGGC CCTGCAGGCC CAGGCTGAGC CACTCCAGGC AAGAGCTGAT GAGGTTGCTG  
181 CAGCCCCGGA GCAGATTGCA GCGGACATCC CAGAAGTGGT TGTTCCTT GCATGGGACG  
241 AAAGCTTGGC TCCAAAGCAT CCAGGCTCAA GGAAAAACAT GGACTGCTAT TGCAGAATAC  
301 CAGCGTGCAT TGCAGGAGAA CGTCGCTATG GAACCTGCAT CTACCAGGA AGACTCTGGG  
361 CATTCTGCTG CTGAGCTTGC AGAAAAAGAA AAATGAGCTC AAAATTTGCT TTGAGAGCTA  
421 CAGGGAATTG CTATTACTCC TGTACCTTCT GCTCAATTC CTTT

## (2) INFORMATION FOR SEQ ID NO:2479:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3781 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2479:

1 CCTGAGACAG AGGCAGCAGT GATACCCACC TGAGAGATCC TGTGTTTGAA CAACTGCTTC  
61 CCAAAACGGA AAGTATTTC AAGCTAAACC TTTGGGTGAA AAGAACTCTT GAAGTCATGA  
121 TTGCTTCACA GTTCTCTCA GCTCTCACTT TGGTGCTTCT CATTAAAGAG AGTGGAGCCT  
181 GGTCTTACAA CACCTCCACG GAAGCTATGA CTTATGATGA GGCCAGTGCT TATTGTGAGC  
241 AAAGGTACAC ACACCTGTTT GCAATTCAAA ACAAGAAGA GATTGAGTAC CTAAGTCCA  
301 TATTGAGCTA TTCACCAAGT TATTACTGGA TTGGAATCAG AAAAGTCAAC AATGTGTGGG  
361 TCTGGGTAGG AACCAGAAA CCTCTGACAG AAGAAGCCAA GAACTGGGCT CCAGGTGAAC  
421 CCAACAATAG GCAAAAAGAT GAGGACTGCG TGGAGATCTA CATCAAGAGA GAAAAAGATG  
481 TGGGCATGTG GAATGATGAG AGGTGCAGCA AGAAGAAGCT TGCCCTATGC TACACAGCTG  
541 CCTGTACCAA TACATCCTGC AGTGGCCACG GTGAATGTGT AGAGACCATC AATAATTACA  
601 CTTGCAAGTG TGACCTGGC TTCAGTGGAC TCAAGTGTGA GCAAAATTGT AACTGTACAG  
661 CCTGGGAATC CCCTGAGCAT GGAAGCCTGG TTTGCAGTCA CCCACTGGGA AACTTCAGCT  
721 ACAATTCTTC CTGCTCTATC AGCTGTGATA GGGGTACCT GCCAAGCAGC ATGGAGACCA  
781 TGCAGTGTAT GTCCTCTGGA GAATGGAGTG CTCCTATTCC AGCCTGCAAT GTGGTTGAGT  
841 GTGATGCTGT GACAAATCCA GCCAATGGGT TCGTGGAAATG TTTCCAAAAC CCTGGAAGCT  
901 TCCCATGGAA CACAACCTGT ACATTTGACT GTGAAGAAGG ATTTGAAC TAAGGGAGCCC  
961 AGAGCCTTCA GTGTACCTCA TCTGGGAATT GGGACAACGA GAAGCCAACG TGTAAGCTG  
1021 TGACATGCAG GGCCGTCCGC CAGCCTCAGA ATGGCTCTGT GAGGTGCAGC CATTCCCTG  
1081 CTGGAGAGTT CACCTTCAA TCATCCTGCA ACTTCACCTG TGAGGAAGGC TTCATTGTTG  
1141 AGGGACAGC CCAGTTGAA TGCAACACTC AAGGGCAGTG GACACAGCA ATCCAGTTT  
1201 GTGAAGCTTT CCAGTGCACA GCCTGTCCA ACCCCGAGCG AGGCTACATG AATTGTCTTC  
1261 CTAGTGCTTC TGGCAGTTTC CGTTATGGGT CCAGCTGTGA GTTCTCCTGT GAGCAGGGTT  
1321 TTGTGTTGAA GGGATCCAAA AGGCTCCAAT GTGGCCCCAC AGGGGAGTGG GACAACGAGA  
1381 AGCCACATG TGAAGCTGTG AGATGCGATG CTGTCCACCA GCCCCGAAG GGTGTTGTTGA  
1441 GGTGTGCTCA TTCCCTATT GGAGAATTCA CCTACAAGTC CTCTTGTGCC TTCAGTGTG  
1501 AGGAGGGATT TGAATTATAT GGATCAACTC AACTTGAGTG CACATCTCAG GGACAATGGA  
1561 CAGAAGAGGT TCCTTCTGTC CAGTGGTAA AATGTTCAAG CCTGGCAGTT CCGGGAAGA  
1621 TCAACATGAG CTGCACTGGG GAGCCCGTGT TTGGCACTGT GTGCAAGTTC GCCTGTCTG  
1681 AAGGATGGAC GCTCAATGGC TCTGCAGCTC GGACATGTGG AGCCACAGGA CACTGCTCTG

1741 GCCTGCTACC TACCTGTGAA GCTCCCACTG AGTCCAACAT TCCCTTGGA GCTGGACTTT  
1801 CTGCTGCTGG ACTCTCCCTC CTGACATTAG CACCATTCTT CCTCTGGCTT CGGAAATGCT  
1861 TACGGAAAGC AAAGAAATTT GTTCTGCCA GCAGCTGCCA AAGCCTTGAA TCAGACGGAA  
1921 GCTACCAAAA GCCTTCTTAC ATCCTTTAAG TTCAAAAGAA TCAGAAACAG GTGCATCTGG  
1981 GGAAGTAGAG GGATACACTG AAGTTAACAG AGACAGATAA CTCTCCTCGG GTCTCTGGCC  
2041 CTCTTTGCCT ACTATGCCAG ATGCCCTTAT GGCTGAAACC GCAACACCCA TCACCATTTC  
2101 AATAGATCAA AGTCCAGCAG GCAAGGACGG CCTTCAACTG AAAAGACTCA GTGTTCCCTT  
2161 TCCTACTCTC AGGATCAAGA AAGTGTGGC TAATGAAGGG AAAGGATATT TTCTTCCAAG  
2221 CAAAGGTGAA GAGACCAAGA CTCTGAAATC TCAGAATTCC TTTTCTAACT CTCCCTTGCT  
2281 CGCTGTAAAA TCTTGGCACA GAAACACAAT ATTTTGTGGC TTTCTTTCTT TTGCCCTTCA  
2341 CAGTGTTCG ACAGCTGATT ACACAGTTGC TGTCATAAGA ATGAATAATA ATTATCCAGA  
2401 GTTTAGAGGA AAAAAATGAC TAAAAATATT ATAACCTAAA AAAATGACAG ATGTTGAATG  
2461 CCCACAGGCA AATGCATGGA GGGTTGTTAA TGGTGCAAT CCTACTGAAT GCTCTGTGCG  
2521 AGGGTTACTA TGCACAATTT AATCACTTTC ATCCCTATGG GATTCACTGC TTCTTAAAGA  
2581 GTTCTTAAGG ATTGTGATAT TTTTACTTGC ATTGAATATA TTATAATCTT CCATACCTCT  
2641 TCATTCAATA CAAGTGTGGT AGGGACTTAA AAAACTTGTA AATGCTGTCA ACTATGATAT  
2701 GGTAAGGTT ACTTATTCTA GATTACCCCT TCATTGTTTA TTAACAAATT ATGTTACATC  
2761 TGTTTTAAAT TTATTTCAA AAGGGAAACT ATTGTCCCT AGCAAGGCAT GATGTTAACC  
2821 AGAATAAAGT TCTGAGTGT TTTACTACAG TTGTTTTTG AAAACATGGT AGAATTGGAG  
2881 AGTAAAGT GAATGGAAGG TTTGTATATT GTCAGATATT TTTTCAGAAA TATGTGGTTT  
2941 CCACGATGAA AAACTTCCAT GAGGCCAAAC GTTTTGAAT AATAAAAGCA TAAATGCAAA  
3001 CACACAAAGG TATAATTTA TGAATGTCTT TGTTGGAAAA GAATACAGAA AGATGGATGT  
3061 GCTTTGCATT CCTACAAAGA TGTTGTCTAG ATGTGATATG TAAACATAAT TCTTGATAT  
3121 TATGGAAGAT TTTAAATTCA CAATAGAAAC TCACCATGTA AAAGAGTCAT CTGGTAGATT  
3181 TTTAACGAAT GAAGATGTCT AATAGTTATT CCTATTGTT TTTCTTCTGT ATGTTAGGGT  
3241 GCTCTGGAAG AGAGGAATGC CTGTGTGAGC AAGCATTAT GTTTATTTAT AAGCAGATTT  
3301 AACCAATTCCA AAGGAATCTC CAGTTTTCAG TTGATCACTG GCAATGAAAA ATTCTCAGTC  
3361 AGTAATTGCC AAAGCTGCTC TAGCCTTGAG GAGTGTGAGA ATCAAACTC TCCTACACTT  
3421 CCATTAACTT AGCATGTGTT GAAAAAAGAA GTTTCAGAGA AGTCTGGCT GAACACTGGC  
3481 AACGACAAAG CCAACAGTCA AAACAGAGAT GTGATAAGGA TCAGAACAGC AGAGGTTCTT  
3541 TTAAAGGGGC AGAAAACTC TGGGAAATAA GAGAGAACAA CTAAGTGAT CAGGCTATGT  
3601 ATGGAATACA GTGTTATTTT CTTTGAAATT GTTTAAGTGT TGTAATATT TATGTAACT  
3661 GCATTAGAAA TTAGCTGTGT GAAATACCAG TGTGGTTGT GTTTGAGTT TATTGAGAT  
3721 TTTAAATTAT AACTTAAAT ATTTTATAAT TTTTAAAGTA TATATTATT TAAGCTTATG  
3781 TCAGACCTAT TTGACATAAC ACTATAAAGG TTGACAATAA ATGTGCTTAT GTTT

## (2) INFORMATION FOR SEQ ID NO:2480:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141541 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2480:

1 GATCAAAATT TTACCTATT ATGCATTGA TATATAATA AGTATATAA TGCACACACA  
61 GACACAGCAA TGATGGTGAA CAGTCTTCAT ACAATTATAT GGATGAATCT CATAAAATGC  
121 TGAGTTAAAG AAATCAGACC AAAGAACATA TACTGAAAGA TTCTCTCTAT ATACAAAGTT  
181 CAAAATAGG TGGACCAATT CATGGTGGTG TTAGAAATCA GAAGAGAGGC TACCTTTGTG  
241 GGGAGGGGAC AGTTTAATGC CCAGAAGCGG TAAATAAGGA ATCCTCTGGG GAGTGGTAAAT  
301 GATCTGGATG CTGCTACAG GATGTGTTGG TTGTAATAAT GCATTTTTTT ATATCTAGCT  
361 TTTTCCATGT GTATATTATA CTTCAAAGAA GTTCAGTTAA TAATTTCTCA TGTCACTGTA  
421 GAGTAGCTCA GTTAGCCCCA GCAAGCCTCT GGCTTAATCT TGTTTTACCT TAAGCCATCA  
481 GTCATTTACA AGTAGGAAAA TTCACAGGGA AAGTTAGAGT ATAAATCCA GAATGAAGGT  
541 TTAGTGGGTA AGAGTCTCTC CATTTTCCAA AGCCCGTTTA TTTCTTGATT CCAGTTCTTA  
601 AGAAGTCTCA GCATTGTGTC TTTTTCATGT ATCTTACAAG AAGACAGCAT GTGCTTCTAA  
661 CACCTGATAC ATTGTATCTA CCAGCACTTG GTAAACAGAA AAGAACCACA TTTTCTTGT  
721 AGGAGAAATT TGGTGCCTAT TTCCTACCAG GCACCAATAA GTGGGACCAA TAGGTGGGAT  
781 TAAAGATACA GTAGAAAGTA TTTAAACTT GCCAGGGGGC AATAGTCTGA AAATAAGTAA  
841 ATTGGTGCTA TAGAATGGAA GTTACAGGCT TCTTCTTTT TTCCCAAG ATCTGCTCCT  
901 TGAGCCCCA GAGACTTTTC TGTCTGTTAC TGTTTCTTCA TTCCTCATCT CCAGAGCCAG  
961 CCTGAGAAG TGCAGACCAA AGCCAGGGAA GGCTCTGCAA AGATGTACAA ATGGAAGTCA  
1021 CCTTAATAAC CTCTGACTGC TGGCATAAT ACATTTCACT CAAAAGAGGG GTTAAACAAT  
1081 GGAACAGAAT ACAGAGGCCA GAAATAATGC TGAACACTGA CAACCATCTG ATCTTTGACA  
1141 AAATCCACAA AAACAAGCAA TGGAGAAAGG ACTCCCTATT CCATAATGTT GCTGGGATAA  
1201 CTGTCTAGCT ATATACAGAA GATTGAACCT GGGCCCTTC CTACATCAT ATACAAAAA  
1261 TAACTCAAGA TGGAGTAAAG ACTTAAATCT AAAACCAAAC ACTATAAAAA CCCTGGAAGA  
1321 TAGCCTGGGA AATACCATTG TGGACATAGG ACCTGGCAAA GACTTCATGA CAAGACACCA  
1381 AAAGCAATAG CAACAAAAC CAAATTGACT AATGAACTA ATGAACTCT TTAGTTGTAC  
1441 AACAGATAGT TTATCTGTAC AACAAAATAA ACTATCAACA GAGTAAACAA CCTACAGAAT  
1501 GGAAAAATTT TTTGCAACT ATGCATCTGA CAAAGGTCTA ATATCCAGAA TCTATAAGGA  
1561 ATTTAAACAA ATTTACAGC AAAAAAATGA CCTCATTAAG AAGTGGGCAA AGGACATGAA  
1621 CAGATGCTTT TCAAAATAAG ACATTCACAC ATCCAACAAC CATATGAAAA GATGTTTAA



1681 ATCACTAATC ATTAGAGGAA TACAAATCAA AAGCATAATA AGATACCATC TAATACCAGT  
1741 AGGAATGACT ACTATTAAAA AGTCAGACAA TAACAGATGC TGGTGAAGGT TGTGGAGAAA  
1801 AGGGAATGTT TATGCACTGC TAGTGGGAAT GTAACTAGT TCAGCCATTG TGGGAAGAGAG  
1861 TGTGGTGATT CCTCAAAGAA TGTAAAACCG AACTGCCTTT CAATCCAGCA ATCCCATTAT  
1921 TGGATATACA CCAAAGGAA TAGAAATTGT TTTACCGTAA AGGCGCATGC ATGCATATGT  
1981 TCATTACAGC ACTATTTACG ATAGCAAAGA CATGGAATCG TCTAAATGCC CATCAGTGGT  
2041 AGACTAGCTA AAAAAAAAAA AATGTGGTAC ATATACATCA CAGAATTGA TGCAGCCATA  
2101 AAAATGAACA AGATCATCAT GTCCTTTGCA GCAACATGGA TGTAGTTGGA GCCATTATC  
2161 CTAAGCAAAT TAATGCAGGA ACAGAAAGCC AAATACCACA TGTTCCTCATT TATAAGTGAC  
2221 AGCTAAATAT TGAGTACACA TGGACACAAA GAAGGGAACA ATAGACATGG GACCTACTTG  
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72661	TTTTACTATT	AATTAGTTGC	TGGTGCCCAA	GTTTTTACTG	AGAAATGGGG	ATAATTTTGG
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72781	CAACACAGCC	TGGCTTTTAG	TAAATGATCA	AAAATACCTG	TTGAATGAAT	AAATGGAGTC
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72961	AGAAAAGCAT	CTGAAAAAAG	CTGCCAGCCG	CTGTGTCTCC	TAATATCAAA	CTGAGCACAG
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73321	CTGGATTCAA	GTGATTCTCC	TGCCCTCAGC	TCCCGAGTAG	CTGGGACAA	AGGTGTGTGC
73381	CATTACACCT	GGCTAATTTT	TGTATTTTGA	GCAGAGATGC	GGTTTCACCA	TGTTGGCCAG
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73501	ATTACAGGCA	TGAGCCACTG	CACCTACCAA	GCACCTTCTAC	TGATAGCATT	TACAAACCCT
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141301 GTGAAACCCC GTCTCTACTA AAAATACAAA AATTAGCCAG GAGTGATGGT GCGCACCTGT
141361 AATGCCAGCT ACTTGGGAGG CTGAGGCAGG AGGATCACTT GAACCCAGGA GGTGGAGGTT
141421 GAAGTAAGCC GAGGTCATGC CACTGCACTC CAGCCTGGGC AACAGAGTGA GACTCCATCT
141481 CAAAAAATAA AAAAATGATC AAAGAAAGGT GAATTTTCAT CTACCCTATT TCTGCTGAGG
141541 AAAATGGACT ATTTTCAAAT ATTTTAAATA AGGGTCAAAA TGAGGGGATC

```

## (2) INFORMATION FOR SEQ ID NO:2481:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1261 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2481:

```

1 GCCACCATGG AAACCTTTG CCTCAGGGCA TCCTTTTGGC TGGCACTGGT TGGATGTGTA
61 ATCAGTGATA ATCCTGAGAG ATACAGCACA AATCTAAGCA ATCATGTGGA TGATTTCAAC
121 ACTTTTCGTG GCACAGAGCT CAGCTTCCTG GTTACCACTC ATCAACCCAC TAATTTGTC
181 CTACCCAGCA ATGGCTCAAT GCACAACATAT TGCCACAGC AGACTAAAAT TACTTCAGCT
241 TTCAAATACA TTAACACTGT GATATCTTGT ACTATTTTCA TCGTGGGAAT GGTGGGGAAT
301 GCAACTCTGC TCAGGATCAT TTACCAGAAC AAATGTATGA GGAATGGCCC CAACGCGCTG
361 ATAGCCAGTC TTGCCCTTGG AGACCTTATC TATGTGGTCA TTGATCTCCC TATCAATGTA
421 TTTAAGCTGC TGGCTGGGCG CTGGCCTTTT GATCACAATG ACTTTGGCGT ATTTCTTTGC
481 AAGCTGTTCC CTTTTTGGCA GAAGTCCTCG GTGGGGATCA CCGTCCTCAA CCTCTGCGCT
541 CTTAGTGTTG ACAGGTACAG AGCAGTTGCC TCCTGGAGTC GTGTTGAGG AATTGGGATT
601 CCTTTGGTAA CTGCCATTGA AATTGCCTCC ATCTGGATCC TGTCCTTTAT CCTGGCCATT
661 CCTGAAGCGA TTGGCTTCGT CATGGTACCC TTTGAATATA GGGGTGGACA GCATAAAACC
721 TGTATGCTCA ATGCCACATC AAAATTCTAT GAGTTCTACC AAGATGTAAA GGACTGGTGG
781 CTCTTCGGGT TCTATTTCTG TATGCCCTTG GTGTGCACTG CGATCTTCTA CACCTCATG
841 ACTGGTGAGA TGTGAACAG AAGGAATGGC AGCTTGAGAA TTGCCCTCAG TGAACATCTT
901 AAGCAGCGTC GAGAAGTGGC AAAAACAGTT TTCTGCTTGG TTGTAATTTT TGCTCTTTGC
961 TGGTTCCTC TTCAATTAAG CCGTATATG AAGAAACTG TGTATAACGA GATGGACAAG
1021 AACCAGATGT AATTACTTAG TTTCTTACTG CTCATGGATT ACATCGGTAT TAACCTGGCA
1081 ACCATGAATT CATGTATAAA CCCCATAGCT CTGTATTTTG TGAGCAAGAA ATTTAAAAAT
1141 TGTATTCAGT CATGCCTCTG CTGCTGCTGT TACCAGTCCA AAAGTCTGAT GACCTCGGTC
1201 CCCATGAACG GAACAAGCAT CCAGTGGGAG AACCACGATC AAAACAACCA CAACACAGAC
1261 CGGAGCAGCC ATAAGGACAG CATGAACTGA CCACCCTTAG AAGCACTCCT

```

## (2) INFORMATION FOR SEQ ID NO:2482:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1861 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2482:

```

1 GAATTCGGGA AAAAGTGAAG GTGTAAAGC AGCACAAGTG CAATAAGAGA TATTTCTCTCA
61 AATTTGCCTC AAGATGGAAA CCCTTTGCCT CAGGGCATCC TTTTGGCTGG CACTGTTTGG
121 ATGTGTAATC AGTGATAATC CTGAGAGATA CAGCACAAAT CTAAGCAATC ATGTGGATGA
181 TTTCACTACT TTTCGTGGCA CAGAGCTCAG CTTCTGGTGT ACCACTCATC AACCCTACTA
241 TTTGGTCCCTA CCCAGCAATG GCTCAATGCA CAACTATTGC CCACAGCAGA CTAAAATTAC
301 TTCAGCTTTC AAATACATTA ACACTGTGAT ATCTTGTAAT ATTTTCATCG TGGGAATGGT
361 GGGGAATGCA ACTCTGCTCA GGATCATTTA CCAGAACAAA TGTATGAGGA ATGGCCCCAA
421 CGCGCTGATA GCCAGTCTTG CCCTTGAGGA CCTTATCTAT GTGGTCATTG ATCTCCCTAT
481 CAATGTATTT AAGCTGCTGG CTGGGCGCTG GCCTTTTGGT CACAATGACT TTGGCGTATT
541 TCTTTGCAAG CTGTTCCCCT TTTTGCAGAA GTCCTCGGTG GGGATCACCG TCCTCAACCT
601 CTGCGCTCTT AGTGTGACA GGTACAGAGC AGTTGCCTCC TGGAGTCGTG TTCAGGGAAT
661 TGGGATTCCT TTGGTAACTG CCATTGAAAT TGTCTCCATC TGGATCCTGT CCTTTATCCT
721 GGCCATTCCCT GAAGCGATTG GCTTCGTCAT GGTACCCTTT GAATATAGGG GTGAACAGCA
781 TAAACCTGT ATGCTCAATG CCACATCAAA ATTCATGGAG TTCTACCAAG ATGTAAGGA
841 CTGGTGGCTC TTCGGGTTCT ATTTCTGTAT GCCCTTGGTG TGCACTGCGA TCTTCTACAC
901 CCTCATGACT TGTGAGATGT TGAACAGAAG GAATGGCAGC TTGAGAATTG CCCTCAGTGA
961 ACATCTTAAG CAGCGTCGAG AAGTGGCAAA AACAGTTTTT TGCTTGGTTG TAATTTTGTG
1021 TCTTTGCTGG TTCCCTCTTC ATTTAAGCCG TATATTGAAG AAAACTGTGT ATAACGAGAT
1081 GGACAAGAAC CGATGTGAAT TACTTAGTTT CTTACTGCTC ATGGATTACA TCGGTATTAA
1141 CTTGGCAACC ATGAATTCAT GTATAAACCC CATAGCTCTG TATTTTGTGA GCAAGAAATT
1201 TAAAAATTGT TTCCAGTCAT GCCTCTGCTG CTGCTGTTAC CAGTCCAAAA GTCTGATGAC
1261 CTCGGTCCCC ATGAACGGAA CAAGCATCCA GTGGAAGAAC CACGATCAAA ACAACCACAA
1321 CACAGACCGG AGCAGCCATA AGGACAGCAT GAACTGACCA CCCTTAGAAG CACTCCTCGG
1381 TACTCCCATATA ATCTCTCGG AGAAAAAAT CACAAGGCAA CTGTGAGTCC GGAATCTCT

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1441 TCTCTGATCC TTCTTCCTTA ATTCACCTCC ACACCCAAGA AGAAATGCTT TCCAAAACCG  
 1501 CAAGGGTAGA CTGGTTTATC CACCCACAAC ATCTACGAAT CGTACTTCTT TAATTGATCT  
 1561 AATTACATA TTCTGCGTGT TGTATTGAGC ACTAAAAAAT GGTGGGAGCT GGGGGAGAAT  
 1621 GAAGACTGTT AAATGAAACC AGAAGGATAT TTACTACTTT TGCATGAAAA TAGAGCTTTC  
 1681 AAGTACATGG CTAGCTTTTA TGGCAGTTCT GGTGAATGTT CAATGGGAAC TGGTCACCAT  
 1741 GAAACTTTAG AGATTAACGA CAAGATTTTC TACTTTTTTT AAGTGATTTT TTTGTCTTTC  
 1801 AGCCAAACAC AATATGGGCT CAAGTCACTT TTATTTGAAA TGTCAATTGG TGCCAGTATC  
 1861 CCGAATTC

## (2) INFORMATION FOR SEQ ID NO:2483:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2431:

1 CACCGCTCCT GTCAGCCAAC AAATATCCAT TGAGCGACAC CTGTGTCCCA GGTGCTGCTC  
 61 TGGGCCCTGG GAGAAGTGCA TCAGTGGGCT TGGTAGTAGA GGGTAGGGAT GGAGTGAAGG  
 121 GTAGGCAGGA AGAATGTCCC CAGGCTGGTA GGAGGTGGGG TGGGGGGTTT CAGTCTCAAA  
 181 ACTCCCATGA AAACCAGAGA GAAGTTTCAG AACTCCACCC AAGAGGCTGG GTTCTAGGG  
 241 CCAGAGCTG CCCTCCCCCA CCCTAGAATG GGCTATAAAA GTCCCTTCCC AGCTACGTCC  
 301 AGAGAAGAGC TGGAGGAAGT GAGAGGTCGG CTGGGGGTCC TCAAAGTGAG AGGGGAGCAG  
 361 AGGATCCTCC CGTGCAGGCT GTGGATGTCA CTCACTTCCC AGCTGGTGAA GCCTCGCTGC  
 421 AGAGATGCAT CTGCTCCAG CCCTGGCAGG GGTCTGGGCC AACTCGTCC TCGCCAGCC  
 481 CTGTGAGGCG ACTGACCAG GTAATAGTCC CTTAGACAGG CAAGGAGGAG GGAGGGGAAA  
 541 TGAAGGGGGA AGCACTTGGG TCTTGGAGGG GGTCTTGTGG CTTGCTGAAC CTTAGTCCC  
 601 CATCTCTTTG AACAGCCTCC CCTGGGCGAG TGGAGACCTC GGTCTGCGA GACTGCATAG  
 661 CAGAGGCCAA GTTGCTGGTG GATGCTGCCT ACAATTGGAC CCAGAAGAGG TGGACTTGGG  
 721 TCTGGGGGCT GCATGGGCCT GGGAGGATCA GT

## (2) INFORMATION FOR SEQ ID NO:2484:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2484:

1 TAATACCTTG TGGGGTCAGG GAGCCCATGT CCCGTGCTGA TGTATTTC CCACCAGGTC  
 61 CGGGCTGTCT CCAACCAGAT TGTGCGCTTC CCCAATGAGA GACTGACCTC CGACCGTGGC  
 121 CGAGCCCTCA TGTTTCATGCA GTGGGGCCAG TTCATTGACC ATGACCTGGA CTTCTCCCCG  
 181 GAGTCCCCCG CCAGAGTGGC CTTCAGTCA GGCCTTGACT GTGAGAGGAC CTGCGCCAG  
 241 CTGCCCCCCT GCTTTCCCAT CAAGGTACCT ACCCTCAGCC AATCTCCCAT GCCCTTGTGT  
 301 GGCCTCCCCC AAAGGCAAGG TGCTGGGGGT GGGGATCTGG AAGACTGGAG CACCATCCTT  
 361 AAGGAGCTGC CTGTGGAGCT AGGTATGAG ACAGAGACAC AAG

## (2) INFORMATION FOR SEQ ID NO:2485:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2485:

1 CACTGTCTCC TCTTCATCT CAGATCCAC CCAATGACCC CCGCATCAAG AACCAGCGTG  
 61 ACTGCATCCC TTTCTCCGC TCGGCACCCT CATGCCCCCA AAACAAGAAC AGAGTCCGCA  
 121 ACCAGATCAA CGCGCTCACC TCCTTTGTGG ACGCCAGCAT GGTGTATGGC AGTGAGGTCT  
 181 CCCTCTCGCT GCGGCTCCGC AACCGGACCA ACTACCTGGG GCTGCTGGCC ATCAACCAGC  
 241 GCTTTCAAGA CAACGGCCGG GCCCTGCTGC CTTTCGACAA CCTGCACGAT GACCCCTGTC  
 301 TCCTCACCAA CCGCTCGGCG CGCATCCCCT GCTTCCTGGC AGGTGAGACA GGGAGGAAGG  
 361 TGGTGTCTTC CCAGGAAACA GCCATCCCTG GGGTCCCAAC TGGGAAGCAA TGGTGGGATG  
 421 TGGTGAAGGT ACATGGTTTG GGACCTCAGT ATTAGGCACA CCATAAGCAT GGATCTGTGC  
 481 AC

## (2) INFORMATION FOR SEQ ID NO:2486:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2486:

1 TGAAGAGATG GAGGTCCAGT GAGGGCCAGG AGTTTGGCCC ACCCGTCTC TCCCATCCCC



61 AGCCCTGGT CTACCCTGGT AGAAAGACAT TTCTCTGGGA AACTCTGCAG TAAATCTGAG  
 121 CTTGGGGTTT TCAAGGTGAC ACCCGATCAA CGGAAACCCC CAAACTGGCA GCCATGCACA  
 181 CCCTCTTTAT GCGAGAGCAC AACC GGCTGG CCACCGAGCT GAGACGCCTG AATCCCCGGT  
 241 GGAATGGAGA CAAACTGTAC AATGAGGCTC GGAAGATCAT GGGGGCCATG GTCCAGGTAA  
 301 GGAGCTCTGC ATCCCAGCAT CCCCC

## (2) INFORMATION FOR SEQ ID NO:2487:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 421 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2487:

1 CTTTGTATCT CCACCCACCA ATAGTAAATT AATGTTGTCA CATTGACGT GATGACAATA  
 61 AAGAATATGT CTGAGCCACC CTTTGAAAAG GCAAGGGTAT GGGTGAGTAG CCTCTGGGGA  
 121 ATGTTCTCTC TGTCTTCCCT TCCAGATCAT CACCTACCGA GACTTTCTGC CCCTGGTTCT  
 181 GGGCAAGGCC CGGGCCAGGA GAACCTGGG GCACTACAGG GGGTACTGCT CCAATGTGGA  
 241 CCCACGGGTG GCCAATGTCT TCACCCTGGC CTTCCGCTTT GGCCACACAA TGCTCCAGCC  
 301 CTTTCATGTT CGCTTGGACA GTCAGTACCG GGCCTCCGCA CCCAACTCGC ATGTCCCACT  
 361 TAGCTCTGCC TTCTTTGCCA GCTGGCGGAT CGTGTATGAA GGTGACCAGG TTTTCCAGGG  
 421 GGCAAATGGG GGTGAGGGTG GGGAGCATGC CCTCCCCTAG GTGG

## (2) INFORMATION FOR SEQ ID NO:2488:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 361 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2488:

1 TCCAGCTGCT TCATGTCTCT CCAGAACTCT GTTTCCTGAC AAACGTTACT AACATACCCG  
 61 ACTGGCTTGT CCAGCTCTGG GCTAGCTTGG CATCATGTGA TAACCCAAAGT AGCTTCCCAG  
 121 AGGCTGGTCC AATCTGTGCT GCTCACATTC CCTGCCACCA GGGGGCATCG ACCCATCCT  
 181 CCGGGGCCCTC ATGGCCACCC CTGCCAAGCT GAACCGTCAG GATGCCATGT TAGTGGATGA  
 241 GCTCCGGGAC CGGCTGTTT GCACAAGTGG GAGGATGGG CTGGACCTGG CAGCTCTCAA  
 301 CATGCAACGA AGCCGGGACC ACGGCCTTCC AGGTGAGGGG GCTGTCCACC TCTTCTCCCA  
 361 GCTTTGCTCG GGCCAGGCTG CTAAGGGGT TCTGGGAAGA CCCTGGTACC

## (2) INFORMATION FOR SEQ ID NO:2489:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 421 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2489:

1 CGACTGCCTG GTAGTTCTG GTGGCAGAAA CGAGGTGTTT TCACCAAAAG ACAGCGCAAG  
 61 GCCCTGAGCA GAATTTCTT GTCTCGAATT ATATGTGACA ATACCGGTAT CACCACGGTT  
 121 TCAAGGGACA TCTTCAGAGC CAACATCTAC CCTCGGGGCT TTGTGAACTG CAGCCGTATC  
 181 CCCAGGTTGA ACCTATCAGC CTGGCGAGGG ACATGAGGCT TCTGCAGGTA AGGGGAGGCC  
 241 ACCTCCAGCA CCCTGGGCTG GTTAAGCCTC ACATCCTTCC CTGGATGGAT GGCTGAGTCC  
 301 TCTTAGGTCT CTAAGCAGAG AAAACAGAAC TTGTCACTAG GTACTCTTTC CAAGTGGCTT  
 361 CCCAATGTGC TAGTTTCTGG GCTGACAGTC AATCCAGGC CCTAGGACTT TGGGGGGAAG  
 421 TTAGGAGCAT CCAACTA

## (2) INFORMATION FOR SEQ ID NO:2490:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2521 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2490:

1 GAATTCCTG GCCAGGACCC CTGCCAGGGC ACTGACCCAG CCTCCCCTGG GGCAGTGGAG  
 61 ACCTCGGTCC TCGGAGACTG CATAGCAGAG GCCAAGTTGC TGGTGGATGC TGCCTACAAT  
 121 TGGACCCAGA AGAGCATCAA GCAGCGGCTT CGCAGCGGTT CAGCCAGCCC CATGGACCTC  
 181 CTGTCCTACT TCAAACAACC GGTAGCAGCC ACCAGGACAG TTGTTCCGGC CGCAGATTAT  
 241 ATGCATGTGG CTTTGGGGCT GCTTGAAGAG AAGTTACAAC CCCAGCGGTC CGGACCCTTC  
 301 ATTGTCACTG ATGTGCTAAC AGAACCACAG CTGCGGCTGC TGTCCCAGGC CAGTGGCTGT  
 361 GCTCTCCGGG ACCAGGCCGA GCGCTGCAGC GACAAGTACC GCACCATCAC TGGACGGTGC  
 421 AACACAAGA GGAGACCCTT GCTAGGGGCC TCCAACCAGG CTCTGGCTCG CTGGCTGCC  
 481 GCCGAGTATG AGGATGGGCT GTCGCTCCCC TTCGGCTGGA CCCCACAGC GAGGCGCAAT  
 541 GGCTTCCTTC TCCCTCTTGT CCGGGCTGTC TCCAACCAGA TTGTGCGCTT CCCCAATGAG

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601 AGACTGACCT CCGACCGTGG CCGAGCCCTC ATGTTTCATGC AGTGGGGCCA GTTCATTGAC
661 CATGACCTGG ACTTCTCCCC GGAGTCCCGG GCCAGAGTGG CCTTCACTGC AGGCGTTGAC
721 TGTGAGAGGA CCGTGCGCCCA GCTGCCCCCC TGCTTTCCCA TCAAGATCCC ACCCAATGAC
781 CCCCAGCATCA AGAACCAGCG TGACTGCATC CCTTTCTTCC GCTCGGCACC CTCATGCCCC
841 CAAAACAAGA ACAGAGTCCG CAACAGATC AACGCGCTCA CCTCCTTTGT GGACGCCAGC
901 ATGGTGTATG GCAGTGAGGT CTCCCTCTCG CTGCGGCTCC GCAACCGGAC CAACTACCTG
961 GGGCTGCTGG CCATCAACCA GCGCTTTCAA GACAACGGCC GGGCCCTGCT GGCCTTCGAC
1021 AACCTGCACG ATGACCCCTG TCTCTCACC AACCGCTCGG CGCGCATCCC CTGCTTCCTG
1081 GCAGGTGACA CCCGATCAAC GGAAACCCCC AAAGTGGCAG CCATGCACAC CCTCTTTATG
1141 CGAGAGCACA ACCGGCTGGC CACCGAGCTG AGACGCCTGA ATCCCCGGTG GAATGGAGAC
1201 AAAGTGTACA ATGAGGCTCG GAAGATCATG GGGGCCATGG TCCAGATCAT CACCTACCGA
1261 GACTTTCTGC CCCTGGTTCT GGGCAAGGCC CGGGCCAGGA GAACCTGGG GCACTACAGG
1321 GGGTACTGCT CCAATGTGGA CCCACGGGTG GCCAATGTCT TCACCTGGC CTTCCGCTTT
1381 GGCCACACAA TGCTCCAGCC CTTCAATGTT CGCTTGAGCA GTCAGTACCG GGCCTTCGCA
1441 CCAACTCGC ATGTCCACT TAGCTCTGCC TTCTTTGCCA GCTGGCGGAT CGTGATGAA
1501 GGGGGCATCG ACCCATCCT CCGGGGCCCTC ATGGCCACCC CTGCCAAGCT GAACCGTCAG
1561 GATGCCATGT TAGTGGATGA GCTCCGGGAC CGCTGTTTC GGCAAGTGAG GAGGATTGGG
1621 CTGGACCTGG CAGCTCTCAA CATGCAACGA AGCCGGGACC ACGGCCTTC AGGTACAAT
1681 CTGTGGAGGC GCTTCTGTGG GCTCTCCAG CCCCGGAATT TGGCACAGCT TAGCCGGGTG
1741 CTGAAAACCC AGGACTTGGC AAGGAAGTTC CTGAATTTGT ATGGAACACC TGACAACATT
1801 GACATCTGGA TTGGGGCCAT CGCTGAGCCT CTTTGGCCG GGGCTCGAGT GGGGCTCTT
1861 CTGGCTTGTC TGTTGAGAA CCAGTTCAGA AGAGCCGAGA CGGAGACAGG TTCTGGTGGC
1921 AGAACGAGGT GTTTTCACCA AAGACAGCGC AAGGCCCTGA GCAGAATTC CTTGTCTCGA
1981 ATTATATGTG ACAATACCGG TATCACCAGG GTTCAAGGG ACATCTTCAG AGCCAACATC
2041 TACCCTCGGG GCTTTGTGAA CTGCAGCCGT ATCCCCAGGT TGAACCTATC AGCCTGGCGA
2101 GGGACATGAG GCTTCTGCAG GAGTCTATCC CAAGTCTCCA ACTTTTGGAG ACAAGGGGAA
2161 GGGGAGGACC ATGAGGCTGC CTTGTCTCCC TGGAGCAAGT GCAGGCTCGT GACGCTTCTG
2221 CTGGCTACAG CTCAGAGCTG GGTCCCCAG CCAGGAGTGA AGGCTGGGG CTCCTATCAG
2281 CAATGGACCT TCCGCCTTGG GAGCCTCTTA GGTATTAGGC TATGAATCAG CGCCACGTGC
2341 AAAGGCTTGG GAGCCAAGCC ATGTGGTCTT GCACCCAGG CAAGAAAAGT CAGCTGGAGG
2401 GTTTACAGCA CTTTCTACTG TTTCCAGCC CTCCTCCCC TCCCTACCA TGACTAAGAG
2461 ACCACTCGGT CCTAGCCTCC AGACACCCCA CAATACTCCT CTGAGCCTGA GGCCAGGCAG
2521 CATGCTCTGC TTCTACCAAT AAAGCACTGC CGGAATTC

```

## (2) INFORMATION FOR SEQ ID NO:2491:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2491:

## (2) INFORMATION FOR SEQ ID NO:2492:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 781 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2431:

```

1 GCATTTTTTC AAGTTTTATG ATTTATTTAA CTTGTGGAAC AAAAAATAAC CAGAAACCAC
61 CACCTCTCAC GCCAAGCTC ACACCTTCAG CCTCCAACAT GAAGGTCTCC GCAGCACTTC
121 TGTGGCTGCT GCTCATAGCA GCTGCCTTCA GCGCCAGGG GCTCGCTGGG CCAGCTTCTG
181 TCCCAACCAC CTGCTGCTTT AACCTGGCCA ATAGGAAGAT ACCCCTTCAG CGACTAGAGA
241 GCTACAGGAG AATCACCAGT GGCAATATG CCCAGAAAGC TGTGATCTTC AAGACCAAC
301 TGGCCAAGGA TATCTGTGCC GACCCCAAGA AGAAGTGGGT GCAGGATTCC ATGAAGTATC
361 TGGACCAAAA ATCTCCAAT CCAAAGCCAT AAATAATCAC CATTTTGTAA ACCAAACCAG
421 AGCCTGAGTG TTGCCTAATT TGTTTTCCCT TCTTACAATG CATTTCTGAG TAACCTCATT
481 ATCAGTCCAA AGGGCATGGG TTTTATTATA TATATATATA TTTTAAAAA AAAAAAACC
541 GTATTGCATT TAATTTATTG AGGCTTTAAA ACTTATCCTC CATGAATATC AGTTATTTTT
601 AAAGTGTAAA GCTTTGTGCA GATTCTTTAC CCCCTGGGAG CCCCAATTCC ATCCCCTGTC
661 ACGTGTGGGC AATGTTCCCC CTCTCCTCTC TTCCTCCCTG GAATCTTGTA AAGGTCCTGG
721 CAAAGATGAT CAGTATGAAA ATGTCATTGT TCTTGTGAAC CCAAAGTGTG ACTCATTAAA
781 TGGAAGTAAA TGTTGTTTTA GGAATAC

```

## (2) INFORMATION FOR SEQ ID NO:2492:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2492:

1 ATGAAGGTCT CCGCAGCACT TCTGTGGCTG CTGCTCATAG CAGCTGCCTT CAGCCCCCAG  
61 GGGCTCGCTG GGCCAGCTTC TGTCCCAACC ACCTGCTGCT TTAACCTGGC CAATAGGAAG  
121 ATACCCCTTC AGCGACTAGA GAGCTACAGG AGAATCACCA GTGGCAAATG TCCCCAGAAA  
181 GCTGTGATCT TCAAGACCAA ACTGGCCAAG GATATCTGTG CCGACCCCAA GAAGAAGTGG  
241 GTGCAGGATT CCATGAAGTA TCTGGACCAA AAATCTCCAA CTCCAAAGCC ATAA

(2) INFORMATION FOR SEQ ID NO:2493:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: 2641 nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2493:

1 CCACATATTC CCCTCCTTTT CCAAGGCAAG ATCCAGATGG ATTAAAAAAT GTACCAAGTC  
61 CCTCCTACTA GCTTGCCCTT CTTCGTCTCT GCTTGACTTC CTAGGATCTG GAATCTGGTC  
121 AGCAATCAGG AATCCCTTCA TCGTGACCCC CGCATGGGCA AAGGCTTCCC TGGAATCTCC  
181 CACACTGTCT GCTCCCTATA AAAGGCAGGC AGATGGGCCA GAGGAGCAGA GAGGCTGAGA  
241 CCAACCCAGA AACCACCACC TCTCAGCCCA AAGCTCACAC CTTAGCCTC CAACATGAAG  
301 GTCTCCGCAG CACTTCTGTG GCTGCTGCTC ATAGCAGCTG CCTTCAGCCC CCAGGGGGCTC  
361 GCTGGGCCAG GTAAGCCCCC CAACTCCTTA CAGGAAAGGT AAGGTAACCA CCTCCAGGCT  
421 ACTAGGTCAG CAAGAATCTT TACAGACTCA CTGCAAATTC TCCATTGAA AAATAGGGAA  
481 ACAGGTTTTG TGGGTGGACA AGAATGCCT CAACCGTCAC ATCCAGTCAC TGGAAGAGCC  
541 AGAACTAGAA AGCTCCCAG TCTTTTCCCC ACATTCAAGA GGGCCGCTGG GTGCATCCTT  
601 ACCCAGCTAT CCTTACAGTG TTTGGGAATG GGAATGGCT CTGTCTTACT GTGGGCATGG  
661 TGGGCATTTT TGGCAGTGGG AGAGAAGGAA AATCTGTGA TTAGAAGCTC AGTATGTTAA  
721 TTCGACTCCA GGACAGCTTT CAGAGACAGT GGCTAAGAGA AGAACGAGGT CCCAGGGGAT  
781 CTCTTGAGGT GACTTATTTT GACACTCTTT GGGAAAGTTA TCTAGGAGAT TTGTTCCATA  
841 ACTCATTTTC CCATACTCTG GTGACAAATT TACTGAGTGT ATCGGTCCCA CTGAGCCAGT  
901 GCATAGCATG GTAACAAACA GTTCTAAATT ATCAATGACT TAACAGAATT AACTAAATTA  
961 ACAAAAGTTA CTTTCTCACT TGTACTAAAT ATCTATAATG TATGGGCTCA GGCTTCTGCA  
1021 TTTTATACTC AGGATTCTAG ACTGATGGAG AAGTTGCCAT GTGGGGGAAC ATTGATGGAT  
1081 ACTGTGATAA AGCAGAAGAA AGCTCTCAGG AGTCTGTCAT AGGCAATGCA CTGTGGCTCA  
1141 AAAATGACAC CCATCACTTT GTCTCTTCTT TTATTGATCA AAATAATTA ATGCCCTCGAA  
1201 CCAAACAAAA GTGGCCAAGA AATGCAAGTC TACCTTGTGT CTCAAAACAG AGGATGGAGA  
1261 ATATTTGGTG AAAATTACCA TGACCATCAC ATGGCCACGT AGGTCTTTAT AATGACAGAG  
1321 CTAGCATTTG TCACATTGAC CAAGCTTTGT CCATACACTC TACAGTAATG ATGAGTCCTC  
1381 AGTGCACAGG GGAGGATGCT GAAGACACAG GACAGCATCC TCCAGACACA TAAGACTTCA  
1441 GAGCAGAGGG ATTCTCCCTC CACCTCTCGC AATTCCCTGC TTTCTCCTAA CTTCCTTTAC  
1501 AAAGTCATGC TTGGAATGT CTATGTATCA TCATGTGGCT CATTTTTTC TCTGTTTATT  
1561 TTTTTTCCCC AAAATTGAGC TTCTGTCCCA ACCACCTGCT GCTTTAACCT GGCCAATAGG  
1621 AAGATACCCC TTCAGCGACT AGAGAGCTAC AGGAGAATCA CCAGTGGCAA ATGTCCCAG  
1681 AAAGCTGTGA TGTAAGTAA TAAAGTTCAC CCTCCCCTAG ACAAAAAAAT AATGTCTAGG  
1741 GCACAGAGTC AAGAACTGTG GGAGTCATAG ACTCTGATAG TTTGACCTCT ATGGTCCAAT  
1801 TCATTAAATT TCACAAGTGA GTGTTCACTC CCAGCTCCCT GCCTGGGAGA TTGCTGTAGT  
1861 CATATCAATT TCTTCAAGTC AAGAGCAAAG ATGGTTTTAC TGGGCCTTTA AGAGCAGCAA  
1921 CTAACCCCAAG AGTCTCATCC TTCCTCTCT CCGTAGCAAC CCTTTGTCCA GGGGCAGATG  
1981 GTCCTTAAAT ATTTAGGGTC AAATGGGCGA AATTTTCAAA AACAATCCTT CCAATTGCAT  
2041 CCTGATTCTC CCCACAGCTT CAAGACCAA CTGGCCAAGG ATATCTGTGC CGACCCCAAG  
2101 AAGAAGTGGG TGCAGGATTC CATGAAGTAT CTGGACCAA AATCTCCAAC TCCAAAGCCA  
2161 TAAATAATCA CCATTTTGA AACCAACCA GAGCCTGAGT GTGCCTAAT TTGTTTTCCC  
2221 TTCTTACAAT GCATTCTGAG GTAACCTCAT TATCAGTCCA AAGGGCATGG GTTTTATTAT  
2281 ATATATATAT ATATATTTT TTTTAAAAA AAACGTATTG CATTTAATT ATTGAGGCTT  
2341 TAAAACTTAT CCTCCATGAA TATCAGTTAT TTTTAACTG TAAAGCTTTG TGCAGATTCT  
2401 TTACCCCTG GGAGCCCCA TTCAGTCCCC TGTCACGTGT GGGCAATGTT CCCCCTCTCC  
2461 TCTCTTCTC CTGGAATCT TGTAAAGTCT CTGGCAAAGA TGATCAGTAT GAAAATGTCA  
2521 TTGTTCTTGT GAACCCAAAG TGTGACTCAT TAAATGGAAG TAATGTTGTT TTAGGAATAC  
2581 ATAAAGTATG TGCATATTTT ATTATAGTCA CTAGTTGTAA TTTTTTTGTG GGAAATCCAC  
2641 ACTGAGCTGA GGGGG

(2) INFORMATION FOR SEQ ID NO:2494:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3663 base pairs

(B) TYPE: 2641 nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2494:

1 GCATTTTTTC AAGTTTTATG ATTTATTTAA CTTGTGGAAC AAAAATAAAC CAGAAACCAC

61 CACCTCTCAC GCCAAAGCTC ACACCTTCAG CCTCCAACAT GAAGGTCTCC GCAGCACTTC  
121 TGTGGCTGCT GCTCATAGCA GCTGCCTTCA GCCCCAGGG GCTCGCTGGG CCAGCTTCTG  
181 TCCCAACCAC CTGCTGCTTT AACCTGGCCA ATAGGAAGAT ACCCCTTCAG CGACTAGAGA  
241 GCTACAGGAG AATCACCAGT GGCAAATGTC CCCAGAAAGC TGTGATCTTC AAGACCAAAAC  
301 TGGCCAAGGA TATCTGTGCC GACCCCAAGA AGAAGTGGGT GCAGGATTCC ATGAAGTATC  
361 TGGACCAAAA ATCTCCAACCT CCAAAGCCAT AAATAATCAC CATTTTTGAA ACCAAACCAG  
421 AGCCTGAGTG TTGCCTAATT TGTTTTCCCT TCTTACAATG CATTCTGAGG TAACCTCATT  
481 ATCAGTCCAA AGGGCATGGG TTTTATTATA TATATATATA TTTTTTTTTT AAAAAAAAC  
541 GTATTGCATT TAATTTATTG AGGCTTTAAA ACTTATCCTC CATGAATATC AGTTATTTTT  
601 AAAGTGATAA GCTTTGTGCA GATTCTTTAC CCCCTGGGAG CCCCAATTCC ATCCCTGTCT  
661 ACGTGTGGGC AATGTTCCCC CTCTCCTCTC TTCTCCTCTG GAATCTTGTA AAGGTCTGG  
721 CAAAGATGAT CAGTATGAAA ATGTCATTGT TCTTGTGAAC CCAAAGTGTG ACTCATTAAA  
781 TGGAAGTAAA TGTGTTTTTA GGAATACATG AAGGTCT CCGCAGACT TCTGTGGCTG  
801 CTGCTCATAG CAGCTGCCTT CAGCCCCAG GGGCTCGCTG GGCCAGCTTC TGTCCCAACC  
861 ACCTGCTGCT TTAACCTGGC CAATAGGAAG ATACCCCTTC AGCGACTAGA GAGCTACAGG  
921 AGAATCACCA GTGGCAAATG TCCCCAGAAA GCTGTGATCT TCAAGACCAA ACTGGCCAAG  
981 GATATCTGTG CCGACCCCAA GAAGAAGTGG GTGCAGGATT CCATGAAGTA TCTGGACCAA  
1005 AAATCTCCAA CTCCAAAGCC ATAA  
1065 CCACATATTC CCTCCTTTT CCAAGGCAAG ATCCAGATGG ATTAATAAAT GTACCAAGTC  
1121 CCTCTACTA GCTTGCTCTT CTCTGTTCT GCTTGACTTC CTAGGATCTG GAATCTGGTC  
1181 AGCAATCAGG AATCCCTTCA TCGTGACCCC CGCATGGGCA AAGGCTTCCC TGGAACTCTC  
1241 CACACTGTCT GCTCCCTATA AAAGGCAGGC AGATGGGCCA GAGGAGCAGA GAGGCTGAGA  
1301 CCAACCCAGA AACCACCACC TCTCAGCCA AAGCTCACAC CTTAGCCTC CAACATGAAG  
1361 GTCTCCGAG CACTTCTGTG GCTGCTGCTC ATAGCAGCTG CCTTCAGCCC CCAGGGGCTC  
1421 GCTGGGCCAG GTAAGCCCC CAACTCCTTA CAGGAAAGGT AAGGTAACCA CCTCCAGGCT  
1481 ACTAGGTCAG CAAGAATCTT TACAGACTCA CTGCAAATTC TCCATTTGAA AAATAGGGAA  
1541 ACAGGTTTTG TGGGTGGACA AGAAATGCCT CAACCGTCAC ATCCAGTCAC TGGAGAGGCC  
1601 AGAAGTAGAA AGCTCCCGAG TCTTTTCCCC ACATTCAAGA GGGCCGCTGG GTGCATCCTT  
1661 ACCCAGCTAT CCTTACAGTG TTTGGGAATG GGAATGGCT CTGTCTTACT GTGGGCATGG  
1721 TGGGCATTTT TGGCAGTGGG AGAGAAGGAA AATCTGTTGA TTAGAAGCTC AGTATGTTAA  
1781 TTCGACTCCA GGACAGCTTT CAGAGACAGT GGCTAAGAGA AGAACGAGGT CCCAGGGAT  
1841 CTCTTGAGGT GACTTATTTT GACACTCTTT GGGAAAGTTA TCTAGGAGAT TTGTTCCATA  
1901 ACTCATTTTC CCATACTCTG GTGACAAATT TACTGAGTGT ATCGGTCCCA CTGAGCCAGT  
1961 GCATAGCATG GTAACAAACA GTTCTAAATT ATCAATGACT TAACAGAATT AACTAAATTA  
2021 AAAAAAGTTA CTTTCTCACT TGTACTAAAT ATCTATAATG TATGGGCTCA GGCTTCTGCA  
2081 TTTTATACTC AGGATTCTAG ACTGATGGAG AAGTTGCCAT GTGGGGGAAC ATTGATGGAT  
2141 ACTGTGATAA AGCAGAAGAA AGCTCTCAGG AGTCTTGCAAT AGGCAATGCA CTGTGGCTCA  
2201 AAAATGACAC CCATCACTTT GTCTCCTTCT TTATTGATCA AAATAATTA ATGCCCTCAA  
2261 CCAAAACAAA GTGGCCAAGA AATGCAAGTC TACCTTGTGT CTCAAAACAG AGGATGGAGA  
2321 ATATTTGGTG AAAATTACCA TGACCATCAC ATGGCCACGT AGGTCTTTAT AATGACAGAG  
2381 CTAGCATTTG TCACATTGAC CAAGCTTTGT CCATACACTC TACAGTAATG ATGAGTCCTC  
2441 AGTGACAGG GGAGGATGCT GAAGACACAG GACAGCATCC TCCAGACACA TAAGACTTCA  
2501 GAGCAGAGGG ATTCTCCCTC CACCTCTCGC AATTCTTGC TTTCTCTAA CTTCTTTAC  
2561 AAAGTCATGC TTGGAATGT CTATGTATCA TCATGTGGCT CATTTTTTTC TCTGTTTATT  
2621 TTTTTTCCCC AAAATTACAG TTCTGTCCA ACCACCTGCT GCTTTAACCT GGCCAATAGG  
2681 AAGATACCCC TTCAGCGACT AGAGAGCTAC AGGAGAATCA CCAGTGGCAA ATGTCCCCAG  
2741 AAAGCTGTGA TGTAAGTAAA TAAAGTTCAC CCTCCCCTAG ACAAAAAAAT AATGTCTAGG  
2801 GCACAGAGTC AAGAACTGTG GGAGTCATAG ACTCTGATAG TTTGACCTCT ATGGTCCAAT  
2861 TCATTAATTT TCACAAGTGA GTGTTCACTC CCAGCTCCCT GCCTGGGAGA TTGCTGTAGT  
2921 CATATCAATT TCTTCAAGTC AAGAGCAAAG ATGGTTTTAC TGGGCCTTTA AGAGCAGCAA  
2981 CTAACCCAAG AGTCTCATCC TTCCTCCTCT CCGTAGCAAC CCTTTGTCCA GGGCAGATG  
3041 GTCCTTAAAT ATTTAGGGTC AAATGGGCAG AATTTTCAA AACAATCCTT CCAATTGCAT  
3101 CCTGATTCTC CCCACAGCTT CAAGACCAA CTGGCCAAGG ATATCTGTGC CGACCCCAAG  
3161 AAGAAGTGGG TGCAGGATTC CATGAAGTAT CTGGACCAA AATCTCCAAC TCCAAAGCCA  
3221 TAAATAATCA CCATTTTTGA AACCAACCA GAGCCTGAGT GTTGCCATAA TTGTTTTCCC  
3281 TTCTTACAAT GCATTCTGAG GTAACCTCAT TATCAGTCCA AAGGGCATGG GTTTTATTAT  
3341 ATATATATAT ATATATTTTT TTTTAAAAAA AAACGTATTG CATTTAATT ATTGAGGCTT  
2341 TAAAACTTAT CCTCCATGAA TATCAGTTAT TTTTAACTG TAAAGCTTTG TGCAGATTCT  
2401 TTACCCCTG GGAGCCCCAA TTCGATCCCC TGTACGCTGT GGGCAATGTT CCCCTCTCC  
2461 TCTCTTCTC CTGGAATCT TGTAAGGTC CTGGCAAAGA TGATCAGTAT GAAATGTCA  
2521 TTGTTCTTGT GAACCCAAAG TGTACTCAT TAAATGGAAG TAATGTTGTT TTAGGAATAC  
2581 ATAAAGTATG TGCATATTTT ATTATAGTCA CTAGTTGTAA TTTTTTTGTG GGAATCCAC  
2641 ACTGAGCTGA GGGGG

## (2) INFORMATION FOR SEQ ID NO:2495:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2495:  
1 GCCAGGTCGC TGTGGTCCA CGCCGCCCGT CGCGCCGCC GCGCGCTCAG CGTCCGCCG  
61 CGCCATGGGA

(2) INFORMATION FOR SEQ ID NO:2496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2496:

1 GGCCGGAGCC GAGCCGGGGT CGGGCAGCAG CAGGGACCCC CCAGAGGCGG GGCTGTGGG  
61 ACCGCTATGG GCGTGGAGAT CGAGACCATC TCCCCGGAG ACGGAAGGAC ATTCCCCAAG  
121 AAGGGCCAAA CGTGTGTGGT GCACTACACA GGAATGCTCC AAAATGGGAA GAAGTTTGAT  
181 TCATCCAGAG ACAGAAACAA ACCTTTCAAG TTCAGAATTG GCAAACAGGA AGTCATCAAA  
241 GGTTTTGAAG AGGGTGCAGC CCAGATGAGC TTGGGGCAGA GGGCGAAGCT GACCTGCACC  
301 CCTGATGTGG CATATGGAGC CACGGGCCAC CCCGGTGTCA TCCCTCCCAA TGCCACCCTC  
361 ATCTTTGACG TGGAGCTGCT CAACCTAGAG TGAAGGCAGG AAGGAAGTCA AGGTGGCTGG  
421 AGATGGCTGC TGCTCACCCT CCTAGCCTGC TCTGCCACTG GGACGGCTCC TGCTTTTGGG  
481 GCTCTTGATC AGTGTGCTAA CCTCACTGCC TCATGGCATC ATCCATTCTC TGTGCCCCAAG  
541 TTGCTCTGTA TGTGTTCTG AGTGTCTATG CGAATTCTTG CTTGAGGAAA CTTGCGTTGC  
601 AGATTGAAGC ATTTTCAGGT GTGCATTTTG TGTGATGCAT GTAGTAGCCT TTCCTGATGA  
661 CAGAACACAG ATCTCTTGT CGCACAATCT AACTGCCTT ACCTTCACTT AAACCACACA  
721 CACAAGGTGC TCAGACATGA AATGTACATG GCGTACCGTA CACAGAGGGA CTTGAGCCAG  
781 TTACCTTTGC TGTCACCTT TCTCTTATAA ATTCTGTTAG CTGCTCACTT AAACAATGTC  
841 CTCTTTGAGA AAATGTAAAA TAAAGGCTCT GTGCTTGACA

(2) INFORMATION FOR SEQ ID NO:2497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2497:

1 GAATTCGGGC CGCCGCCAGG TCGCTGTTGG TCCACGCCGC CCGTCGCGCC GCGCGCCCGC  
61 TCAGCGTCCG CCGCCGCCAT GGGAGTGCAG GTGGAACCA TCTCCCCAGG AGACGGGCGC  
121 ACCTTCCCA AGCGCGGCCA GACCTGCGTG GTGCACTACA CCGGGATGCT TGAAGATGGA  
181 AAGAAATTTG ATTCCTCCCG GGACAGAAAC AAGCCCTTTA AGTTTATGCT AGGCAAGCAG  
241 GAGGTGATCC GAGGCTGGGA AGAAGGGGTT GCCCAGATGA GTGTGGGTCA GAGAGCCAAA  
301 CTGACTATAT CTCCAGATTA TGCTATGGT GCCACTGGGC ACCCAGGCAT CATCCACCA  
361 CATGCCACTC TCGTCTTCCA TGTGGAGCTT CTAAGACTGG AATGACAGGA ATGGCCTCCT  
421 CCCTTAGCTC CCTGTTCTTG GATCTGCCAT GGAGGGATCT GGTGCCTCCA GACATGTGCA  
481 CATGAGTCCA TATGGAGCTT TTCCTGATGT TCCACTCCAC TTTGTATAGA CATCTGCCCT  
541 GACTGAATGT GTTCTGTAC TCAGCTTTGC TTCCGACACC TCTGTTCTCT CTTCCCTTTT  
601 CTCCTCGTAT GTGTGTTTAC CTAAGCTATA TGCCATAAAC CTCAGTTAT TCATTTTAT  
661 TTGTTTTTCA TTTGGGGTGA AGATTAGTT TCAGTCTTTT GGATATAGGT TTCCAATTAA  
721 GTACATGGTC AAGTATTAAC AGCACAAGTG GTAGGTTAAC ATTAGAATAG GAATTGGTGT  
781 TGGGGGGGGG GTTTGCAAGA ATATTTTAT TTAATTTTTT GGATGAAATT TTTATCTATT  
841 ATATATTAAA CATTCTTGCT GCTGCGCTGC AAAGCCATAG CAGATTTGAG GCGCTGTTGA  
901 GGAAGTGAAT ACTCTCCAAG TTGAGAGATG TCTTTGGGTT AAATTAAGG CCCTACCTAA  
961 AACTGAGGTG GGGATGGGGA GAGCCTTTC CTCCACCATT CCCACCCACC CTCCCCTTAA  
1021 ACCCTCTGCC TTTGAAAGTA GATCATGTT ACTGCAATGC TGGACACTAC AGGTATCTGT  
1081 CCCTGGGCCA GCAGGGACCT CTGAAGCCTT CTTTGTGGCC TTTTTTTTTT TTCATCCTGT  
1141 GGTTTTTCTA ATGGACTTTC AGGAATTTTG TAATCTCATA ACTTTCCAAG CTCCACCACT  
1201 TCCTAAATCT TAAGAACTTT AATTGACAGT TTCAATTGAA GGTGCTGTTT GTAGACTTAA  
1261 CACCCAGTGA AAGCCAGCC ATCATGACAA ATCCTTGAAT GTTCTCTTAA GAAATGATG  
1321 CTGGTCATCG CAGCTTCAGC ATCTCCTGTT TTTTGATGCT TGCTCCCTC TGCTGATCTC  
1381 AGTTTCTTGG CTTTTCCTCC CTCAGCCCTT TCTCACCCTT TTGCTGTCCT GTGTAGTGAT  
1441 TTGGTGAGAA ATCGTTGCTG CACCCTTCCC CCAGCACCAT TTATGAGTCT CAAGTTTTAT  
1501 TATTGCAATA AAAGTGCTTT ATGCCCGAAT TC

(2) INFORMATION FOR SEQ ID NO:2498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2498:

1 GCCCGGCCA TGGGAGTGCA GGTGGAAACC ATCTCCCGAG GAGACGGGCG CACCTTCCCC

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61 AAGCGCGGCC AGACCTGCGT GGTGCACTAC ACCGGGATGC TTGAAGATGG AAAGAAATTT
121 GATTCCCTCCC GGGACAGAAA CAAGCCCTTT AAGTTTATGC TAGGCAAGCA GGAGGTGATC
181 CGAGGCTGGG AAGAAGGGGT TGCCAGATG AGTGTTGGGTC AGAGAGCCAA ACTGACTATA
241 TCTCCAGATT ATGCTTATGG TGCCACTGGG CACCCAGGCA TCATCCCACC ACATGCCACT
301 CTCGTCTTCG ATGTGGAGCT TCTAAACTG GAATGACAGG AATGGCCTCC TCCCTTAGCT
361 CCCTGTTCTT GGATCTGCCR TGGAGGGATC TGGTGCCTCC AGACATGTGC ACATGARTCC
421 ATATGGAGCT TTTCTGATG TTCCACTCCA CTTTGTATAG ACATCTGCCC TGACTGAATG
481 TGTTCGTGCA CTCAGCTTTG CTTCCGACAC CTCTGTTTCC TCTTCCCCTT TCTCCTCGTA
541 TGTGTGTTTA CCTAAACTAT ATGCCATAAA CCTCAAGTTA TTCA

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(2) INFORMATION FOR SEQ ID NO:2499:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3135 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2499:

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1 GCCAGGTCGC TGTTGGTCCA CGCCGCCCGT CGCGCCGCCG GCGCGCTCAG CGTCCGCCGC
61 CGCCATGGGA GCGCGGAGCC GAGCCGGGGT CGGGCAGCAG CAGGGACCCC CCAGAGGCGG
121 GGCCTGTGGG ACCGCTATGG GCGTGAGAT CGAGACCATC TCCCCCGGAG ACGGAAGGAC
181 ATTCCCAAG AAGGGCCAAA CGTGTGTGGT GCACTACACA GGAATGCTCC AAAATGGGAA
241 GAAGTTTGAT TCATCCAGAG ACAGAAACAA ACCTTTCAAG TTCAGAATTG GCAAACAGGA
301 AGTCATCAAA GGTTTTGAAG AGGGTGCAGC CCAGATGAGC TTGGGGCAGA GGGCGAAGCT
361 GACCTGCACC CCTGATGTGG CATATGGAGC CACGGGGCAC CCCGGTGTCA TCCCTCCCAA
421 TGCCACCCTC ATCTTTGACG TGGAGCTGCT CAACTTAGAG TGAAGGCAGG AAGGAACACA
481 AGGTGGCTGG AGATGGCTGC TGCTCACCTT CCTAGCCTGC TCTGCCACTG GGACGGCTCC
541 TGCTTTTGGG GCTCTTGATC AGTGTGCTAA CCTCACTGCC TCATGGCATC ATCCATTCTC
601 TCTGCCCAAG TTGCTCTGTA TGTGTTGCTC AGTGTTCATG CGAATTCTTG CTTGAGGAAA
661 CTTGCGTTGC AGATTGAAGC ATTTCAAGGT GTGCATTTTG TGTGATGCAT GTAGTAGCCT
721 TTCCTGATGA CAGAACACAG ATCTCTTGTT CGCACATCT ACCTGCCTT ACCTTCACTT
781 AAACCACACA CACAAGGTGC TCAGACATGA AATGTACATG CGGTACCGTA CACAGAGGGA
841 CTTGAGCCAG TTACCTTTGC TGCTACTTTC TCTCTTATAA ATTCTGTTAG CTGCTCACTT
901 AAACAATGTC CTCTTTGAGA AAATGTAAAA TAAAGGCTCT GTGCTTGACA GAATTCGGGC
961 CGCCGCCAGG TCGCTGTTGG TCCACGCCGC CCGTCGCCGC GCGCGCCGCG
1011 TCAGCGTCCG CCGCCGCCAT GGGAGTGCAG GTGGAAACCA TCTCCCAGG AGACGGGCGC
1171 ACCTTCCCA AGCGCGGCCA GACCTGCGTG GTGCACTACA CCGGATGCT TGAAGATGGA
1231 AAGAAATTTG ATTCTCCCG GGACAGAAAC AAGCCCTTTA AGTTTATGCT AGGCAAGCAG
1291 GAGGTGATCC GAGGTGGGA AGAAGGGGTT GCCAGATGA GTGTGGGTCA GAGAGCCAAA
1351 CTGACTATAT CTCCAGATTA TGCCTATGGT GCCACTGGGC ACCCAGCAT CATCCACCA
1411 CATGCCACTC TCGTCTTCGA TGTGGAGCTT CTAAACTGG AATGACAGGA ATGGCCTCCT
1471 CCCTTAGCTC CCTGTCTTG GATCTGCCAT GGAGGGATCT GGTGCCTCCA GACATGTGCA
1531 CATGAGTCCA TATGGAGCTT TTCCTGATGT TCCACTCCAC TTTGTATAGA CATCTGCCCT
1591 GACTGAATGT GTTCTGTCAC TCAGCTTTGC TCCGACACC TCTGTTTCTT CTTCCTTTT
1651 CTCCTCGTAT GTGTGTTTAC CTAACTATA TGCCATAAAC CTCAAGTTAT TCATTTTATT
1711 TTGTTTTTCA TTTGGGGTGA AGATTCAATT TCAGTCTTTT GGATATAGGT TTCCAATTAA
1771 GTACATGGTC AAGTATTAAC AGCACAAGTG GTAGGTTAAC ATTAGAATAG GAATTGGTGT
1831 TGGGGGGGGG GTTTGCAAGA ATATTTTATT TTAATTTTGT GGATGAAATT TTTATCTATT
1891 ATATATTTAA CATTCTTGCT GCTGCGCTGC AAAGCCATAG CAGATTTGAG GCGCTGTTGA
1951 GGAATGAATT ACTCTCCAAG TTGAGAGATG TCTTTGGGTT AAATTTAAAG CCTACCTAA
2011 AACTGAGGTG GGGATGGGGA GAGCCTTTGC TCCACCATT CCCACCACC CTCCCTTAA
2071 ACCCTCTGCC TTTGAAAGTA GATCATGTTT ACTGCAATGC TGGACACTAC AGGTATCTGT
2131 CCTGGGCCA GCAGGACCTT CTGAAGCCTT CTTTGTGGCC TTTTCTTTT TTCATCCTGT
2191 GGTTTTTTCTA ATGGACTTTC AGGAATTTTG TAATCTCATA ACTTTCCAAG CTCCACCACT
2251 TCCTAAATCT TAAGAACTTT AATTGACAGT TTCAATTGAA GGTGCTGTTT GTAGACTTAA
2331 CACCCAGTGA AAGCCAGGCC ATCATGACAA ATCCTTGAAT GTTCTCTTAA GAAAATGATG
2391 CTGGTCATCG CAGCTTCAGC ATCTCCTGTT TTTTGATGCT TGGCTCCCTC TGCTGATCTC
2451 AGTTTCCTGG CTTTTCTTCC CTCAGCCCCT TCTCACCCTT TTGCTGTCTT GTGTAGTGAT
2511 TTGGTGAGAA ATCGTTGCTG CACCTTCCC CCAGCACCAT TTATGAGTCT CAAGTTTTAT
2561 TATTGCAATA AAAGTGCTTT ATGCCGAAT TC
2594 GCGCCGCCA TGGGAGTGCA GGTGGAACAC ATCTCCCAG GAGACGGGCG CACCTTCCCC
2655 AAGCGCGGCC AGACCTGCGT GGTGCACTAC ACCGGGATGC TTGAAGATGG AAAGAAATTT
2715 GATTCCCTCCC GGGACAGAAA CAAGCCCTTT AAGTTTATGC TAGGCAAGCA GGAGGTGATC
2775 CGAGGCTGGG AAGAAGGGGT TGCCAGATG AGTGTTGGGTC AGAGAGCCAA ACTGACTATA
2835 TCTCCAGATT ATGCCTATGG TGCCACTGGG CACCCAGGCA TCATCCCACC ACATGCCACT
2895 CTCGTCTTCG ATGTGGAGCT TCTAAACTG GAATGACAGG AATGGCCTCC TCCCTTAGCT
2955 CCCTGTTCTT GGATCTGCCR TGGAGGGATC TGGTGCCTCC AGACATGTGC ACATGARTCC
3015 ATATGGAGCT TTTCTGATG TTCCACTCCA CTTTGTATAG ACATCTGCCC TGACTGAATG
3075 TGTTCGTGCA CTCAGCTTTG CTTCCGACAC CTCTGTTTCC TCTTCCCCTT TCTCCTCGTA
3135 TGTGTGTTTA CCTAAACTAT ATGCCATAAA CCTCAAGTTA TTCA

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## (2) INFORMATION FOR SEQ ID NO:2500:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7621 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2500:

1 AACAGAAAA GCGTTGGTAG CTCTGGTGAA TCCCAAAAGA ATGTGGCAGT TGCTAGCCAT  
61 GCTCCTGAAT ATGTATTAAC AGTACATCAT ATGACTAAGA GTTGTACTTA GGGGTTAGAT  
121 TTTATGTGTT TGAACCCCAA ATTAGTTATT TAATAGTTGG CACCCCAAAA CAAGTTACTT  
181 AACCTCACTA AGGTTCACTT TTCTGTGTTA TAAATGTAG ATAGTGATAG TATGTACTTT  
241 ATAGGATTAT TGTGAAATAA AAATGAAATA TCAGATTTAT TTAGGATAAC ACCTGGCATA  
301 TGTGTTGGTAT TCAGAATTAG TTGCTGCTGT TTTATTCTGC TCTCCCTTGC ATCCCACTTT  
361 TCTAAGTTGT AAACATAATA GTTGTACACA GATTGACAGA TTAAGAAAGG CTTGTGATTG  
421 TGCTAGACCT ATGCCTATGC CTCTGTCTCA CCAGATTCCA GGTGTATATG TGGAGGTGGG  
481 ATAGGGAGTG GAGTAAGTGG GTAAATATTA AATTGCCAG TGGGGCACCA TCCTGAATAT  
541 TATCTCTAAA GAAAGAAGCA AAACCAGGCA CAGCTGATGG GTTAACCAGA TATGATACAG  
601 AAAACATTTC CTTCTGCTTT TTGTTTAA GCCTATATT GAAGCCTTAG ATCTCTCCAG  
661 CACAGTAAGC ACCAGGAGTC CATGAAGAAG ATG

## (2) INFORMATION FOR SEQ ID NO:2501:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7621 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2501:

1 GATCTTCATG TGGAAAGTACT GGTTTCATTC AATAGACTTA ATTCAGCAGT CTGTGGGGAA  
61 GAGCAAGGTA TGATAGAATG GTTCCTCAAG TGCTTCAGAT GTGAAGTGGG TTTAAATATA  
121 CTGTCCCTGT CTTCTTCAGA GTTTTGGTAA AGATAAAATA GGACACTCAT TTTAAAGCAA  
181 TCTTTGCAAA TGACAAGCCA CTATAGACAT TAATAGAGTT TTCATTTCCTA GTATTATCAT  
241 TAATATCAGA TCCTGGAAGA AGGTTGAGCC TTGACCTAGA GCAAAAAAAC AGAAGAATTA  
301 GTAAAGGAAT CCTGGAGAAA GCCCCTGCTG TGTATTTAAA GGAGAAAGGG AGATCATGTT  
361 GGGAAATTAT AATATTAATA GTAAACAAAA GCTAGGAAGT AAAATAAAAT AAATTATATG  
421 GCCTAGATCC CCATAAGTAA TGGTTTAACT TCTGCCTTCC TGTGTTCTGA GCCAGATTAG  
481 GGCACAGTAG AGAAAGAGGA GTCTCTGAAA ATGTTTCCAA TTTGCTGGT CAGACAGCGG  
541 ATCATCAGTG AATCAGATGA AAATTTGTGG ATTTATGCAC TAACTGATCA GCAGGAAATT  
601 AAACAAGAAA AGCGTTGGTA GCTCTGGTGA ATCCCAAAAG AATTTGGCAG TTGCTAGCCA  
661 TGCTCCTGAA TATGTATAAA CAGTACATCA TATGACTAAG AGTTTGACTT AGGGGTTAGA  
721 TTTTATGTGT TTGAACCCCA AATTAGTTAT TTAATAGTTG GCACCCCAAA ACAAGTTACT  
781 TAACCTCACT AAGATTCAGT TTTCTGTTT ATAAAATGTA GATAGTGATA GTATGTACTT  
841 TATAGGATTA TTGTGAAAAA TAAATGAAAT ATCAGATTTA TTTAGGATA CACCTGGCAT  
901 ATGTTTGGTA TTCAGTAATT AGTTGCTGCT GTTTTATTCT GCTCTCCCT GCATCCCACT  
961 TTTCTAAGTT GTAAACTAAA TAGTTGTACA CAGATTGACA GATTAAGAAA GCCTTGTGAT  
1021 TGTGCTAGAC CTATGCCTCT CTCTCACCAG ATTCCAGGTG TATATGTGGA GGTGGGATAG  
1081 GGAGTGGAGT AAGTGGGTAA ATATTAAATT GCCCAGTTGG GCACCATCCT GAATATTATC  
1141 TCTAAAGAAA GAAGCAAAAC CAGGCACAGC TGATGGGTAA ACCAGATATG ATACAGAAAA  
1201 CATTTCCCTC TGCTTTTGGG TTTTAAAGCCT ATATTGTAAG CCTTAGATCT CTCCAGCACA  
1261 GTAAGCACCA GGAGTCCATG AAGAAGATGG CTCCTGCCAT GGAATCCCCT ACTCTACTGT  
1321 GTGTAGCCTT ACTGTTCTTC GGTAAGTAGA GATTCAATTA CCCCTCCCCT TTTCTAGGA  
1381 ATGAATTTGG GGAGCAGCTG GGGTAGGAAC CTTTACTGTG GGTGGTGACT TTTCTAGGA  
1441 CATGTGCAAA CTATTGGGCA TTTCCAGGG ACTCTGTAGT GGAGCCAAGC TAGAAAGCAG  
1501 AGGCAAGTGG GCTGAGCAAC ACCTAAGGAG GAAGCCAGAC TGAAAGCTTG GTTCCTTGCA  
1561 TTTGCTCTGG CATCTCCAG AGTGCAAAAT TCCTACCAAG GTAATGAGGG TAGAGGAGAG  
1621 AAAGAAGCTC TTTCTTCCCC TGATTCTCAT TCCTGAAAAG ACGGTTGGTC CTTAAATTC  
1681 CATGGATGTA GATCTTATCC CCACACCCAG ATTCTAGTCC TCTGGAGATA AAGAAGACTG  
1741 CTGGACACTA ATGTATCCTC TCTGGACTTT TGCAGCTCCA GATGGCGTGT TAGCAGGTGA  
1801 GTCCTCTGTT CTTGTTCCCT TGGTGTATCA ACATGTCTGG GCATTGCTTT CCTCTACTA  
1861 TTTCTTCTGT CCCATCACTT CTGCTTTCTA ATGAGCATGA ATCTGTTCTT TGGCCAGACT  
1921 ACTTCCCTC TCCACCTTGC CTTGTCTTTC TTTTTTCCC TGATTCATTG CATTCTCTCA  
1981 AGTCATTCTC TCCTCTGTTT TAGTCAATAA CCATGTCTGT TGCACATATA CATGTCTCAT  
2041 TCTCTCTCCT AGACACTTTG GCATGATCTC GCTCAATAAT TACATTATTA TTATTATTGC  
2101 CATTTTATAA TTGAGGATGC TGAAACTCAG TGATTTTCTG GTGGTTACAT GGCTAAGGAA  
2161 CTGGATTTCA ACGTAAGTTC CTTGGATCTA AGTCCAGTTC TCTTCTGACT ATATCACCTT  
2221 TTTGTTATCA CCATGTATCT ACTTCTTTGG TCTCTGTTCA AATTGCACT ACATCCCCTT  
2281 GTTCCAGGAA GCCATTCAAG ACTGACTTTC TTAGTGCTC TCACTACTTT CTGGAACCTGA  
2341 CATATGTTTT TCACTCTGTA TATACTTACA ATTAATAGT CATAAATATT CAGAGCTTGG  
2401 AGAAACCTTA TATTTCAATC AGTCCAGTAA ATTTATCCAT CCATAATTCA CTCATTCAAT  
2461 CACATAATAA ATATTTAATG TAACAATGGT TGAACATGGC AGACAGTGTT TCTACCTCAA  
2521 AAGAGATTGC AGTCTCTCATT TACAGATACT GAATTGAAAT TAACAGAAGT AGAGTGAGTC

2581 AGCTCAAATC ACATAGTGAA TTGGTTTCTT TGTTTTTTAAA TCTCCTGCAT ATGTGTCCTG  
2641 TCTTTCTCCC TGTGTTGGGC GTTCCCTGGG GCACCAATAC TAATTTCTCC TTCCCTTAGA  
2701 AATCAAAACA GGGTCTTATC ACCAACAGAA TAAGGACAGG TTGACCACTG ATTGTCAGAA  
2761 TATTGCTTCG TTTGTACTTT TAAGCCTAGA CAGTTTTTCAA TGACTTTTTT TCTCTCTACA  
2821 TGTCTTTTCA TATTTTTATC TTCTTGAAGT CCCTCAGAAA CCTAAGGTCT CCTTGAACCC  
2881 TCCATGGAAAT AGAATATTTA AAGGAGAGAA TGTGACTCTT ACATGTAATG GGAACAATTT  
2941 CTTTGAAGTC AGTTCCACCA AATGGTTCCA CAATGGCAGC CTTTCAGAAG AGACAAATTC  
3001 AAGTTTGAAT ATTGTGAATG CCAAATTTGA AGACAGTGGA GAATACAAAT GTGAGCACC  
3061 ACAAGTTAAT GAGAGTGAAC CTGTGTACCT GGAAGTCTTC AGTGGTAAGT TCCAGGGATA  
3121 TGGAAATACA GATCTCTCAT GTGAGGGATG GCTCATCTGA AGATGGGAAA AAACAGGTTA  
3181 TTCCAAGGGT TAGGACACCA GAGTGGGATT CAAGGCCTCT CATTTTTAAG ACCCCTGCAT  
3241 TGGCTGGGCA CAGTGGCTCA CGCCTGTAAT CCCAGCACTT TGGGAGGCTG AGGCAGGTGG  
3301 ATCAGGAGGT CAGGAGATCG AGACCATCCG GCTAACATGG TGAACCCCA TCTCTGCTAA  
3361 AAAATATATA TATATAAAT TAGCCGGCGG TAGTGGTGGG CACCTGTAGT CCCAGGTACT  
3421 CGGGAGGCTG AGGCAGGAGA ATGGTGTGAA CCCAGGAGGT GGAGGTTGCA GTGAGCTGAG  
3481 ATCAGCCAC TGCCCTCCAG CCTGGGCTAC AGAGCAAGAC TCCGTCTCAA AAAATAAATA  
3541 AATAAATAAA AAAGACCCCT GCATCTCTTT TCTTCTACCC CCTTCCCTTT TGATTACTTG  
3601 TATGCCTTCT TTCAATATTC TAGTCATCTC TCAATATTAT TCCTCCACCC TATTTTCTCTC  
3661 TATCTTTTCT GCCTAGATTC AGGTATATAT TATGTGGTCA AACAGCATGA CATATATGTG  
3721 AACATTTCAA AGAGCTGTGT ATCTGGAATA GGATCAAAAG GTTTGACTTA AAGTTTTGCT  
3781 CTGCATAATC CATATGGCAG GACCTGAATA TTAGGTTGTA CTCTTCGTTA TGAAACATAT  
3841 CTGGGTACAT TTCCTTATGT CCTCTGTTGT TACTTAAGAA CACATATTTC ATGCTTGTCTT  
3901 CATTTTTATC ACTCCTACTG CCAACAAATA GCATAGCATG CTTAGGCACA TGTGGCTTAA  
3961 TTAGCAAATG TTGAATAAAC AAATTAATGA TTTTGAATAG TGACCAATAG GTCTCTTTTA  
4021 TACTCTATAT TTTTCTCTTG AGTGAAAAA AATGTTTCAA CCTCCATATG TAAATCCAA  
4081 ACACAACTA AAGCAATGTA GAATAGCTTC TTTATTCCCT GGAGTAGGTT CTAGAGAAGT  
4141 CCTAAAGGAT TGGTCCTAAA TTAATTATGC TTATTATGCT AGCGATATTT CCTTTCAAAA  
4201 TTTCTCTTTA ATGAATGCTT TTAATTTTT ACAAAAGCAT TAACCATAGA ATGTGATTCT  
4261 TGTCTTTTAC TGACTCATTG GTGACAAATA TTTGTTGAGT ACCTACCAAC TCCTAAGTAT  
4321 TGCTACCAAC TCCTAAATAC TGTGTTGGGC ATTCAGAATA GAATGTAGAA CTAGACAGGG  
4381 TCCCTGACTT CTTGGAGCAC AGAGCAGTAT GGGAGAGGA CATTAAATAA AGAATTACAT  
4441 AAGTAATTAA TTTAAATTAT ACATGTTTGG AAGAAGTTTT TTTTGTACAA CTATAATTAA  
4501 CACTAGAACT GGGAAAGTTT TATAAGGTAA GAGAGGACAA AATAGACACT CTCCTAAGCT  
4561 AAAATTCCCA AGAAAGACTG TTTATTTTCC CCTAACTAAC TAGAACTAGC AACAGAAGAT  
4621 CTGAAGGAA TTCTGGCTTT CAAGTGTTC ATGTATGGAC TCATCAGGGA GGTCCGAGAG  
4681 GCTTTTGGC CCCGACTGA CTTTTCAGGA GGGGAAAGGA TTTATCAATA CACAAGACAG  
4741 GCTCTAAGCA TTATTTTGTG CCCTTTAAAA ATCCACTTTA TGAGCCAAAA AGTGAGTTAA  
4801 TGATAATTCA TAGTTTCTGA CACATGCTCT ATGCGTGGCT CTCTTTTCTC TATTCATTCT  
4861 CTCTCTCTTC ATTTATTGTT AAATAAATAA TGTAATGAAT GTTCTTCAGA CTGGCTGCTC  
4921 CTTCAGGCTT CTGCTGAGGT GGTGATGGAG GGCCAGCCCC TCTTCTCAG GTGCCATGGT  
4981 TGGAGGAACT GGGATGTGTA CAAGGTGATC TATTATAAGG ATGGTGAAGC TCTCAAGTAC  
5041 TGGTATGAGA ACCACAACAT CTCCATTACA AATGCCACAG TTGAAGACAG TGAACCTAC  
5101 TACTGTACGG GCAAAGTGTG GCAGCTGGAC TATGAGTCTG AGCCCCCAA CATTACTGTA  
5161 ATAAAAGGTG AGTTGGTAAA GGAAGGAAA AGCATCCATA GCAGGGGAA AGAAGAGAA  
5221 CTTCTGAGCC TGAGCAGTTG CAGCTTGTAG AAGGGGGGCA CCTGTGATAC ACTGGAAAGC  
5281 CTACCAGACT TGCAATGAGG AGACCTGGGT GATAGTATAT ATCTCAATCT CTGTTTCAAA  
5341 GCCTTGACTT GTTAAATGGT GATAGTAATA CCTGCTTGCA CTATGAAAT TTTATGAAGA  
5401 TTAATGTGGT AATATTTGTG AAATGACTTT GTAACTGTT AAGCACTACC CAAGCATAAC  
5461 AGATTGTGAT TACTATTTTG ATCTCAAAGT CATCTGTTGC TCCTGGGGGA ACACCTATAT  
5521 TTATCAAATT GAAAAAAGT TTCAAAGTTG AATGAAGAAA GGATATAAAG AGCTTGAGGA  
5581 GCCCATTCCA GCTTAGGAGG GCTGGGAAAG GAAACCAGCA AGTCAGTAAG CTGTGTGCCT  
5641 GTGTATTGAG GGAGGAGGGA ATGGACTTGA TATGGAGAGG GTAGGGAGGT GGACTGCCTC  
5701 TATGGCCTGT AAGAAAACT GCTCTCTCCA AACTCTTTAT AAGAGAGGGA GCCTGTGAAG  
5761 TATCACTTT TGAAGGAGAA AGTTAGACTT TTCCTTCACA CACTTTGTAC ATAATAATGT  
5821 TTAATAAAGC ATGAGGTCAA AATACATAAT TAAGTCCTAG CAGTTCTCTG TTAACATAAT  
5881 TGAGACTGAA GTGCTATGTA CTGTCTCTA GGCTTCCAGT ATCTTCATCT GTAAACAGA  
5941 ATATTGGTC TAGATTCCAT TAGAATCATT TGATAACTTA AAAAATATAT TGATGCTCAT  
6001 GTCTCATTTT TTGAGATTCT GATTTAATTG GTTTGGGGTG CAGCCTGGGT ATACGTATTT  
6061 TTCATAGGTC TTTCACATAA TGGTAATGGG TAGCCAATAT TGAGAATCAC TTGTCTAGGT  
6121 GATCTTTAAA TGATTTCTGG ATGTAATATT CTGAGGCTCT ATAATTTGAG ACTAATCACA  
6181 AAAATCGGTA CAGTTTATAA ACAGACTAAC AGAACCACAA AATAATAGAA TTGGAAGGCA  
6241 ATTTAACTAG TGCAATTTCT TCATTTTGCC TAACAGGCAT GTAAGAAATG ATGATTGATT  
6301 GAGTAATAGG CATTGATGAC CCCTGTCTC ACTTTGTCCC CTTTCCACCC CTTAATTATA  
6361 TGTGAATTCT GGTCTTGTCA TTTCGAATAA GGGGTTTATC TTTCTATTG TCTTCCCTC  
6421 TGGGCACGGC AACTGGCTA CTGGAGTTAA GAGGAAATGC TTAGGACTCC CTGTGGCTCC  
6481 AGGAGCACC AACAGAGCAA CTCAACCTAG TGTTAATCTG AGTGTCTTCT CTGTGCTTCT  
6541 GGATGCCACA TCACGCTAAA AATGAAGGAC AAAGCTTGGT CTTTCTCTTA GGGAGGATGA  
6601 AACTCTGAAC CTCATTTTTC AGTTCCCAAG ATGAATTATG TTTCTCATTG CATCTGTGTT



6661 CCA GC TCCGCGTGAG AAGTACTGGC TACAATTTTT CCATTG TTGGTGGTGA  
 6721 TTCTGTTTGC TGTGGACACA GGATTATTTA TCTCAACTCA GCAGCAGGTC ACATTTCTCT  
 6781 TGAGATTAA GAGAACCAGG AAAGGCTTCA GACTTCTGAA CCCACATCCT AAGCCAAACC  
 6841 CCAAAAACAA CTGATATAAT TACTCAAGAA ATATTTGCAA CATTAGTTTT TTTCCAGCAT  
 6901 CAGCAATTGC TACTCAATTG TCAAACACAG CTTGCAATAT ACATAGAAAC GTCTGTGCTC  
 6961 AAGGATTTAT AGAAATGCTT CATTAAACTG AGTGAAGTGT GTTAAGTGGC ATGTAATAGT  
 7021 AAGTGCTCAA TTAACATTGG TTGAATAAAT GAGAGAATGA ATAGATTCAT TTATTAGCAT  
 7081 TTGTAAAAGA GATGTTCAAT TTCAATAAAA TAAATATAAA ACCATGTAAC AGAATGCTTC  
 7141 TGAGTATTCA AGGCTTGCTA GTTTGTTTGT TTGTTTCTA CTAAAGGCAA GGACCATGAA  
 7201 GTTCTAGATT GGAATGTCC TCTCTTGACT ATTGCAAGTG CGATCTAGGA ATGAAAAGAC  
 7261 ATAGGAGGAT GCCAGTGAGG TGGATCATT TTAGCTTCT TCTTCAGCTT ACTAAATATG  
 7321 AACTTTCACT TCTTGGCAGA ATCAGGGACA GTCTCAAGAC ATAGGACTCT CAGGATGAAG  
 7381 TAGAGTCCAG GATTCCTCTG TGATTGTTTT GCCCTCCCA AATTTATATC TTGAACCTAT  
 7441 GTCTTGATC TTTATACAGC ACCTGAACCA AGCATTTTGG AGAAATTCCA GCTAATAATA  
 7501 ATAACCAAAA CCTTCGGCTC TGAAAACAGT CCAGGACTGA ATAAGATCTT GGGCAAAAGA  
 7561 ACTAGACAGT TTTGGTTTAT TTTCCCTTTC ATTTTATGTC TTCATCATAG TCATTGGAGG  
 7621 CTCATTCTTC TTGTCATGGA GTAAATGGGA TTAAAGTTC

## (2) INFORMATION FOR SEQ ID NO:2502:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1198 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2502:

1 TACTAAGAGT CTCCAGCATC CTCCACCTGT CTACCACCGA GCATGGGCCCT ATATTTGAAG  
 61 CCTTAGATCT CTCCAGCACA GTAAGCACCA GGAGTCCATG AAGAAGATGG CTCCTGCCAT  
 121 GGAATCCCTT ACTCTACTGT GTGTAGCCTT ACTGTTCTTC GCTCCAGATG GCGTGTTAGC  
 181 AGTCCCTCAG AAACCTAAGG TCTCCTTGAA CCCTCCATGG AATAGAATAT TTAAAGGAGA  
 241 GAATGTGACT CTTACATGTA ATGGGAACAA TTTCTTTGAA GTCAGTTCCA CCAAATGGTT  
 301 CCACAATGGC AGCCTTTCAG AAGAGACAAA TTCAAGTTG AATATTGTGA ATGCCAAATT  
 361 TGAAGACAGT GGAGAATACA AATGTCAGCA CCAACAAGTT AATGAGAGTG AACCTGTGTA  
 421 CCTGGAAGTC TTCAGTGAAT GGCTGCTCCT TCAGGCCTCT GCTGAGGTGG TGATGGAGGG  
 481 CCAGCCCCTC TTCCTCAGGT GCCATGGTTG GAGGAACTGG GATGTGTACA AGGTGATCTA  
 541 TTATAAGGAT GGTGAAGCTC TCAAGTACTG GTATGAGAAC CACAACATCT CCATTACAAA  
 601 TGCCACAGTT GAAGACAGTG GAACCTACTA CTGTACGGGC AAAGTGTGGC AGCTGGACTA  
 661 TGAGTCTGAG CCCCTCAACA TTAGTGTAAT AAAAGCTCCG CGTGAGAAGT ACTGGCTACA  
 721 ATTTTTTATC CCATTGTTGG TGGTGATTCT GTTTGCTGTG GACACAGGAT TATTTATCTC  
 781 AACTCAGCAG CAGGTCACAT TTCTCTTGAA GATTAAGAGA ACCAGGAAG GCTTCAGACT  
 841 TCTGAACCCA CATCCTAAGC CAAACCCCAA AAACAAGTGA TATAATTACT CAAGAAATAT  
 901 TTGCAACATT AGTTTTTTTC CAGCATCAGC AATTGCTACT CAATTGTCAA ACACAGCTTG  
 961 CAATATACAT AGAAACGTCT GTGCTCAAGG ATTTATAGAA ATGCTTCATT AAACCTGAGT  
 1021 AAACCTGGTTA AGTGGCATGT AATAGTAAGT GCTCAATTAA CATTGGTTGA ATAAATGAGA  
 1081 GAATGAATAG ATTCAATTTAT TAGCATTGTG AAAAGAGATG TTCAATTTCA ATAAATAAAA  
 1141 TATAAAACCA TGTAACAGAA TGCTTCTGAG TAAAAAATAA AAAAAAATAA AAAAAAATAA

## (2) INFORMATION FOR SEQ ID NO:2503:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2503:

1 TCTCAATATA ATAATATTCT TTATTCCTGG ACAGCTCGGT TAATGAAAAA ATGGACACAG  
 61 AAAGTAATAG GAGAGCAAAT CTTGCTCTCC CACAGGAGCC TTCCAGTGTG CCTGCATTTG  
 121 AAGTCTTGA AATATCTCCC CAGGAAGTAT CTTGAGGAG ACTATTGAAG TCGGCCTCAT  
 181 CCCCACCACT GCATACATGG CTGACAGTTT TGAAAAAAGA GCAGGAGTTC CTGGGGGTAA  
 241 CACAAATTCT GACTGCTATG ATATGCCTTT GTTTTGGAAC AGTTGTCTGC TCTGTACTTG  
 301 ATATTTTACA CATTGAGGGA GACATTTTTT CATCATTTAA AGCAGGTTAT CCATTCTGGG  
 361 GAGCCATATT TTTTCTATT TCTGGAATGT TGTCAATTAT ATCTGAAAGG AGAAATGCAA  
 421 CATATCTGGT GAGAGGAAGC CTGGGAGCAA AACTGCTGAG CAGCATAGCT GGGGGAACGG  
 481 GAATTACCAT CCTGATCATC AACCTGAAGA AGAGCTTGGC CTATATCCAC ATCCACAGTT  
 541 GCCAGAAATT TTTGAGACC AAGTGCTTTA TGGCTTCCTT TTCCACTGAA ATTGTAGTGA  
 601 TGATGCTGTT TCTCACCATT CTGGGACTTG GTAGTGCTGT GTCACTCACA ATCTGTGGAG  
 661 CTGGGGAAGA ACTCAAAGGA AACAAAGTTC CAGAGGATCG TGTTTATGAA GAATTAAACA  
 721 TATATTCAGC TACTTACAGT GAGTTGGAAG ACCCAGGGGA AATGTCTCCT CCCATTGATT  
 781 TATAAGAATC ACGTGTCCAG AACACTCTGA TTCACAGCCA AGGATCCAGA AGGCCAAGGT  
 841 CTTGTTAAGG GGCTACTGGA AAAATTTCTA TTCTCTCCAC AGCCTGCTGG TTTT

## (2) INFORMATION FOR SEQ ID NO:2504:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11298 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2504:

1 AAGCTTTTCA AAGGTGCAAT TGGATAACTT CTGCCATGAG AAATGGCTGA ATTGGGACAC  
61 AAGTGGGGAC AATTCCAGAA GAAGGGCACA TCTCTTCTT TTCTGCAGT CTTTCTCACC  
121 TTCTCAACTC CTACTAAAAT GTCTCATTTT CAGGTTCTGT AAATCCTGCT AGTCTCAGGC  
181 AAAATTATGC TCCAGGAGTC TCAAATTTTC TTATTTTATA TTAGTCTTTA TTTAGTAGAC  
241 TTCTCAATTT TTCTATTCAT CACAAGTAAA AGCCTGTTGA TCTTAATCAG CCAAGAAACT  
301 TATCTGTCTG GCAAATGACT TATGTATAAA GAGAATCATC AATGTCATGA GGTAAACCCAT  
361 TTCAACTGCC TATTCAGAGC ATGCAGTAAG AGGAAATCCA CCAAGTCTCA ATATAATAAT  
421 ATTCTTTATT CCTGGACAGC TCGGTTAATG AAAAAATGGA CACAGAAAGT AATAGGAGAG  
481 CAAATCTTGC TCTCCACAG GAGCCTTCCA GGTAGGTACA AGGTATTATT TTTTCTTACC  
541 CTCAGTCACT TGTGGCAGGG GAAGTCATAG TCACGGTGT TAGGAGATGA AACTTTATTG  
601 ATTTAGGCAT GGATCCATCT AGTTTAATTA ATATATTGGG TATGAGGAAG CTACTTGCTG  
661 TACTTTCCAT GTGGTCTCT CTCCCTGGAG AGGAACATTT TTAATCAGCT TGCAAACCTGG  
721 AAATAGATTT TCTCACATTA GAAGCTCATT TTCTGGGTAT GAGACAGGAG AGTTCATACT  
781 GTGTATGTAG ATCTCTGGCT TCTGGGTCTG ACATGTGCTG AGGGACACAT ATCCTTCACA  
841 CATGCTTTTA TAAATACTTG ATAAAGTAAC CTGCTTCTTG ATTGGTCTTT ATAATCCATA  
901 AGCTGTGGGA TGCTTCTCTG AAGATGAAAA TAGTAATAGA GTCCCATCTA GCTATTCAAA  
961 GCCATTCTTT CATGTATTG TGTGCATAG AAGTTGGGGT TGTTTACTGA CAAAATATAT  
1021 TCAGATACAT TTCTATGTTA AAAGGATTGT GAGATGCATA GGTAAATGTG TTTATTTTCA  
1081 GTTTTACTTG TCAACATAGA TGAATGAGAA AGAACTTGAA AGTAACACTG GATTAAAGAT  
1141 AGGAAAATTT GGCATGGATT TTGCTCCATT TTGTCCCATC TAATCACTTG GATAGTGTTT  
1201 AGGTGTCTTT GGTGAGTTAC TTGGATGCTC TGAGCTTTAG TTTCTTGGTG ATTACAATGA  
1261 AGATTTGAAT TACAGGATGG CTTTGAAGAA ATAAACAAAA CTCCCCTTTC TGTCTGTCGA  
1321 GAATGTTGCA CAGGGAGTTA CAGAATGTTT TCATGACTGA ATTGCTTTTA AATTTACACG  
1381 TGTGCTGCA TTTGAAGTCT TGGAAATATC TCCCAGGAA GTATCTTCAG GCAGACTATT  
1441 GAAGTCGGCC GTGAGTGAGC CTCCTCCAAC TTTGACTAGA GTAAGGGTTG GGTCTAGAAA  
1501 GTTCTGGGG GTGAGTGAGC CTCCTCCAAC TTTGACTAGA GTAAGGGTTG GGTCTAGAAA  
1561 AGAATATTGA GTTGCATCAA CTGTTTCCC ACTTGGATTC ATGAGAGGTG TTAGGTCCTT  
1621 TAAAAACAT GGTAGATAAA GAGTTGACAC TAACTGGGTC CTTTTGGGAA GAGCCAGAAG  
1681 CATTTCCTCA TAAAGACTTT AAATTGCTAG GACGAGAATG GCCAACAGGA GTGAAGGATT  
1741 CATAACTTTA TCTTTACTTA GATGTAAGA ACAATTACTG ATGTTCAACA TGAATACATA  
1801 CATAAGGCG CATGGAGAAA AGTATTGGCC TTCCATGCAT TAGGTAGTGC TGTATCAAT  
1861 TCTTATAGTG GCTAGGGTAT CCTGGAAAT CTTACGTGTG GATCATTCT CAGGACAGTC  
1921 TAGGACACTA ACGCAGTTTC TCATGTTTGG CTTCTATTAT TAAAAAATGA TACAATCTCG  
1981 GGAAATTTT TTTGATTTTC ATGAAATTCA TGTGTTTTTC TATAGGTAAC ACAAAATCTG  
2041 ACTGCTATGA TATGCCTTTG TTTTGAACA GTTGTCTGCT CTGTACTTGA TATTTACAC  
2101 ATTGAGGGAG ACATTTTTTC ATCATTAAAA GCAGGTTATC CATTCTGGGG AGCCATATTT  
2161 GTGAGTATAT ATCTATAATT GTTTCTGAAA TAACACTGAA CATAGGTTTT TCTCTTCTC  
2221 AGATCTAACC AGTTGTTTAT TCCCAGTATT AAGATGATAT TTATAATTCT TAATTATAAA  
2281 TATATGTGAG CATATATAAC ATAGATATGC TCATTAACAA CAACAAAAGA TTCTTTTTAC  
2341 AATTAACGGT GGGTTAAACA TTTAGCCAC AGTTTTATCC CATGAGAAAC CTGAATCTAA  
2401 TACAAGTTAA ATGACTTGCC TAAGGGCCAC TTGACTAATA GTAATTGAAC CTAAACTTTC  
2461 AGAATCCAAC TCCAGGAACA TACTTCTAGC ACTATTCATC AATAAAGTTA TATGATAAAT  
2521 ACATACAAC TATCTGTCA ACTAAAAATA ACAACAGAGG CTGGGCATGG TGGCTCACAC  
2581 CCGTAATCCC AGCACTTTGG GAGGCTGAGG CAGGTGGATC ACCTGAGGTC AGGAGTTTGA  
2641 GACCAGCCTG ACCAACATGG TGAAACCTCA TCTCTACTAA ATATAAAAAA TTAGCTGAGT  
2701 GTGATAGTGC ATACCTGTAA TCCAGCTACT TAAGAGGCTG AGGCAGGAGG CTGTTTGA  
2761 CCTGGAAGGC AGAGGTTGCA GTGAGCTGAG ATTGTGCCAT TGCACTCCAG CCTGGGCAAT  
2821 AAGTGCGAAC TCTGTCTCAA AATAATAATA ATAATAATAG AAAATAAAGT TGTCTTCATG  
2881 AAAATGAGG AAAGAGATTG CTGGGGTGAG AAACATTAAG ATCAATGGGC ATATGGTGAC  
2941 CTTCTATGCC CTAGAACTC TTTTANGGTA TTTTCTCCTG GTATCTCTTT TACNATCGT  
3001 TCTATCTGGA AAAATAGGTG GATGAGTGAG ATAATAACGG TATATACTTT TAAAGGTCT  
3061 AATTGACATA TATAAATTGC AAGTATTTCA GATGTCAATT TGCTAACCTT GACACACATA  
3121 GACACACATG AAAACATCAC CACATTAATA CAATGTATGT ATCCATCATT CAAAAGCTT  
3181 CCTGTGTAT CTTTGTAAT CTTTCTCTCT CCCTCCACTC CTTGCTCTCT CGTTCCCAAG  
3241 AAAACATTGA TCTGCTTCT GTGAATATAA ATTAACCTAC ATTTTGTAGA GCTTTATATA  
3301 AGTATGTTCT CTTTACTGTT TGCTTCTCT CGCTGCACAG TTATTTTGTG ATTCTTCAAG  
3361 TTTTTTCTTT ATATCGATAC TTCATTACAA AGAATATATT TTAATTCTAG ACTATGTCAC  
3421 ATTGACTTTG TCGTCTGCTA AATCCTTAGT GCTCAGATGA CTTGTTTCTG ACTCTCCTTG  
3481 AACCTGTACC TCTGTTANAT TGAAACTTGT CTCTACTGTC TTTTATTTTC AAACACAGCT  
3541 TATTAGGTGT CTCTCAACCC ATCAAACNCA CAATCTGAGT CTTTAGGAGA TTGCTTTGAA  
3601 TTTGTGCTAT TGACTTATAT NTATATNAAA TNTGTAAATG TTTGGTAAAA ATATCATCAT  
3661 GTACNTTTTC ATAATTACGC TATNTNCACA TGATATATGT CAGACTCTGG AAATATGCAT

3721 GCCACACA CGTGTTCCTT GCCTAAAGGG GCTGATGGAA CACATA CNAATAGACG  
3781 ATTGCAGTAG AATGAGAGTG GTGGTCTAAN CAGTACATGT CCTGATGTTG CTCGGACAGT  
3841 TACTACNCCA AGAGTACCCC CTGCATTGTC AGGGTTAGCA TCTCCTGGAA GCCTCATGTA  
3901 AATGAAGAAT TTCATGCTCC ATCCAGGACC TAATGAATAA GAATCTGCAT TTTAGCAAGA  
3961 CCCTCATATG ATTCATATAC ACTTTTTTTT TTTTTTTTGA GATGGAGTCT CACTCTTGTC  
4021 GCCCAGGCTG GAGTGCAATG GCATGATCTT GGCTCACTGC AACCTCTGCC TCCCAGGTTT  
4081 AAGTGATTCT CCTGTCTCAG CCTCCCTAGT AGCTGGGACT ACAGGTGCAT GCCACAGTGG  
4141 CTGGCTAATT TTTGTATTTT TAGTAGAGAC AGGGTTTCAC CATTTTGGTC AGGCTGGTCT  
4201 TGAACATCATG ACCTCCGCTG ATTCCCCCGC CTCGGCTTCC CAAAGTGCTG GGATTACAGA  
4261 CATGAGCCAC CACACCCGCC TTATTCGTAT ACNCATTAA TTCTGAGAAG CACTCTATAG  
4321 AAAATAAGAA TAAGAAAATA TTGGGCTCAC AGGTGACATT AATAAGTAAC TTTATCGAGT  
4381 ACCCCAAATT TTACCTATGT TTGGAAGATG GGGTTAAAAG GACACATTGA AAACAAGAAC  
4441 TCATTGTGGC TTTTTTTTCC TCCTTTTTGA ACAGTTTTCT ATTTCTGGAA TGTGTCAAT  
4501 TATATCTGAA AGGAGAAATG CAACATATCT GGTGAGTTGC CCGTTTCTGT CTTTGTCCAT  
4561 CTTGAAAAG ATAAGAAGAA CAGAGTTTAA AGAGTCTTAA GGGAAACACA TCTTGTCTC  
4621 CTATATTACT TGTGAATGTG GATATATGAT TTTGTTTCAA TCTATTTGT GTCCTAAGGC  
4681 TTTTGCACAC AGAAGTTGGA TATATCATT GAAACATAAA TTGTACCATT TAACATACAT  
4741 GAAGTTTATG TTTACCTTGA CGTTCTTCTA AAAAGTGTCC TACACCGGCA TTGTCTTGT  
4801 AGGCATATTC ACATGATCAA ATAAAATAAT TAGTTTTCAA TTAAGGAGAA TATTTGAGGA  
4861 AAGACCGTAC GTGTTTCATGT GGTTCCTGAA GGCAGTCCAG TGAGAAAGTA ATATATGCTT  
4921 CATTAAACAA TCGCGACATT TTCAGGGTTT CCCTTTTTAA CCAAATTTG GAAGCAATGT  
4981 GGAATTTACT GGATGCATCC AGCCCTGAAA TGAAGATAGG TTTATTGAAT GTGCCAGCAA  
5041 GTGCAGGCCC AGGTCTGAGT GTTCTTCATT ATTATCAGGT GAGAGGAAGC CTGGGAGCAA  
5101 ACACTGCCAG CAGCATAGCT GGGGGAACGG GAATTACCAT CCTGATCATC AACCTGAAGA  
5161 AGAGCTTGGC CTATATCCAC ATCCACAGTT GCCAGAAAT TTTTGAGACC AAGTGCTTTA  
5221 TGGCTTCCTT TTCCACTGTA TGTATTTTTT TTTGTGTGGG AAGACTAAGA TTCTGGGTCC  
5281 TAATGTAAGT AAGAAGCCCT CTCTCCTGT TCCATGAACA CCATCCTTTT CTGTAACCTC  
5341 TATTACACAG TATAGTGGTT CTGTAAGTTC ACACAGCCCA GGGAGATGCT GGCTGCCAC  
5401 TCCCCTCAAC CCAGGCAAAAT TCCTCGGGGT TAAAGTTATC TACTGCAAGT GACGATCTCT  
5461 GGGTTTTTCT GTGCCTGTGT TTGTGTGTGT GTGTGTGTGT GTGTGTGTGT GTATGTGTCA  
5521 CTTTAAAAGG ACTGGTCAGA TGGTAGGGAG ATGAAAACAG GAGATGCTAT AAGAAAATAA  
5581 ACTTTTGGGG CGAATACCAA TGTACTCTT TTTGTTTGTG ATTTGTTGCT GTTCAATAGG  
5641 AAATTGTAAGT GATGATGCTG TTTCTCACCA TTCTGGGACT TGGTAGTCTG GTGTCACTCA  
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(2) INFORMATION FOR SEQ ID NO:2505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: - base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2505:

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## (2) INFORMATION FOR SEQ ID NO:2506:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2506:

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1021 CCTTTATGCA AAAACAATC TCTGGATGGC ATGGGGTGAG TATAAATACT TCTTGGCTGC
1081 CAGTGTGTTT ATAATTGT AGCGAGTCGA AAAGTGAGGC TCCGGCCGCA GAGAACTCAG
1141 CCTCATTCCT GCTTTAAAT CTCTCGGCCA CCTTTGATGA GGGGACTGGG CAGTTCTAGA
1201 CAGTCCCGAA GTTCTCAAGG CACAGGTCTC TTCCTGGTTT GACTGTCCTT ACCCGGGGA
1261 GGCAGTGCAG CCAGCTGCAA GGTGAGTTGC C

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## (2) INFORMATION FOR SEQ ID NO:2507:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2507:

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1 CTGCTTTTAA ATCTCTCGGC CACCTTTGAT GAGGGGACTG GGCAGTTCTA GACAGTCCCCG
61 AAGTTCTCAA GGCACAGGTC TCTTCCTGGT TTGACTGTCC TTACCCCGGG GAGGCAGTGC
121 AGCCAGCTGC AAGCCCCACA GTGAAGAACA TCTGAGTCA AATCCAGATA AGTGACATAA
181 GTGACCTGCT TTGTAAAGCC ATAGAGATGG CCTGTCCTTG GAAATTTCTG TTCAAGACCA
241 AATTCCACCA GTATGCAATG AATGGGGAAA AAGACATCAA CAACAATGTG GAGAAAGCCC
301 CCTGTGCCAC CTCCAGTCCA GTGACACAGG ATGACCTTCA GTATCACAAC CTCAGCAAGC
361 AGCAGAATGA GTCCCCGAG CCCCTCGTGG AGACGGGAAA GAAGTCTCCA GAATCTCTGG
421 TCAAGCTGGA TGCAACCCCA TTGTCTCCC CACGGCATGT GAGGATCAAA AACTGGGGCA
481 GCGGGATGAC TTTCCAAGAC AACTTCAACC ATAAGGCCAA AGGGATTTTA ACTTGCAGGT
541 CCAATCTTG CCTGGGTCC ATTATGACTC CCAAAGTTT GACCAGAGGA CCCAGGGACA

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601 AGCC...CCC.TCCAGATGAG CTCTACCTC AAGCTATCGA A...GTCAAC CAATATTACG  
 661 GCTCCTTCAA AGAGGCAAAA ATAGAGGAAC ATCTGGCCAG GGTGGAAGCG GTAACAAAGG  
 721 AGATAGAAAC AACAGGAACC TACCAACTGA CGGGAGATGA GCTCATCTTC GCCACCAAGC  
 781 AGGCCTGGCG CAATGCCCA CGCTGCATTG GGAGGATCCA GTGGTCCAAC CTGCAGGTCT  
 841 TCGATGCCCG CAGCTGTTCC ACTGCCCCGG AAATGTTTGA ACACATCTGC AGACACGTGC  
 901 GTTACTCCAC CAACAATGGC AACATCAGGT CGGCCATCAC CGTGTTCCCC CAGCGGAGTG  
 961 ATGGCAAGCA CGACTTCCGG GTGTGGAATG CTCAGCTCAT CCGCTATGCT GGCTACCAGA  
 1021 TGCCAGATGG CAGCATCAGA GGGGACCCTG CCAACGTGGA ATTCACCTAG CTGTGCATCG  
 1081 ACCTGGGCTG GAAGCCCAAG TACGGCCGCT TCGATGTGGT CCCCCTGGTC CTGCAGGCCA  
 1141 ATGGCCGTGA CCTGAGCTC TTGAAATCC CACCTGACCT TGTGCTTGAG GTGGCCATGG  
 1201 AACATCCCAA ATACGAGTGG TTTCGGGAAC TGGAGCTAAA GTGGTACGCC CTGCCTGCAG  
 1261 TGGCCACAT GCTGCTTGAG GTGGGCGGCC TGGAGTTCCT AGGGTGGCCC TTCAATGGCT  
 1321 GGTACATGGG CACAGAGATC GGAGTCCGGG ACTTCTGTGA CGTCCAGCGC TACAACATCC  
 1381 TGGAGGAAGT GGGCAGGAGA ATGGGCTGG AAACGCACAA GCTGGCCTCG CTCTGGAAAG  
 1441 ACCAGCTGT CGTTGAGATC AACATTGCTG TGATCCATAG TTTTCAGAAG CAGAATGTGA  
 1501 CCATCATGGA CCACCACTCG GCTGCAGAAAT CCTTCATGAA GTACATGCAG AATGAATACC  
 1561 GGTCCCGTGG GGGCTGCCCG GCAGACTGGA TTTGGCTGGT CCCTCCCATG TCTGGGAGCA  
 1621 TCACCCCGT GTTTCACCAG GAGATGCTGA ACTACGTCCT GTCCCTTTTC TACTACTATC  
 1681 AGGTAGAGGC CTGGAAAACC CATGTCTGGC AGGACGAGAA GCGGAGACCC AAGAGAAGAG  
 1741 AGATTCCATT GAAAGTCTTG GTCAAAGCTG TGCTCTTTGC CTGTATGCTG ATGCGCAAGA  
 1801 CAATGGCGTC CCGAGTCAGA GTCACCATCC TCTTTGCGAC AGAGACAGGA AAATCAGAGG  
 1861 CGCTGGCCTG GGACCTGGGG GCCTTATTCA GCTGTGCCTT CAACCCCAAG GTTGTCTGCA  
 1921 TGGATAAGTA CAGGCTGAGC TGCCCTGGAGG AGGAACGGCT GCTGTTGGTG GTGACCAGTA  
 1981 CGTTTGGCAA TGGAGACTGC CCTGGCAATG GAGAGAACT GAAGAAATCG CTCTTCATGC  
 2041 TGAAAGAGCT CAACAACAAA TTCAGGTACG CTGTGTTTGG CCTCGGCTCC AGCATGTACC  
 2101 CTCGGTTCTG CGCCTTTGCT CATGACATTG ATCAGAAGCT GTCCACCTG GGGGCTCTC  
 2161 AGCTCACCCC GATGGGAGAA GGGGATGAGC TCAGTGGGCA GGAGGACGCC TTCCGAGCT  
 2221 GGGCCGTGCA AACCTTCAAG GCAGCCTGTG AGACGTTTGA TGTCCGAGGC AAACAGCACA  
 2281 TTCAGATCCC CAAGCTCTAC ACCTCCAATG TGACCTGGGA CCCGCACCAC TACAGGCTCG  
 2341 TGCAGGACTC ACAGCCTTG GACCTCAGCA AAGCCCTCAG CAGCATGCAT GCCAAGAACG  
 2401 TGTTACCAT GAGGCTCAAA TCTCGGCAGA ATCTACAAAG TCCGACATCC AGCCGTGCCA  
 2461 CCATCCTGGT GGAACCTCTC TGTGAGGATG GCCAAGGCCT GAACCTACCTG CCGGGGAGC  
 2521 ACCTTGGGGT TTGCCCAGGC AACCAGCCGG CCCTGGTCCA AGGCATCCTG GAGCGAGTGG  
 2581 TGGATGGCCC CACACCCAC CAGACAGTGC GCCTGGAGGA CCTGGATGAG AGTGGCAGCT  
 2641 ACTGGGTGAG TGACAAGAGG CTGCCCCCT GCTCACTCAG CCAGGCCCTC ACCTACTCCC  
 2701 CGGACATCAC CACACCCCA ACCAGCTGC TGCTCCAAA GCTGGCCAG GTGGCCACAG  
 2761 AAGAGCCTGA GAGACAGAGG CTGGAGGCC TGTGCCAGCC CTCAGAGTAC AGCAAGTGGA  
 2821 AGTTCACCAA CAGCCCCACA TTCCTGGAGG TGCTAGAGGA GTTCCGTCCT CTGCGGGTGT  
 2881 CTGCTGGCTT CCTGCTTTCC CAGCTCCCCA TTCTGAAGCC CAGGTTCTAC TCCATCAGCT  
 2941 CCTCCCGGGA TCACACGCCC ACGGAGATCC ACCTGACTGT GGCCGTGGTC ACCTACCACA  
 3001 CCGGAGATGG CCAGGTCCC CTGCACCAG GTGTCTGCAG CACATGGCTC AACAGCCTGA  
 3061 AGCCCCAAGA CCCAGTGCCC TGCTTTGTGC GGAATGCCAG CGCCTTCCAC CTCCCCGAGG  
 3121 ATCCCTCCA TCCTGTCATC CTCATCGGGC CTGGCACAGG CATCGTGCCC TTCCGAGTT  
 3181 TCTGGCAGCA ACGGCTCCAT GACTCCAGC ACAAGGGAGT GCGGGGAGGC CGCATGACCT  
 3241 TGGTGTGTTG GTGCCGCCGC CCAGATGAGG ACCACATCTA CCAGGAGGAG ATGCTGGAGA  
 3301 TGGCCAGAA GGGGTGCTG CATGCGGTGC ACACAGCCTA TTCCCGCCTG CCTGGCAAGC  
 3361 CCAAGTCTA TGTTCAAGAC ATCTGCGGC AGCAGCTGGC CAGCGAGGTG CTCCGTGTGC  
 3421 TCCACAAGGA GCCAGGCCAC CTCTATGTTT GCGGGGATGT GCGCATGGCC CGGGACGTGG  
 3481 CCCACACCT GAAGCAGCTG GTGGCTGCCA AGCTGAAAT GAATGAGGAG CAGGTCGAGG  
 3541 ACTATTCTT TCAGCTCAAG AGCCAGAAGC GCTATCACGA AGATATCTTC GGTGCTGTAT  
 3601 TTCCTTACGA GGCGAAGAAG GACAGGGTGG CGGTGCAGCC CAGCAGCCTG GAGATGTACG  
 3661 CGCTCTGAGG GCCTACAGGA GGGGTAAAG CTGCCGGCAC AGAACTTAAG GATGGAGCCA  
 3721 GCTCTGCATT ATCTGAGGTC ACAGGGCCTG GGGAGATGGA GGAAAGTGAT ATCCCCAGC  
 3781 CTCAAGTCTT ATTTCTCAA CGTTGCTCCC CATCAAGCCC TTTACTTGAC CTCCTAACAA  
 3841 GTAGCACCTT GGATTGATCG GAGCCTCCTC TCTCAAACCTG GGGCCTCCCT GTCCCTTGG  
 3901 AGACAAAATC TTAATGCCA GGCCTGGCGA GTGGGTGAAA GATGGAACCT GCTGCTGAGT  
 3961 GCACCACTT AAGTGACCAC CAGGAGGTGC TATCGCACCA CTGTGATTTT AACTGCCTTG  
 4021 TGTACAGTTA TTTATGCCTC TGTATTTAAA AAATAACAC CCAGTCTGTT CCCCATGGCC  
 4081 ACTTGGGTCT TCCCTGTATG ATTCCTTGAT GGAGATATTT ACATGAATTG CATTTTACTT  
 4141 TAATC

## (2) INFORMATION FOR SEQ ID NO:2508:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4077 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2508:

1 GAATTCAC TCTGCTGCT GCTCCAGCAG ACGGACGCAC AGTAACATGG GCAACTTGAA

61	GAGCGTGGCC	CAGGAGCCTG	GGCCACCCTG	CGGCCTGGGG	CTGGGGCTGG	GCCTTGGGCT
121	GTGCGGCAAG	CAGGGCCAG	CCACCCCGGC	CCCTGAGCCC	AGCCGGGGCC	CAGCATCCCT
181	ACTCCCACCA	GCGCCAGAAC	ACAGCCCCCG	GAGCTCCCCG	CTAACCCAGC	CCCCAGAGGG
241	GCCCAAGTTC	CCTCGTGTGA	AGAACTGGGA	GGTGGGGAGC	ATCACTATG	ACACCTCAG
301	CGCCCAGGCG	CAGCAGGATG	GGCCTGCAC	CCCAAGACGC	TGCTGGGCT	CCCTGTATT
361	TCCACGGAAA	CTACAGGGCC	GGCCTCCCC	CGGCCCCCG	GCCCTGAGC	AGCTGTGAG
421	TCAGGCCCGG	GACTTCATCA	ACCAGTACTA	CAGCTCCATT	AAGAGGAGCG	GCTCCCAGGC
481	CCACGAACAG	CGGCTTCAAG	AGGTGGAAGC	CGAGGTGGCA	GCCACAGGCA	CCTACCAGCT
541	TAGGGAGAGC	GAGCTGGTGT	TCGGGGCTAA	GCAGGCCTGG	CGCAACGCTC	CCCGCTGCGT
601	GGGCCGGATC	CAGTGGGGGA	AGCTGCAGGT	GTTTCGATGCC	CGGGAAGTGA	GGTCTGCACA
661	GGAAATGTTT	ACCTACATCT	GCAACCACAT	CAAGTATGCC	ACCAACCGGG	GCAACCTTCG
721	CTCGGCCATC	ACAGTGTTC	CGCAGCGCTG	CCCTGGCCGA	GGAGACTTCC	GAATCTGGAA
781	CAGCCAGCTG	GTGCGCTACG	CGGGCTACCG	GCAGCAGGAC	GGCTCTGTGC	GGGGGGACCC
841	AGCCAACGTG	GAGATCACCG	AGCTCTGCAT	TCAGCACGGC	TGGACCCAG	GAAACGGTCG
901	CTTCGACGTG	CTGCCCTGCG	TGCTGCAGGC	CCCAGATGAG	CCCCCAGAAC	TCTTCTTCT
961	GCCCCCCGAG	CTGGTCCTTG	AGGTGCCCTT	GGAGCACCCC	ACGCTGGAGT	GGTTTGCAGC
1021	CCTGGGCTTG	CGCTGGTACG	CCCTCCCGGC	AGTGTCCAAC	ATGCTGTCTG	AAATTGGGGG
1081	CTGGAGTTC	CCCGCAGCCC	CCTTCAGTGG	CTGGTACATG	AGCACTGAGA	TCGGCACGAG
1141	GAACCTGTGT	GACCCTCACC	GCTACAACAT	CCTGGAGGAT	GTGGCTGTCT	GCATGGACCT
1201	GGATACCCGG	ACCACCTCGT	CCCTGTGGAA	AGACAAGGCA	GCAGTGGAAA	TCAACGTGGC
1261	CGTGTGCAC	AGTTACCAGC	TAGCCAAAGT	CACCATCGTG	GACCACCAGC	CCGCCACGGC
1321	CTCTTTCATG	AAGCACCTGG	AGAATGAGCA	GAAGGCCAGG	GGGGGCTGCC	CTGCAGACTG
1381	GGCCTGGATC	GTGCCCCCCA	TCTCGGGCAG	CCTCACTCCT	GTTTTCCATC	AGGAGATGGT
1441	CAACTATTTC	CTGTCCCCGG	CCTTCCGCTA	CCAGCCAGAC	CCCTGGAAGG	GGAGTGCCGC
1501	CAAGGGCACC	GGCATCACCA	GGAAGAAGAC	CTTTAAAGAA	GTGGCCACCG	CCGTGAAGAT
1561	CTCCGCCCTG	CTCATGGGCA	CGGTGATGGC	GAAGCGAGTG	AAGGCGACAA	TCCTGTATGG
1621	CTCCGAGACC	GGCCGGGCCC	AGAGCTACGC	ACAGCAGCTG	GGGAGACTCT	TCCGGAAGGC
1681	TTTTGATCCC	CGGGTCCTGT	GTATGGATGA	GTATGACGTG	GTGTCCCTCG	AACACGAGAC
1741	GCTGGTGCTG	GTGGTAACCA	GCACATTGG	GAATGGGGAT	CCCCCGGAGA	ATGGAGAGAG
1801	CTTTGCAGCT	GCCCTGATGG	AGATGTCCGG	CCCCTACAAC	AGCTCCCTC	GGCCGGAACA
1861	GCACAAGAGT	TATAAGATCC	GCTTCAACAG	CATCTCCTGC	TCAGACCCAC	TGGTGTCTCT
1921	TTGGCGGCGG	AAGAGGAAGG	AGTCCAGTAA	CACAGACAGT	GCAGGGGGCC	TGGGCACCCT
1981	CAGGTTCTGT	GTGTTGCGGC	TCGGCTCCCC	GGCATACCCC	CACTTCTGCG	CCTTTGCTCG
2041	TGCCGTGGAC	ACACGGCTGG	AGGAAGTGGG	CGGGGAGCGG	CTGCTGCAGC	TGGGCCAGGG
2101	CGACGAGCTG	TGCGGCCAGG	AGGAGGCCTT	CCGAGGCTGG	GCCCAGGCTG	CCTTCCAGGC
2161	CGCTGTGAG	ACCTTCTGTG	TGGGAGAGGA	TGCCAAGGCC	GCCGCCGAG	ACATCTTCAG
2221	CCCCAAACGG	AGCTGGAAGC	GCCAGAGGTA	CCGGCTGAGC	GCCCAGGCCG	AGGGCCTGCA
2281	GTTGCTGCCA	GGTCTGATCC	ACGTGCACAG	GCGGAAGATG	TTCCAGGCTA	CAATCCGCTC
2341	AGTGGAAGAC	CTGCAAAGCA	GCAAGTCCAC	GAGGGCCACC	ATCCTGGTGC	GCCTGGACAC
2401	CGGAGGCCAG	GAGGGGCTGC	AGTACCAGCC	GGGGGACCAC	ATAGGTGTCT	GCCCCCCCAA
2461	CCGGCCCGGC	CTTGTGGAGG	CGCTGTGAG	CCGCGTGGAG	GACCCGCCCG	CGCCCACTGA
2521	GCCCGTGGCA	GTAGAGCAGC	TGGAGAAGGG	CAGCCCTGGT	GGCCCTCCCG	CCGGCTGGGT
2581	GCGGGACCCC	CGGCTGCCCC	CGTGCACGCT	GCGCCAGGCT	CTCACCTTCT	TCCTGGACAT
2641	CACCTCCCCA	CCCAGCCCTC	AGCTCTTGCG	GCTGCTCAGC	ACCTTGGCAG	AAGAGCCCAG
2701	GGAACAGCAG	GAGCTGGAGG	CCCTCAGCCA	GGATCCCCGA	CGCTACGAGG	AGTGGAAGTG
2761	GTTCCGCTGC	CCCACGCTGC	TGGAGGTGCT	GGAGCAGTTC	CCGTCCGTGG	CGTGCCTGC
2821	CCCACTGCTC	CTCACCAGC	TGCCCTGCT	CCAGCCCCGG	TACTACTCAG	TCAGCTCGGC
2881	ACCCAGCACC	CACCCAGGAG	AGATCCACCT	CACTGTAGCT	GTGCTGGCAT	ACAGGACTCA
2941	GGATGGGCTG	GGCCCCCTGC	ACTATGGAGT	CTGCTCCAGC	TGGCTAAGCC	AGCTCAAGCC
3001	CGGAGACCCT	GTGCCCTGCT	TCATCCGGGG	GGCTCCCTCC	TTCCGGCTGC	CACCCGATCC
3061	CAGCTTGCCC	TGCATCCTGG	TGGGTCCAGG	CACTGGCATT	GCCCCCTTCC	GGGGATTCTG
3121	GCAGGAGCGG	CTGCATGACA	TTGAGAGCAA	AGGGCTGCAG	CCCACTCCCA	TGACTTTGGT
3181	GTTCCGCTGC	CGATGCTCCC	AACTTGACCA	TCTCTACCGC	GACGAGGTGC	AGAACGCCCA
3241	GCAGCGCGGG	GTGTTTGGCC	GAGTCCTCAC	CGCCTTCTCC	CGGGAACCTG	ACAACCCCAA
3301	GACCTACGTG	CAGGACATCC	TGAGGACGGA	GCTGGCTGCG	GAGGTGCACC	GCGTGTGTG
3361	CCTCGAGCGG	GGCCACATGT	TTGTCTGCGG	CGATGTTACC	ATGGCAACCA	ACGTCTGCA
3421	GACCGTGCAG	CGCATCCTGG	CGACGGAGGG	CGACATGGAG	CTGGACGAGG	CCGGCGACGT
3481	CATCGGCGTG	CTGCGGGATC	AGCAACGCTA	CCACGAAGAC	ATTTTCGGGC	TCACGCTGCG
3541	CACCCAGGAG	GTGACAAGCC	GCATACGCAC	CCAGAGCTTT	TCCTTGCAGG	AGCGTCAGTT
3601	GCGGGGCGCA	GTGCCCTGGG	CGTTCGACCC	TCCCGGCTCA	GACACCAACA	GCCCCTGAGA
3661	GCCGCTGGC	TTTCCCTTCC	AGTTCGGGGA	GAGCGGCTGC	CCGACTCAGG	TCCGCCCCGAC
3721	CAGGATCAGC	CCCGCTCCTC	CCCTCTTGAG	GTGGTGCTT	CTCACATCTG	TCCAGAGGCT
3781	GCAAGGATT	AGCATTATTC	CTCCAGGAAG	GAGCAAAACG	CCTCTTTTCC	CTCTTAGGC
3841	CTGTTGCCCT	GGGCCTGGGT	CCGCCTTAAT	CTGGAAGGCC	CCTCCAGCA	GCGGTACCCC
3901	AGGGCCTACT	GCCACCCGCT	TCCTGTTTCT	TAGTCCGAAT	GTTAGATTCC	TCTTGCCTCT
3961	CTCAGGAGTA	TCTTACCTGT	AAAGTCTAAT	CTCTAAATCA	AGTATTTATT	ATTGAAGATT
4021	TACCATAAGG	GACTGTGCCA	GATGTTAGGA	GAACCTACTAA	AGTGCCCTACC	CCAGCTC

(2) INFORMATION FOR SEQ ID NO:2509:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2- base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2509:

1 CATATGTATG GGAATACTGT ATTTCAAGCA TTATAAGGAA TGAAATTATA GGCCGGGCAT  
61 TGTGGCTAAC CCTTGTATC CTAGCACTTT GAGAGGCTGA AGTGGGCAGA TCACTTGAGC  
121 TTCAGAGTTC GAGACCAGCA TGGACAACAT GGTGAAACCC AGTCTCTACC AAAACACAA  
181 AAATATTAGC TGGGTGTGGT GGTGCATGCC TGTAGTCCCA GCTACTCAGG AGGCTGAGGT  
241 GGGAGGATCG CTTGAGCCTG GGAGGCAGAA GTTGCAATGA GCAGAGATCG TGCCACTCCG  
301 CTCAGTCTT GGTGACAGAA TGAGACTCCA TCTCAAAAT AAATAAATAA ATAAATAAAA  
361 TAAATGAAAT GAAATTATAA GAAATTACCA CTTTTTCATG TAAGAAGTGA TCATTTCCAT  
421 TATAAGGGAA GGAATTTAAT CCTACCTGCC ATTCCACCAA AGCTTACCTA GTGCTAAAGG  
481 ATGAGGTGTT AGTAAGACCA ACATCTCAGA GGCCTCTCTG TGCCAATAGC CTTCTTCTCT  
541 TTCCCTTCCA AAAACCTCAA GTGACTAGTT CAGAGGCCTG TCTGGAATAA TGGCATCATC  
601 TAATATCACT GGCCTTCTGG AACCTGGGCA TTTTCCAGT TGTTCATAT TGTCAATATT  
661 CCCCCAGCTT CCTGGACTCC TGTCACAAGC TGGAAAAGTG AGAGGATGGA CAGGGATTAA  
721 CCAGAGAGCT CCCTGCTGAG GAAAAATCT CCCAGATGCT GAAAGTGAGG CCATGTGGCT  
781 TGCCCAAATA AAACCTGGCT CCGTGGTGCC TCTGTCTTAG CAGCCACCCT GCTGATGAAC  
841 TGCCACCTTG GACTTGGGAC CAGAAAGAGG TGGGTTGGGT GAAGAGGCAC CACACAGAGT  
901 GATGTAACAG CAAGATCAGG TCACCCACAG GCCCTGGCAG TCACAGTCAT AAATTAGCTA  
961 ACTGTACACA AGCTGGGGAC ACTCCCTTTG GAAACCAAAA AAAAAAAAAA AAAAAAGAGA  
1021 CCTTTATGCA AAAACAATC TCTGGATGGC ATGGGGTGAG TATAAATCT TCTTGGCTGC  
1081 CAGTGTGTTT ATAACCTTGT AGCGAGTCGA AAAGTGGGC TCCGGCCGCA GAGAGCTCAG  
1141 CCTCATCTCT GCTTTAAAT CTCTCGGCA CCTTTGATGA GGGGACTGGG CAGTTCTAGA  
1201 CAGTCCCGAA GTTCTCAAG CACAGGTCTC TTCCTGGTTT GACTGTCTT ACCCCGGGGA  
1261 GGCAGTGCA CCAGCTGCAA GGTGAGTTGC C  
1 CTGCTTTAAA ATCTCTCGC CACCTTTGAT GAGGGGACTG GGCAGTTCTA GACAGTCCCG  
61 AAGTTCTCAA GGCACAGGTC TCTTCTGGT TTGACTGTCC TTACCCCGGG GAGGCAGTGC  
121 AGCCAGTGC AAGCCACACA GTGAAGAACA TCTGAGCTCA AATCCAGATA AGTGACATAA  
181 GTGACCTGCT TTGTAAAGCC ATAGAGATGG CTTGCTCTTG GAAATTTCTG TTCAAGACCA  
241 AATTCCACCA GTATGCAATG AATGGGAAA AAGACATCAA CAACAATGTG GAGAAAGCCC  
301 CCTGTGCCAC CTCCAGTCCA GTGACACAGG ATGACCTTCA GTATCACAAC CTCAGCAAGC  
361 AGCAGAAATG GTCCCGCAG CCCTCGTGG AGACGGGAAA GAAGTCTCCA GAATCTCTGG  
421 TCAAGCTGGA TGCAACCCCA TTGTCTCTCC CACGGCATGT GAGGATCAAA AACTGGGGCA  
481 GCGGGATGAC TTCCAAGAC AACTTCAACC ATAAGGCCAA AGGGATTTTA ACTTGCAGGT  
541 CCAAATCTTG CCTGGGGTCC ATTATGACTC CCAAAGTTT GACCAGAGGA CCCAGGGACA  
601 AGCCTACCCC TCCAGATGAG CTTCTACCTC AAGCTATCGA ATTTGTCAAC CAATATTACG  
661 GCTCCTTCAA AGAGGCAAAA ATAGAGGAAC ATCTGGCCAG GGTGGAAGCG GTAACAAAGG  
721 AGATAGAAAC AACAGGAACC TACCAACTGA CGGGAGATGA GTCATCTTC GCCACCAAGC  
781 AGGCCTGGCG CAATGCCCA CGCTGCATTG GGAGGATCCA GTGGTCCAAC CTGCAGGTCT  
841 TCGATGCCCG CAGCTGTTCC ACTGCCCGGG AAATGTTTGA ACACATCTGC AGACACGTGC  
901 GTTACTCCAC CAACAATGGC AACATCAGGT CGGCCATCAC CGTGTTCGCC CAGCGGAGTG  
961 ATGGCAAGCA CGACTTCCGG GTGTGGAATG CTCAGCTCAT CCGCTATGCT GGCTACCAGA  
1021 TGCCAGATGG CAGCATCAGA GGGGACCTG CCAACGTGGA ATTCATCAG CTGTGCATCG  
1081 ACCTGGGCTG GAAGCCCAAG TACGGCCGCT TCGATGTGGT CCCCCTGTGC CTGCAGGCA  
1141 ATGGCCGTGA CCCTGAGCTC TTCGAAATCC CACCTGACCT TGTGCTTGA GTGGCCATGG  
1201 AACATCCCAA ATACGAGTGG TTTCCGGAAC TGGAGCTAAA GTGGTACGCC CTGCCTGCAG  
1261 TGGCCAACAT GCTGCTTGA GTGGGCGGCC TGGAGTTCCC AGGGTGCCCC TTCAATGGCT  
1321 GGTACATGGG CACAGAGATC GGAGTCCGGG ACTTCTGTGA CGTCCAGCGC TACAACATCC  
1381 TGGAGGAAGT GGGCAGGAGA ATGGGCTGG AAACGCACAA GCTGGCCTCG CTCTGGAAAG  
1441 ACCAGGCTGT CGTTGAGATC AACATTGCTG TGATCCATAG TTTTCAGAAG CAGAATGTGA  
1501 CCATCATGGA CCACCACTCG GCTGCAGAA CTTTCATGAA GTACATGCA AATGAATACC  
1561 GGTCCCGTGG GGGCTGCCCG GCAGACTGGA TTTGGCTGGT CCTCCCATG TCTGGGAGCA  
1621 TCACCCCGGT GTTTCACCAG GAGATGCTGA ACTACGTCCT GTCCCTTTT TACTACTATC  
1681 AGGTAGAGGC CTGGAACACC CATGTCTGGC AGGACGAGAA GCGGAGACCC AAGAGAAGAG  
1741 AGATTCCATT GAAAGTCTTG GTCAAAGCTG TGCTCTTTG CTGTATGCTG ATGCGCAAGA  
1801 CAATGGCGTC CCGAGTCAGA GTCACCATCC TCTTTGCGAC AGAGACAGGA AAATCAGAGG  
1861 CGCTGGCCTG GGACCTGGGG GCCTTATTCA GCTGTGCCTT CAACCCCAAG GTTGTCTGCA  
1921 TGGATAAGTA CAGGCTGAG TGCCCTGGAG AGGAACGGCT GCTGTTGGT GTGACCAGTA  
1981 CGTTTGGCAA TGGAGACTGC CCTGGCAATG GAGAGAACT GAAGAAATCG CTCTTCATGC  
2041 TGAAAGAGCT CAACAACAAA TTCAGGTACG CTGTGTTTGG CCTCGGCTCC AGCATGTACC  
2101 CTCGGTTCTG CGCCTTTGCT CATGACATTG ATCAGAAGCT GTCCACCTG GGGGCTCTC  
2161 AGCTACCCCC GATGGGAGAA GGGGATGAG TCAGTGGGCA GGAGGACGCC TTCCGAGCT  
2221 GGGCCGTGCA AACCTTCAAG GCAGCTGTG AGACGTTTGA TGTCCAGGC AACAGCACA  
2281 TTCAGATCCC CAAGCTCTAC ACCTCCAATG TGACCTGGGA CCCGCACCAC TACAGGCTCG  
2341 TGCAGGACTC ACAGCCTTTG GACCTCAGCA AAGCCCTCAG CAGCATGCAT GCCAAGAAGC

2401 TGTTACCAT GAGGCTCAA TCTCGGCAGA ATCTACAAAG TCCGACATCC AGCCGTGCCA  
2461 CCATCCTGGT GGAACCTCTC TGTGAGGATG GCCAAGGCCCT GAACTACCTG CCGGGGGAGC  
2521 ACCTTGGGGT TTGCCCAGGC AACCCAGCCGG CCTTGGTCCA AGGCATCCTG GAGCGAGTGG  
2581 TGGATGGCCC CACACCCAC CAGACAGTGC GCCTGGAGGA CCTGGATGAG AGTGGCAGCT  
2641 ACTGGGTGAG TGACAAGAGG CTGCCCCCTT GCTCACTCAG CCAGGCCCTC ACCTACTCCC  
2701 CGGACATCAC CACACCCCA ACCCAGCTGC TGCTCCAAA GCTGGCCAG GTGGCCACAG  
2761 AAGAGCCTGA GAGACAGAGG CTGGAGGCC TGTGCCAGCC CTCAGAGTAC AGCAAGTGA  
2821 AGTTACCAA CAGCCCCACA TTCTGGAGG TGCTAGAGGA GTTCCCGTCC CTGCGGGTGT  
2881 CTGCTGGCTT CCTGCTTCC CAGCTCCCA TTCTGAAGCC CAGGTTCTAC TCCATCAGCT  
2941 CCTCCCGGGA TCACACGCC ACGGAGATCC ACCTGACTGT GGCCGTGGTC ACCTACCACA  
3001 CCGGAGATGG CCAGGGTCCC CTGCACCAG GTGTCTGCAG CACATGGCTC AACAGCCTGA  
3061 AGCCCCAAGA CCCAGTGCCC TGCTTTGTGC GGAATGCCAG CGCCTTCCAC CTCCCCGAGG  
3121 ATCCCTCCCA TCCTTGCATC CTCTATCGGC CTGGCACAGG CATCGTGCCC TTCCGCAGTT  
3181 TCTGGCAGCA ACGGCTCCAT GACTCCAGC ACAAGGGAGT GCGGGGAGGC CGCATGACCT  
3241 TGGTGTGTTG GTGCCGCCG CCAGATGAGG ACCACATCTA CCAGGAGGAG ATGCTGGAGA  
3301 TGGCCAGAA GGGGGTGCTG CATGCGGTGC ACACAGCCTA TTCCCGCCTG CCTGGCAAGC  
3361 CCAAGGTCTA TGTTCAAGAC ATCCTGCGGC AGCAGCTGGC CAGCGAGGTG CTCCGTGTGC  
3421 TCCACAAGGA GCCAGGCCAC CTCTATGTTT GCGGGGATGT GCGCATGGCC CGGGACGTGG  
3481 CCCACACCTT GAAGCAGCTG GTGGCTGCCA AGCTGAAATT GAATGAGGAG CAGGTCGAGG  
3541 ACTATTTCTT TCAGCTCAAG AGCCAGAAGC GCTATCACGA AGATATCTTC GGTGCTGTAT  
3601 TTCTTACGA GCGGAAGAAG GACAGGGTGG CGGTGCAGCC CAGCAGCCTG GAGATGTCAG  
3661 CGCTCTGAGG GCCTACAGGA GGGGTAAAG CTGCCGGCAC AGAACTTAAG GATGGAGCCA  
3721 GCTCTGCATT ATCTGAGGTC ACAGGGCCTG GGGAGATGGA GGAAAGTGAT ATCCCCCAGC  
3781 CTCAAGTCTT ATTTCTCAA CGTTGCTCCC CATCAAGCCC TTTACTTGAC CTCCTAACAA  
3841 GTAGCACCTT GGATTGATCG GAGCCTCCTC TCTCAAAGT GGGCCTCCCT GGTCCCTTGG  
3901 AGACAAAATC TTAAATGCCA GGCCTGGCGA GTGGGTGAAA GATGGAATT GCTGCTGAGT  
3961 GCACCACTT AAGTGACCAC CAGGAGGTGC TATCGCACCA CTGTGTATTT AACTGCCTTG  
4021 TGTACAGTTA TTTATGCCTC TGTATTTAAA AAACCTAACAC CCAGTCTGTT CCCCATGGCC  
4081 ACTTGGGTCT TCCCTGTATG ATTCCTTGAT GGAGATATTT ACATGAATTG CATTTTACTT  
4141 TAATC  
1 GAATTCAC TCTGCTGCCT GCTCCAGCAG ACGGACGCAC AGTAACATGG GCAACTTGAA  
61 GAGCGTGGCC CAGGAGCCTG GGCCACCCTG CGGCCTGGGG CTGGGGCTGG GCCTTGGGCT  
121 GTGCGGCAAG CAGGGCCCAG CCACCCCGGC CCTGAGCCC AGCCGGGGCC CAGCATCCCT  
181 ACTCCCACCA GCGCCAGAAC ACAGCCCCC GAGCTCCCCG CTAACCCAGC CCCCAGAGGG  
241 GCCCAAGTTC CCTCGTGTGA AGAACTGGGA GGTGGGGAGC ATCACCTATG ACACCTCAG  
301 CGCCCAGGCG CAGCAGGATG GGCCCTGCAC CCAAGACGC TGCCCTGGGT TGCCTGGTATT  
361 TCCACGGAAA CTACAGGGCC GGCCCTCCCC CGGCCCCCGG GCCCTGAGC AGCTGCTGAG  
421 TCAGGCCCCG GACTTCATCA ACCAGTACTA CAGCTCCATT AAGAGGAGCG GCTCCCAGGC  
481 CCACGAACAG CCGCTTCAAG AGGTGGAAGC CGAGGTGGCA GCCACAGGCA CCTACCAGCT  
541 TAGGGAGAGC GAGCTGGTGT TCGGGGCTAA GCAGGCTGG CGCAACGCTC CCCGCTGCGT  
601 GGGCCGGATC CAGTGGGGGA AGCTGCAGGT GTTCGATGCC CGGGACTGCA GGTCTGCACA  
661 GGAATGTTC ACCTACATCT GCAACCACAT CAAGTATGCC ACCAACCGGG GCAACCTTCG  
721 CTCGGCCATC ACAGTGTTC CGCAGCGCTG CCCTGGCCGA GGAGACTTCC GAATCTGGAA  
781 CAGCCAGCTG GTGCGTACG CGGGCTACCG GCAGCAGGAC GGCTCTGTGC GGGGGGACCC  
841 AGCCAACGTG GAGATACCG AGCTCTGCAT TCAGCACGGC TGGACCCAG GAAACGGTCG  
901 CTTGACGTG CTGCCCCGCT TGCTGCAGGC CCCAGATGAG CCCCAGAAC TCTTCTTCT  
961 GCCCCCGGAG CTGGTCTTGG AGGTGCCCTT GGAGCAGCCC ACGCTGGAGT GGTTCGAGC  
1021 CCTGGGCTG CGCTGGTACG CCCTCCCGGC AGTGTCCAAC ATGCTGCTGG AAATGGGGG  
1081 CCTGGAGTTC CCCGAGCCC CCTTCAGTGG CTGGTACATG AGCACTGAGA TCGGCACGAG  
1141 GAACCTGTG GACCTCACC GTACAACAT CCTGGAGGAT GTGGCTGTCT GCATGGACCT  
1201 GGATACCCGG ACCACCTCGT CCCTGTGGA AGACAAGGCA GCAGTGGA TCAACGTGGC  
1261 CGTGCTGCAC AGTTACCAGC TAGCCAAAGT CACCATCGTG GACCACCAG CCGCCACGGC  
1321 CTCTTTCATG AAGCACCTGG AGAATGAGCA GAAGGCCAGG GGGGGCTGCC CTGCAGACTG  
1381 GGCCTGGATC GTGCCCCCA TCTCGGGCAG CCTCACTCCT GTTTTCCATC AGGAGATGGT  
1441 CAACTATTTC CTGTCCCCGG CCTTCCGCTA CCAGCCAGAC CCCTGGAAGG GGAGTGCCGC  
1501 CAAGGGCACC GGATCACCA GGAAGAAGAC CTTTAAAGAA GTGGCCAAAG CCGTGAAGAT  
1561 CTCCGCTCG CTCATGGGCA CGGTGATGGC GAAGCGAGTG AAGGCGACAA TCCTGTATGG  
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1741 GCTGGTGCTG GTGGTAACCA GCACATTGG GAATGGGGAT CCCCCGGAGA ATGGAGAGAG  
1801 CTTTGAGCT GCCCTGATGG AGATGTCCGG CCCCTACAAC AGCTCCCCCTC GGCCGGAACA  
1861 GCACAAGAGT TATAAGATCC GCTTCAACAG CATCTCCTGC TCAGACCCAC TGGTGTCTC  
1921 TTGGCGGCGG AAGAGGAAG AGTCCAGTAA CACAGACAGT GCAGGGGGCC TGGGCACCCT  
1981 CAGGTTCTGT GTGTTCCGGC TCGGCTCCCG GGCATACCCC CACTTCTGCG CTTTGTCTG  
2041 TGCCGTGGAC ACACGGCTGG AGGAACTGGG CGGGGAGCGG CTGCTGCAGC TGGGCCAGGG  
2101 CGACGAGCTG TGCGGCCAGG AGGAGGCTT CCGAGGCTGG GCCCAGGCTG CTTTCCAGGC  
2161 CGCCTGTGAG ACCTTCTGTG TGGGAGAGGA TGCCAAGGCC GCCGCCCTAG ACATCTTCAG  
2221 CCCCAAACCG AGCTGGAAGC GCCAGAGGTA CCGGCTGAGC GCCAGGGCCG AGGGCCTGCA

2281 GTTCGCGCCA GGTCTGATCC ACGTGCACAG GCGGAAGATG TTCCAGGCTA CAATCCGCTC  
2341 AGTGGAAAAC CTGCAAAGCA GCAAGTCCAC GAGGGCCACC ATCCTGGTGC GCCTGGACAC  
2401 CGGAGGCCAG GAGGGGCTGC AGTACCAGCC GGGGGACCAC ATAGGTGTCT GCCCGCCCAA  
2461 CCGGCCCGGC CTTGTGGAGG CGTGCTGAG CCGCGTGGAG GACCCGCCGG CGCCACTGA  
2521 GCCCGTGGCA GTAGAGCAGC TGGAGAAGGG CAGCCCTGGT GGCCCTCCCC CCGGCTGGGT  
2581 GCGGGACCCC CGGCTGCCCC CGTGACAGCT GCGCCAGGCT CTCACCTTCT TCCTGGACAT  
2641 CACCTCCCCA CCCAGCCCTC AGCTCTTGGC GCTGCTCAGC ACCTTGGCAG AAGAGCCCAG  
2701 GGAACAGCAG GAGCTGGAGG CCCTCAGCCA GGATCCCCGA CGCTACGAGG AGTGGAAAGTG  
2761 GTTCCGCTGC CCCACGCTGC TGGAGGTGCT GGAGCAGTTC CCGTCGGTGG CGCTGCCTGC  
2821 CCCACTGTCT CTCACCCAGC TGCCTCTGCT CCAGCCCGG TACTACTCAG TCAGCTCGGC  
2881 ACCCAGCACC CACCCAGGAG AGATCCACCT CACTGTAGCT GTGCTGGCAT ACAGGACTCA  
2941 GGATGGGCTG GGCCCCCTGC ACTATGGAGT CTGCTCCACG TGGCTAAGCC AGCTCAAGCC  
3001 CGGAGACCCT GTGCCCTGCT TCATCCGGGG GGCTCCCTCC TTCCGGCTGC CACCCGATCC  
3061 CAGCTTGCCC TGCATCTGG TGGGTCCAGG CACTGGCATT GCCCCTTCC GGGGATTCTG  
3121 GCAGGAGCGG CTGCATGACA TTGAGAGCAA AGGGCTGCAG CCCACTCCCA TGACTTTGGT  
3181 GTTCGGCTGC CGATGCTCCC AACTTGACCA TCTCTACGC GACGAGGTGC AGAACGCCCA  
3241 GCAGCGCGGG GTGTTTGCC GAGTCTCTAC CGCCTTCTCC CGGGAACCTG ACAACCCCAA  
3301 GACCTACGTG CAGGACATCC TGAGGACGGA GCTGGCTGCG GAGGTGCACC GCGTGTCTG  
3361 CCTCGAGCGG GGCCACATGT TTGTCTGCGG CGATGTTACC ATGGCAACCA ACGTCTGCA  
3421 GACCGTGCAG CGCATCTGG CGACGGAGGG CGACATGGAG CTGGACGAGG CCGGCGACGT  
3481 CATCGGCGTG CTGCGGGATC AGCAACGCTA CCAGGAAGAC ATTTTCGGGC TCACGCTGCG  
3541 CACCCAGGAG GTGACAAGCC GCATACGCAC CCAGAGCTTT TCCTTGCAGG AGCGTCAATT  
3601 GCGGGGCGCA GTGCCCTGGG CGTTCGACCC TCCCGGCTCA GACACCAACA GCCCCTGAGA  
3661 GCGGCTGGC TTTCCCTTCC AGTTCGGGA GAGCGGCTGC CCGACTCAGG TCCGCCCCGAC  
3721 CAGGATCAGC CCGCTCTCTC CCTCTTGAG GTGGTGCCTT CTCACATCTG TCCAGAGGCT  
3781 GCAAGGATTC AGCATTATTC CTCCAGGAG GAGCAAAACG CCTCTTTTCC CTCTCTAGGC  
3841 CTGTTGCCTC GGGCCTGGGT CCGCCTTAAT CTGGAAGGCC CCTCCAGCA GCGGTACCCC  
3901 AGGGCCTACT GCCACCCGCT TCCTGTTTCT TAGTCCGAAT GTTAGATTCC TCTTGCTCT  
3961 CTCAGGAGTA TCTTACCTGT AAAGTCTAAT CTCTAAATCA AGTATTTATT ATTGAAGATT  
4021 TACCATAAGG GACTGTGCCA GATGTTAGGA GAACTACTAA AGTGCCTACC CCAGCTC

## (2) INFORMATION FOR SEQ ID NO:2510:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11970 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2510:

1 AAGCTTCTAC CTAGTCTGG TGCTACACTT ACATTGCTTA CATCCAAGTG TGTTATTTT  
61 TGTGGCTCCT GTTATAACTA TTATAGCACC AGGTCTATGA CCAGGAGAAT TAGACTGGCA  
121 TTAATCAGA ATAAGAGATT TTGCACCTGC AATAGACCTT ATGACACCTA ACCAACCCCA  
181 TTATTACAA TTAACAGGA ACAGAGGGAA TACTTTATCC AACTCACACA AGCTGTTTTT  
241 CTCCCAGATC CATGCTTTTT TGCGTTTATT ATTTTTTAGA GATGGGGGCT TCACTATGTT  
301 GCCCACACTG GACTAAAACT CTGGGCCTCA AGTGATTGTC CTGCCCTCAG CTCCTGAATA  
361 GCTGGGACTA CAGGGGCTAG CCATCACACC TAGTTCATTT CCTCTATTTA AATATACAT  
421 GGCTTAAACT CCAACTGGGA ACCCAAAACA TTCATTTGCT AAGAGTCTGG TGTTCTACCA  
481 CCTGAAGTAG GCTGGCCACA GGAATTATAA AAGCTGAGAA ATTCTTTAAT AATAGTAACC  
541 AGGCAACATC ATTGAAGGCT CATATGTAAG AATCCATGCC TTCCTTTCTC CCAATCTCCA  
601 TTCCCAAACCT TAGCCACTGG TTCTGGCTGA GGCCTTACGC ATACCTCCCG GGGCTTGCAC  
661 ACACCTTTCT CTACAGAAGA CACACCTTGG GCATATCCTA CAGAAGACCA GGCTTCTCTC  
721 TGTCCTTGG TAGAGGGCTA CTTTACTGTA ACAGGGCCAG GGTGGAGAGT TCTCTCTGTA  
781 AGCTCCATCC CCTCTATAGG AAATGTGTTG ACAATATTCA GAAGAGTAAG AGGATCAAGA  
841 CTTCTTTGTG CTCAAATACC ACTGTTCTCT TCTCTACCTT GCCCTAACCA GGAGCTTGTG  
901 ACCCCAAACT CTGAGGTGAT TTATGCCTTA ATCAAGCAAA CTTCCCTCTT CAGAAAAGAT  
961 GGCTCATTTT CCTCAAAG TTGCCAGGAG CTGCCAAGTA TTCTGCCAAT TCACCCTGGA  
1021 GCACAATCAA CAAATTGAGC CAGAACACAA CTACAGCTAC TATTAGAAT ATTATTATTA  
1081 ATAAATTCCT CTCAAATCT AGCCCTTGA CTTCCGATTT CACGATTTCT CCCTTCTCTC  
1141 TAGAAACTTG ATAAGTTTCC CGCGCTTCCC TTTTCTAAG ACTACATGTT TGTCATCTTA  
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1261 AATAATATCA GCTATGCCAT CTTTCACTAT TTTAGCCAGT ATCGAGTTGA ATGAACATAG  
1321 AAAAATACAA AACTGAATTC TTCCCTGTAA ATTCCCGGTT TTGACGACGC ACTTGTAGCC  
1381 ACCTAGCCAC GCCTACTTAA GACAATTACA AAAGGCGAAG AAGACTGACT CAGGCTTAAG  
1441 CTGCCAGCCA GAGAGGGAGT CATTTCATTG GCGTTTGAGT CAGCAAAGGT ATTGCTCTCA  
1501 CATCTCTGGC TATTAAAGTA TTTTCTGTTG TTGTTTTTCT CTTTGGCTGT TTTCTCTCAC  
1561 ATTGCCTTCT CTAAAGCTAC AGTCTCTCCT TTCTTTTCTT GTCCCTCCCT GGTGTTGGTAT  
1621 GTGACCTAGA ATTACAGTCA GATTTTCAGAA AATGATTCTC TCATTTTGGT GATAAGGACT  
1681 GATTGCTTTT ACTGAGGGAC GGCAGAACTA GTTTCCTATG AGGCGATGGG TGAATACAAC  
1741 TGAGGCTTCT CATGGGAGGG AATCTCTACT ATCCAAAATT ATTAGGAGAA AATTGAAAT  
1801 TTCAAACCTCT GTCTCTCTCT TACCTCTGTG TAAGGCAAAAT ACCTTATTCT TGTGGTGT



1861 TTGTAACCTC TTCAAACCTT CATTGATTGA ATGCCTGTTC TGGCAATACA TTAGGTTGGG  
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1981 AGACAGGTAC ATAGCAAAC AATTCAAAGG AGCTAGAAGA TGGAGAAAAT GCTGAATGTG  
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2161 ATGGCCAAAG TTCCAGACAT GTTTGAAGAC CTGAAGAACT GTTACAGGTA AGGAATAAGA  
2221 TTTATCTCTT GTGATTTAAT GAGGGTTTCA AGGCTCACCA GAATCCAGCT AGGCATAACA  
2281 GTGGCCAGCA TGGGGGCGAG CCGGCAGAGG TTGTAGAGAT GTGTACTAGT CCTGAAGTCA  
2341 GAGCAGGTTT AGAGAAGACC CAGAAAAACT AAGCATTGAG CATGTTAAAC TGAGATTACA  
2401 TTGGCAGGGA GACCGCCATT TTAGAAAAAT TATTTTTGAG GTCTGCTGAG CCCTACATGA  
2461 ATATCAGCAT CAACTAGAC ACAGCCTCTG TTGAGATCAC ATGCCCTGAT ATAAGAATGG  
2521 GTTTTACTGG TCCATTCTCA GGAAAACTTG ATCTCATTCA GGAACAGGAA ATGGCTCCAC  
2581 AGCAAGCTGG GCATGTGAAC TCACATATGC AGGCAAATCT CACTCAGATG TAGAAGAAAG  
2641 GTAAATGAAC ACAAAGATAA AATTACGGAA CATATTAAAC TAACATGATG TTTCCATTAT  
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2941 AAGCACAGGT AAAGCTCAA GCCTGTCTTG ATGACTACTA ATTCCAGATT AGTAAGATAT  
3001 GAATTACTCT ACCTATGTGT ATGTGTAGAA GTCCTTAAAT TTCAAAGATG ACAGTAATGG  
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3241 GGACTGCTAT TCTTACACAG TGGTTTCTTC ATCCAAAGAG AACAGCAATG ACTTGAATCT  
3301 TAAATACTTT TGTTTTACCC TCACTAGAGA TCCAGAGACC TGCTTTTCAT TATAAGTGAG  
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3601 GCTGAGAGAG AGGAAGCAAG CCAGCTGAAA GTGAGAAGTC TACAGCCACT CATCAATCTG  
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4141 AGGCTGCATG GATCAATCTG TGTCTCTGAG TATCTCTGAA ACCTCTAAAA CATCCAAGCT  
4201 TACCTTCAAG GAGAGCATGG TGGTAGTAGC AACCAACGGG AAGGTTCTGA AGAAGAGACG  
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4321 GGAAGGTAAG GGGTCAAGCA CAATAATATC TTTCTTTTAC AGTTTTAAGC AAGTAGGGAC  
4381 AGTAGAATTT AGGGGAAAAT TAAACGTGGA GTCAGAATAA CAAGAAGACA ACCAAGCATT  
4441 AGTCTGGTAA CTATACAGAG GAAAATTAAT TTTTATCCTT CTCCAGGAGG GAGAAATGAG  
4501 CAGTGGCCTG AATCGAGAAT ACTTGCTCAC AGCCATTATT TCTTAGCCAT ATTGTAAAGG  
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4621 CTCTCATACT AACTATGCCT CCTTGGTCAT GTTACATAAT CTTTTCGTGA TTCAGTTTCC  
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4981 TCCTGGGTTT ATGCCATTCT CCTGCCCTCAG CCTCCCGAGT AAGCTGGGAA TACAGGCACC  
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5581 TATGTTTCCT TAAAACTTT GCTATACACA TACCTACATG TGAACAAATA TGTCTAACAT  
5641 CAAGACCACA CTATTTACAA CTTTATATCC AGCTTTTCTT ACTTAGCAAT GTATTGAGGA  
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5821 CCAGAGCCAT GAGGATTTGT GACGCTATTG ATATGTGCCA CTTTGCACTC TCTGTGACAT  
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5941 CGGGAAATAC TGGTAGTCTT CCTTGTCAGT TAGAAACACC CAAATCAATGA AAAATGAAAA  
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6601 AGGGCAGAAG GTTCAACTAA ATCTGGAAGT TCCACAAGAG AGAAGTTTCC TATCTTTGAG  
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7021 TCCAGAGAGG CAATTTTGCA ATAAACAAGC AAGACTTTTT CTGATTGGAT GCACTTCAGC  
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7201 AGACAATTCA ATCAGGTTGC TACGTTGGTC CCTTGGGTTT ACTCTAAATA GCTTGATTGC  
7261 AAATATCTTT GTATATATTA TTGTTTTTTC TCCTATCTTG TAATTTCTTT GAGCACATCC  
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7921 CCAACCAGTG CTGCTGAAGG TCAGTTGTCC TTTGTCTCCA ACTTACCTTC ATTTACATCT  
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8401 CTCTGCATTG ATGTCAGCAT TATCCTTCGT CCCAGTCTG TCTCCACTAC CACTTTCCCC  
8461 CTCAAACACA CACACACACA ACAGCCTTAG ATGTTTTCTC CACTGATAAG TAGGTGACTC  
8521 AATTTGTAAG TATATAATCC AAGACCTTCT ATTCCCAAGT AGAATTTATG TGCCTGCCTG  
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9001 GAGGAGGGGG CGGGTCGTGG TTGTGGGTTT TTGGGTAGGA CATTAGAGG AGGGGGCGGG  
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9481 TTGGAGATAG AACCACAGA AGGAAGAGGA GAAACAACAT TTAGTGAGAA GGGAAAAAGT  
9541 AGGAGAGGAA TAGGTTTGGG AAATAAATCC TGCTGACATT GGAAACCCCA AGGAAGCCTC  
9601 AAAAGTATAT TTAATTGCTT TAGATTTAAA AGAATAGGAA AGAAGCATCT CAACCTGGAA  
9661 TTTGAAATCT ATTTTCCAT AAAAGTATTG TTAATTCTA CTCATACTCA CAAGAAAAGT  
9721 ACATTCTAAA GAGTATATTG AAAGAGTTTA CTGATATACT TAGGAATTTT GTGTGTATGT  
9781 GTGTGTGTGT ATGTGTGTGT GTGTGTTTAA CCTTCAATTG TTGACTTAAA TACTGAGATA  
9841 AATGTCATCT AAATGCTAAA TTGATTTCCC AAAGGTATGA TTTGTTCACT TGGAGATCAA  
9901 AATGTTTAGG GGGCTTAGAA TCACTGTAGT GCTCAGATTG GATGCAAAAT GTCTTAGGCC  
9961 TATGTTGAAG GCAGGACAGA AACAATGTTT CCCTCCTACC TGCCTGGATA CAGTAAGATA

10021 CTAGTGTAC TGACAATCTT CATAACTAAT TTAGATCTCT CTCCAATCAA CTAAGGAAAT  
10081 CAACTCTTAT TAATAGACTG GGCCACACAT CTACTAGGCA TGTAAATAAT GCTTGTGAA  
10141 TGAACAAATG AATGAAGAGC CTATAGCATC ATGTACAGC CATAGTCCTA AAGTGGTGT  
10201 TCTCATGAAG GCCAAATGCT AAGGGATTGA GCTTCAGTCC TTTTCTAAC ATCTTGTCT  
10261 CTAACAGAAT TCTCTTCTTT TCTTCATAGG AGATGCCTGA GATACCCAAA ACCATCACAG  
10321 GTAGTGAGAC CAACCTCCTC TCTTCTGGG AAACCTCACGG CACTAAGAAC TATTTTCAT  
10381 CAGTTGCCCA TCCAAACTTG TTTATTGCCA CAAAGCAAGA CTACTGGGTG TGCTTGGCAG  
10441 GGGGGCCACC CTCTATCACT GACTTTCAGA TACTGGAAAA CCAGGCGTAG GTCTGGAGTC  
10501 TCACTTGTCT CACTTGTGCA GTGTTGACAG TTCATATGTA CCATGTACAT GAAGAAGCTA  
10561 AATCCTTTAC TGTTAGTCAT TTGCTGAGCA TGTACTGAGC CTTGTAATTC TAAATGAATG  
10621 TTTACACTCT TTGTAAGAGT GGAACCAACA CTAACATATA ATGTTGTAT TTAAGAACA  
10681 CCCTATATTT TGCATAGTAC CAATCATTTT AATTATTATT CTTCATAACA ATTTTAGGAG  
10741 GACCAGAGCT ACTGACTATG GCTACCAAAA AGACTCTACC CATATTACAG ATGGGCAAA  
10801 TAAGGCATAA GAAAACTAAG AAATATGCAC AATAGCAGTT GAAACAAGAA GCCACAGACC  
10861 TAGGATTTC TGAATTCATT TCAACTGTTT GCCTTCTGCT TTTAAGTTGC TGATGAATC  
10921 TTAATCAAAT AGCATAAGTT TCTGGGACCT CAGTTTTATC ATTTTCAAAA TGGAGGGAAT  
10981 AATACCTAAG CCTTCCTGCC GCAACAGTTT TTTATGCTAA TCAGGGAGGT CATTTTGGTA  
11041 AAATACTTCT CGAAGCCGAG CCTCAAGATG AAGGCAAAGC ACGAAATGTT ATTTTAAAT  
11101 TATTATTTAT ATATGTATTT ATAAATATAT TTAAGATAAT TATAATATAC TATATTTATG  
11161 GGAACCCCTT CATCCTCTGA GTGTGACCAG GCATCCTCCA CAATAGCAGA CAGTGTTTTT  
11221 TGGGATAAGT AAGTTTGATT TCATTATATC AGGGCATTTT GGTCCAAGTT GTGCTTATCC  
11281 CATAGCCAGG AAACCTCTGCA TTCTAGTACT TGGGAGACCT GTAATCATAT AATAAATGTA  
11341 CATTAATTAC CTTGAGCCAG TAATTGGTCC GATCTTTGAC TCTTTTGCCA TTAACTTAC  
11401 CTGGGCATT CTTGTTTATT CAATCCACC TGCAATCAAG TCCTACAAGC TAAAATTAGA  
11461 TGAAGTCAAC TTTGACAACC ATGAGACCAC TGTATCAAA ACTTTCTTTT CTGGAATGTA  
11521 ATCAATGTTT CTTCTAGGTT CTAAAATTG TGATCAGACC ATAATGTAC ATTATATCA  
11581 ACAATAGTGA TTGATAGAGT GTTATCAGTC ATAATAAAT AAAGCTTGCA ACAAATTTCT  
11641 CTGACACATA GTTATTCATT GCCTTAATCA TTATTTTACT GCATGGTAAT TAGGGACAAA  
11701 TGTAAATGT TTACATAAAT AATTGTATTT AGTGTACTT TATAAATCA AACCAAGATT  
11761 TTATATTTTT TTCTCCTCTT TGTTAGCTGC CAGTATGCAT AAATGGCATT AAGAATGATA  
11821 ATATTTCCGG GTTCACTTAA AGCTCATATT ACACATACAC AAAACATGTG TTCCCATCTT  
11881 TATACAACT CACACATACA GAGCTACATT AAAACAACCT AATAGGCCAG GCACGGTGGC  
11941 TCAGACCTGT AATCCAGCA CTTTGGGAGG

## (2) INFORMATION FOR SEQ ID NO:2511:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1497 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2511:

1 ACCAACCTCT TCGAGGCACA AGGCACAACA GGCTGCTCTG GGATTCTCTT CAGCCAATCT  
61 TCATTGCTCA AGTGTCTGAA GCAGCCATGG CAGAAGTACC TGAGCTCGCC AGTGAAATGA  
121 TGGCTTATTA CAGTGGCAAT GAGGATGACT TGTCTTTGA AGCTGATGGC CCTAAACAGA  
181 TGAAGTGCTC CTTCCAGGAC CTGGACCTCT GCCCTCTGGA TGGCGGCATC CAGCTACGAA  
241 TCTCCGACCA CCACTACAGC AAGGGCTTCA GGCAGGCCGC GTCAGTTGTT GTGGCCATGG  
301 ACAAGCTGAG GAAGATGCTG GTTCCCTGCC CACAGACCTT CCAGGAGAAT GACCTGAGCA  
361 CTTCTTTTCC CTTTCTCTTT GAAGAAGAAC CTATCTTCTT CGACACATGG GATAACGAGG  
421 CTTATGTGCA CGATGCACCT GTACGATCAC TGAAGTGCAC GCTCCGGGAC TCACAGCAAA  
481 AAAGCTTGGT GATGTCTGGT CCATATGAAC TGAAAGCTCT CCACCTCCAG GGACAGGATA  
541 TGGAGCAACA AGTGGTGTTC TCCATGTCCT TTGTACAAGG AGAAGAAAGT AATGACAAAA  
601 TACCTGTGGC CTTGGGCCTC AAGGAAAAGA ATCTGTACCT GTCCTGCGTG TTGAAAGATG  
661 ATAAGCCAC TCTACAGCTG GAGAGTGTAG ATCCCAAAA TTACCCAAAG AAGAAGATGG  
721 AAAAGCGATT TGTCTTCAAC AAGATAGAAA TCAATAACAA GCTGGAATTT GAGTCTGCCC  
781 AGTTCCCAA CTGGTACATC AGCACCTCTC AAGCAGAAAA CATGCCCGTC TTCCTGGGAG  
841 GGACCAAAGG CGGCCAGGAT ATAAGTACTC TACCATGCA ATTTGTGTCT TCCTAAAGAG  
901 AGCTGTACCC AGAGAGTCTT GTGCTGAATG TGGACTCAAT CCCTAGGGCT GGCAGAAAGG  
961 GAACAGAAAG GTTTTTGAGT ACGGCTATAG CCTGGACTTT CCTGTTGTCT ACACCAATGC  
1021 CCAACTGCCT GCCTTAGGGT AGTGCTAAGA GGATCTCCTG TCCATCAGCC AGGACAGTCA  
1081 GCTCTCTCCT TTCAGGGCCA ATCCCAGGCC CTTTTGTGA GCCAGGCCTC TCTCACCTCT  
1141 CCTACTCACT TAAAGCCCGC CTGACAGAAA CCACGGCCAC ATTTGGTTCT AAGAAACCTT  
1201 CTGTCATTCT CTCCCACATT CTGATGAGCA ACCGCTTCCC TATTTATTTA TTTATTTGTT  
1261 TGTTTGTGTT ATTCAATGTT CTAATTTATT CAAAGGGGGC AAGAAGTAGC AGTGTCTGTA  
1321 AAAGAGCCTA GTTTTTAATA GCTATGGAAT CAATTCAATT TGGACTGGTG TGCTCTCTTT  
1381 AAATCAAGTC CTTTAATTA GACTGAAAT ATATAAGCTC AGATTATTTA AATGGGAATA  
1441 TTTATAAATG AGCAAATATC ATACTGTTCA ATGGTTCTGA AATAAACTTC TCTGAAG

## (2) INFORMATION FOR SEQ ID NO:2512:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9721 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2512:

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1 AGAAAGAAAG AGAGAGAGAA AGAAAAGAAA GAGGAAGGAA GGAAGGAAGG AAGAAAGACA
61 GGCTCTGAGG AAGGTGGCAG TTCCTACAC GGGAGAACCA GTGGTTAATT TGCAAAGTGG
121 ATCCTGTGGA GGCANN CAGA GGAGTCCCT AGGCCACCCA GACAGGGCTT TTAGCTATCT
181 GCAGGCCAGA CACCAAATTT CAGGAGGGCT CAGTGTTAGG AATGGATTAT GGCTTATCAA
241 ATTCACAGGA AACTAACATG TTGAACAGCT TTTAGATTTT CTGTGGAAAA TATAACTTAC
301 TAAAGATGGA GTTCTTGTGA CTGACTCCTG ATATCAAGAT ACTGGGAGCC AAATTAAGAA
361 TCAGAAGGCT GCTTGGAGAG CAAGTCCATG AAATGCTCTT TTTCCACAG TAGAACCTAT
421 TTCCCTCGTG TCTCAAATAC TTGCACAGAG GCTCACTCCC TTGGATAATG CAGAGCGAGC
481 ACGATACCTG GCACATACTA ATTTGAATAA AATGCTGTCA AATTTCCATT CACCCATTCA
541 AGCAGCAAAC TCTATCTCAC CTGAATGTAC ATGCCAGGCA CTGTGCTAGA CTGGGCTCAA
601 AAAGATTTC A GTTTCCTGGA GGAACCAGGA GGGCAAGGTT TCAACTCAGT GCTATAAGAA
661 GTGTTACAGG CTGGACACGG TGGCTCACGC CTGTAATCCC AACATTTGGG AGGCCGAGGC
721 GGGCAGATCA CAAGGTCAGG AGATCGAGAC CATCTGGCT AACATGTGA AACCTGTCT
781 CTAATAAAAA TACAAAAAAT TAGCCGGGCG TTGGCGGCG GTGCCTGTAG TCCAGCTGC
841 TGGGGAGGCT GAGGCAGGAG AATGGTGTGA ACCCGGGAGG CGGAAGTTC AGGGGGCCGA
901 GATCGTGCCA CTGCACTCCA GCCTGGGCGA CAGAGTGAGA CTCTGTCTCA AAAAAAAAAA
961 AAAAGTGTTA TGATGCAGAC CTGTCAAAGA GGCAAGGAG GGTGTTCTTA CACTCCAGGC
1021 ACTGTTTATA ACCTGGACTC TCATTCAATC TACAAATGGA GGGTCCCCCT GGGCAGATCC
1081 CTGGAGCAGG CACTTTGCTG GTGTCTCGT TAAAGAGAAA CTGATAACTC TTGGTATTAC
1141 CAAGAGATAG AGTCTCAGAT GGATATTCTT ACAGAAACAA TATTTCCCAT TTTCAGAGTT
1201 CACCAAAAAA TCATTTTAGG CAGAGCTCAT CTGGCATTGA TCTGGTTCAT CCATGAGATT
1261 GGCTAGGGTA ACAGCACCTG GTCTTGCAGG GTTGTGTGAG CTTATCTCCA GGGTTGCCCC
1321 AACTCCGTCA GGAGCCTGAA CCCTGCATAC CGTATGTTCT CTGCCCCAGC CAAGAAAGGT
1381 CAATTTTCTC CTCAGAGGCT CCTGCAATTG ACAGAGAGCT CCCGAGGCAG AGAACAGCAC
1441 CCAAGGTAGA GACCCACACC CTCAATACAG ACAGGGAGGG CTATTGGCCC TTCATTGTAC
1501 CCATTTATCC ATCTGTAAGT GGGAGATTTC CTAACCTTAA GTACAAAGAA GTGAATGAAG
1561 AAAAGTATGT GCATGTATAA ATCTGTGTGT CTCCACTTT GTCCACATA TACTAAATTT
1621 AAACATTCTT CTAACGTGGG AAAATCCAGT ATTTTAATGT GGACATCAAC TGCACAACGA
1681 TTGTCAAGAA AACAATGCAT ATTTGCATGG TGATACATTT GCAAAATGTG TCATAGTTTG
1741 CTACTCCTTG CCCTTCCATG AACCAGAGAA TTATCTCAGT TTATTAGTCC CCTCCCTTAA
1801 GAAGCTTCCA CCAATACTCT TTTCCCTTTT CCTTTAAGTT GATTGTGAAA TCAGGTATTC
1861 AACAGAGAAA TTTCTCAGCC TCCTACTTCT GCTTTTGAAA GCTATAAAAA CAGCGAGGGA
1921 GAAACTGGCA GATACCAAAC CTCTTCGAGG CACAAGGCAC AACAGGCTGC TCTGGGATTC
1981 TCTTCAGCCA ATCTTCATG CTCAAGTATG ACTTTAATCT TCCTTACAAC TAGGTGCTAA
2041 GGGAGTCTCT CTGTCTCTCT GCCTCTTTGT GTGTATGCAT ATTCTCTCTT TCTCTCTCTT
2101 TCTTTCTCTG TCTCTCTCTC CTTCCTCTC TGCCTCTCT CTCAGCTTTT TGCAAAAATG
2161 CCAGGTGTAA TATAATGCTT ATGACTCGGG AAATATTCTG GGAATGGATA CTGCTTATCT
2221 AACAGCTGAC ACCCTAAAGG TTAGTGTCAG AGCCTCTGCT CCAGCTCTCC TAGCCAATAC
2281 ATTGCTAGTT GGGGTTTGGT TTAGCAAATG CTTTTCTCTA GACCCAAAGG ACTTCTCTTT
2341 CACACATTCA TTCATTTACT CAGAGATCAT TTCTTTGCAT GACTGCCATG CACTGGATGC
2401 TGAGAGAAAT CACACATGAA CGTAGCCGTC ATGGGGAAGT CACTCATTTT CTCCTTTTAA
2461 CACAGGTGTC TGAAGCAGCC ATGGCAGAAG TACCTGAGCT CGCCAGTGAA ATGATGGCTT
2521 ATTACAGGTC AGTGGAGACG CTGAGACCAG TAACATGAGC AGGTCTCTCT TTTCAAGAGT
2581 AGAGTGTAT CTGTGCTTGG AGACCAGATT TTTCCCTTAA ATTGCCTCTT TCAGTGGCAA
2641 ACAGGGTGCC AAGTAAATCT GATTTAAAGA CTACTTTCCC ATTACAAGTC CCTCCAGCCT
2701 TGGGACCTGG AGGCTATCCA GATGTGTTGT TGCAAGGGCT TCCTGCAGAG GCAAATGGGG
2761 AGAAAAGATT CCAAGCCAC AATACAAGGA ATCCCTTTGC AAAGTGTGGC TTGGAGGGAG
2821 AGGGAGAGCT CAGATTTAG CTGACTCTGC TGGGCTAGAG GTTAGGCCTC AAGATCCAAC
2881 AGGGAGCACC AGGGTGCCCA CTGCCAGGC CTAGAATCTG CTTCTGAC TGTTCTGCGC
2941 ATATCACTGT GAAACTTGCC AGGTGTTTCA GGCAGCTTTG AGAGGCAGGC TGTTCAGAT
3001 TTCTTATGAA CAGTCAAGTC TTGTACACAG GGAAGGAAAA ATAAACCTGT TTAGAAGACA
3061 TAATTGAGAC ATGTCCCTGT TTTTATTACA GTGGCAATGA GGATGACTTG TTCTTTGAAG
3121 CTGATGGCCC TAAACAGATG AAGGTAAGAC TATGGGTTTA ACTCCAACC CAAGGAAGGG
3181 CTCTAACACA GGGAAAGCTC AAAGAAGGGA GTTCTGGGCC ACTTTGATGC CATGGTATTT
3241 TGTTTTAGAA AGACTTTAAC CTCTCCAGT GAGACACAGG CTGCACCACT TGCTGACCTG
3301 GCCACTTGGT CATCATATCA CCACAGTCAC TCACTAACGT TGGTGGTGGT GGCCACACTT
3361 GGTGGTGACA GGGGAGGAGT AGTGATAATG TTCCCATTTT ATAGTAGGAA GACAACCAAG
3421 TCTTCAACAT AAATTTGATT ATCCTTTTAA GAGATGGATT CAGCCTATGC CAATCACTTG
3481 AGTTAACTC TGAAACCAAG AGATGATCTT GAGAACTAAC ATATGTCTAC CCTTTTGGAG
3541 TAGAATAGTT TTTTGCTACC TGGGGTGAAG CTTATAACAA CAAGACATAG ATGATATAAA
3601 CAAAAGATG AATTGAGACT TGAAAGAAAA CCATTCACTT GCTGTTTGAC CTGACAAGT
3661 CATTTTACCC GCTTTGGACC TCATCTGAAA AATAAAGGGC TGAGCTGGAT GATCTCTGAG
3721 ATTCAGCAT CCTGCAACCT CCAGTTCTGA AATATTTTCA GTTGTAGCTA AGGGCATTTG
3781 GGCAGCAAAT GGTCAATTTT CAGACTCATC CTTACAAAGA GCCATGTTAT ATTCTGCTG
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3841 TCCCTTCTGT TTTATATGAT GCTCAGTAGC CTTCTAGGT GCCCAGCCAT CAGCCTAGCT  
3901 AGGTCAGTTG TGCAGGTTGG AGGCAGCCAC TTTTCTCTGG CTTTATTTTA TTCCAGTTTG  
3961 TGATAGCCTC CCCTAGCCTC ATAATCCAGT CCTCAATCTT GTTAAAAACA TATTTCTTTA  
4021 GAAGTTTTAA GACTGGCATA ACTTCTTGGC TGCAGCTGTG GGAGGAGCCC ATTGGCTTGT  
4081 CTGCTGGGCC TTTGCCCCC ATTGCCTCTT CCAGCAGCTT GGCTCTGCTC CAGGCAGGAA  
4141 ATTCTCTCCT GCTCAACTTT CTTTGTGTGA CTTACAGGTC TCTTTAAGC TCTTCAAGC  
4201 CTTTGAACCA TTATCAGCCT TAAGGCAACC TCAGTGAAGC CTTAATACGG AGCTTCTCTG  
4261 AATAAGAGGA AAGTGGTAAC ATTTCAAAA AAGTACTCTC ACAGGATTTG CAGAATGCCT  
4321 ATGAGACAGT GTTATGAAAA AGGAAAAAAA AGAACAGTGT AGAAAAATTG AATACTTGCT  
4381 GAGTGAGCAT AGGTGAATGG AAAATGTTAT GGTCACTGTC ATGAAAAAGC AAATCATAGT  
4441 GTGACAGCAT TAGGGATACA AAAAGATATA GAGAAGGTAT ACATGTATGG TGTAGGTGGG  
4501 GCATGTACAA AAAGATGACA AGTAGAATCG GGATTTATTC TAAAGAATAG CCTGTAAGGT  
4561 GTCCAGAAGC CACATTCTAG TCTTGAGTCT GCCTCTACCT GCTGTGTGCC CTTGAGTACA  
4621 CCTTAAACCT CCTTGAGCTT CAGAGAGGGA TAATCTTTT ATTTTATTTT ATTTTATTTT  
4681 GTTTTGT TTTTGT TTTTGT TTTTGT TTTTGT TTTTGT TTTTGT TTTTGT TTTTGT TTTTGT  
4741 GTGCAGTGGT ACAATCTTGG CTTACTGCAT CCTCCACCTC CTGAGTTCAA GCGATTCTCC  
4801 TTCTCAGTC TCCTGAATAG CTAGGATTAC AGGTGCACCC CACCACACC AGCTAATTTT  
4861 TGTATTTTGA GTAGAGAAGG GGTTTCGCCA TGTGCGCCAG GCTGTTTGTG AAGTCCTGAC  
4921 CTAATGATT CATCCACCTC GGCTTCCCAA AGTGCTGGGA TTACAGGCAT GAGCCACCAC  
4981 GCCTGGCCCA GAGAGGGATG ATCTTTAGAA GCTCGGGATT CTTTCAAGCC CTTTCTCCT  
5041 CTCTGAGCTT TCTACTCTCT GATGTCAAAG CATGGTTCCT GGCAGGACCA CCTCACCAGG  
5101 TCCTCTCCT CGCTCTCTCC GCAGTGCTCC TTCCAGGACC TGGACCTCTG CCTCTGGAT  
5161 GCGGCGCATCC AGCTACGAAT CTCCGACCAC CACTACAGCA AGGGCTTCAG GCAGGCCGCG  
5221 TCAGTTGTTG TGGCCATGGA CAAGCTGAGG AAGATGCTGG TTCCCTGCCC ACAGACCTTC  
5281 CAGGAGAATG ACCTGAGCAC CTCTTTCCC TTCTCTTTG AAGAAGGTAG TTAGCCAAGA  
5341 GCAGGCAGTA GATCTCCACT TGTGTCCTCT TGGAAATCAT CAAGCCCCAG CCAACTCAAT  
5401 TCCCCCAGAG CCAAAGCCCT TTAAGGTAG AAGGCCCAGC GGGGAGACAA AACAAAGAAG  
5461 GCTGGAAACC AAAGCAATCA TCTCTTAGT GGAAACTATT CTTAAAGAAG ATCTTGATGG  
5521 CTACTGACAT TTGCAACTCC CTCACTTTT CTCAGGGGCC TTCACTTAC ATTTGTCACCA  
5581 GAGGTTTCGT ACCTCCCTGT GGGCTAGTGT TATGACCATC ACCATTTTAC CTAAGTAGCT  
5641 CTGTTGCTCG GCCACAGTGA GCAGTAATAG ACCTGAAGCT GGAACCCATG TCTAATAGTG  
5701 TCAGGTCCAG TGTTCTTAGC CACCCACTC CCAGCTTCAT CCCTACTGGT GTTGTCTATCA  
5761 GACTTTGACC GTATATGCTC AGGTGTCTCT CAAGAAATCA AATTTTGCCA CCTCGCTCA  
5821 CGAGGCCTGC CTTCTGATT TTATACCTAA ACAACATGTG CTCCACATTT CAGAACCTAT  
5881 CTTCTTCGAC ACATGGGATA ACGAGGCTTA TGTGCACGAT GCACCTGTAC GATCACTGAA  
5941 CTGACGCTC CGGACTCAC AGCAAAAAAG CTTGGTGATG TCTGGTCCAT ATGAACTGAA  
6001 AGCTCTCCAC CTCCAGGGAC AGGATATGGA GCAACAAGGT AAATGGAAAC ATCCTGTTT  
6061 CCCTGCCTGG CCTCCTGGCA GCTTGCTAAT TCTCCATGTT TTAACAAAG TAGAAAGTTA  
6121 ATTTAAGGCA AATGATCAAC ACAAGTGAAG AAAAATATTA AAAAGGAATA TACAACTTT  
6181 GGTCTTAGAA ATGGCACATT TGATTGCACT GGCCAGTGCA TTTGTTAACA GGAGTGTGAC  
6241 CCTGAGAAAT TAGACGGCTC AAGCACTCCC AGGACCATGT CCACCCAAGT CTCTTGGGCA  
6301 TAGTGCAGTG TCAATCTTTC CACAATATGG GGTCAATTGA TGGACATGGC CTAAGTGCCT  
6361 GTGGGTTCTC TCTTCTGTT GTTGAGGCTG AAACAAGAGT GCTGGAGCGA TAATGTGTCC  
6421 ATCCCCCTCC CCAGTCTTCC CCCCTTGCCC CAACATCCGT CCCACCCAAT GCCAGTGGT  
6481 TCCTTGTAGG GAAATTTTAC CGCCAGCAG GAACTTATAT CTCTCCGCTG TAACGGGCAA  
6541 AAGTTTCAAG TGCGGTGAAC CCATCATTAG CTGTGGTGAT CTGCCTGGCA TCGTGCCACA  
6601 GTAGCCAAAG CCTCTGCACA GGAGTGTGGG CAACTAAGGC TGCTGACTTT GAAGGACAGC  
6661 CTCACTCAGG GGAAGCTAT TTGCTCTCAG CCAGGCCAAG AAAATCCTGT TTCTTTGGAA  
6721 TCGGGTAGTA AGAGTGATCC CAGGGCCTCC AATTGACACT GCTGTGACTG AGGAAGATCA  
6781 AAATGAGTGT CTCTCTTGG AGCCACTTTC CCAGCTCAGC CTCTCCTCTC CCAGTTTCTT  
6841 CCCATGGGCT ACTCTGTGT CCTGAAACAG TTCTGGTGCC TGATTTCTGG CAGAAGTACA  
6901 GCTTACCTC TTTCTTTCC TTCCACATTG ATCAAGTTGT TCCGCTCCTG TGGATGGGCA  
6961 CATTGCCAGC CAGTGACACA ATGGCTTCTC TCCTTCTTTC CTTGAGCATT TAAATGTAG  
7021 ACCCTCTTTC ATTCTCCGTT CTTACTGCTA TGAGGCTCTG AGAAACCCTC AGGCCTTTGA  
7081 GGGGAAACCC TAAATCAACA AAATGACCCT GCTATTGTCT GTGAGAAGTC AAGTTATCCT  
7141 GTGTCTTAGG CCAAGGAACC TCACTGTGGG TTCCACAGA GGCTACCAAT TACATGTATC  
7201 CTACTCTCGG GGCTAGGGGT TGGGGTGACC CTGCATGCTG TGTCCTTAAC CACAAGACCC  
7261 CCTTCTTTCT TCAAGTGTGT TCTCCATGTC CTTTGTACAA GGAGAAGAAA GTAATGACAA  
7321 AATACTGTG GCCTTGGGCC TCAAGGAAAA GAATCTGTAC CTGTCTGCG TGTGAAAGA  
7381 TGATAAGCCC ACTCTACAGC TGGAGGTAAG TGAATGCTAT GGAATGAAGC CCTTCTCAGC  
7441 CTCCTGCTAC CACTTATTCC CAGACAATTC ACCTTCTCCC CGCCCCATC CCTAGGAAAA  
7501 GCTGGGAACA GGTCTATTTG ACAAGTTTTG CATTAAATGA AATAAATTTA ACATAATTTT  
7561 TAACTGCGTG CAACCTTCAA TCCTGCTGCA GAAAATTAAA TCATTTTGCC GATGTTATTA  
7621 TGTCCTACCA TAGTTACAAC CCCAACAGAT TATATATTGT TAGGGCTGCT CTCATTTGAT  
7681 AGACACCTTG GGAAATAGAT GACTTAAAGG GTCCCATAT CACGTCCACT CCACTCCCAA  
7741 AATCAACCAC ACTATCACCT CCAGCTTTCT CAGCAAAAGC TTCATTTCCA AGTTGATGTC  
7801 ATTCTAGGAC CATAAGGAAA AATACAATAA AAAGCCCTG GAACTAGGT ACTTCAAGAA  
7861 GCTCTAGCTT AATTTTCACC CCCCCAAAA AAAAAAATTC TCACCTACAT TATGCTCCTC

7921 AGCATGC ACTAAGTTTT AGAAAAGAAG AAGGGCTCTT TTTAAAGC CACAGAAAGT  
7981 TGGGGGCCCA GTTACAACCTC AGGAGTCTGG CTCCTGATCA TGTGACCTGC TCCTCAGTTT  
8041 CCTTCTGGC CAACCCAAAG AACATCTTTC CCATAGGCAT CTTTGTCCCT TGCCCCACAA  
8101 AAATTCTTCT TTCTCTTTCG CTGCAGAGTG TAGATCCCAA AAATTACCCA AAGAAGAAGA  
8161 TGGAAAAGCG ATTTGTCTTC AACAAGATAG AAATCAATAA CAAGCTGGAA TTTGAGTCTG  
8221 CCCAGTTCCC CAACTGGTAC ATCAGCACCT CTCAAGCAGA AAACATGCCC GTCTTCCTGG  
8281 GAGGGACCAA AGGCGGCCAG GATATAACTG ACTTCACCAT GCAATTGTG TCTTCTTAAA  
8341 GAGAGCTGTA CCCAGAGAGT CCTGTGCTGA ATGTGGACTC AATCCCTAGG GCTGGCAGAA  
8401 AGGGAACAGA AAGGTTTTTG AGTACGGCTA TAGCCTGGAC TTTCTGTGTG TCTACACCAA  
8461 TGCCCAACTG CCTGCCCTAG GGTAGTGCTA AGAGGATCTC CTGTCCATCA GCCAGGACAG  
8521 TCAGCTCTCT CCTTTCAGGG CCAATCCCA GGCCTTTTGT TGAGCCAGGC CTCTCTCACC  
8581 TCTCCTACTC ACTTAAAGCC CGCCTGACAG AAACCACGGC CACATTGGT TCTAAGAAAC  
8641 CCTCTGTCAT TCGCTCCAC ATTCTGATGA GCAACCGCTT CCCTATTTAT TTATTTATTT  
8701 GTTTGTTTGT TTTGATTAT TGGTCTAATT TATTCAAAGG GGGCAAGAAG TAGCAGTGTC  
8761 TGTAAAGAG CCTAGTTTTT AATAGCTATG GAATCAATTC AATTGGACT GGTGTGCTCT  
8821 CTTTAAATCA AGTCCTTTAA TTAAGACTGA AAATATATAA GCTCAGATTA TTTAAATGGG  
8881 AATATTTATA AATGAGCAA TATCATACTG TTCAATGGT CTGAAATAAA CTTCAGTAA  
8941 GAAAAAAGAA AAAGGGTCTC TCCTGATCAT TGAATGTCTG GATTGACACT GACAGTAAGC  
9001 AAACAGGCTG TGAGAGTTCT TGGGACTAAG CCCACTCCTC ATTGCTGAGT GCTGCAAGTA  
9061 CCTAGAAATA TCCTTGGCCA CCGAAGACTA TCCTCCTCAC CCATCCCCTT TATTTCTGTTG  
9121 TTCAACAGAA GGATATTCAG TGCACATCTG GAACAGGATC AGCTGAAGCA CTGCAAGGAG  
9181 TCAGGACTGG TAGTAACAGC TACCATGATT TATCTATCAA TGCACCAAAC ATCTGTTGAG  
9241 CAAGCGCTAT GTACTAGGAG CTGGGAGTAC AGAGATGAGA ACAGTCACAA GTCCCTCCTC  
9301 AGATAGGAGA GGCAGCTAGT TATAAGCAGA ACAAGGTAAC ATGACAAGTA GAGTAAGATA  
9361 GAAGAACGAA GAGGAGTAGC CAGGAAGGAG GGAGGAGAAC GACATAAGAA TCAAGCCTAA  
9421 AGGATAAAGC AGAAGATTTC CACACATGGG CTGGGCCAAT TGGGTGTCTG TTACGCCTGT  
9481 AATCCCAGCA CTTTGGGTGG CAGGGGAGCA AAGATCGCTT GAGCCCAGGA GTTCAAGACC  
9541 AGCCTGGGCA ACATAGTGAG ACTCCCATCT CTACAAAAA TAAATAAATA AATAAAACAA  
9601 TCAGCCAGGC ATGCTGGCAT GCACCTGTAG TCCTAGCTAC TTGGGAAGCT GACACTGGAG  
9661 GATTGCTTGA GCCCAGAAGT TCAAGACTGC AGTGAGCTTA TCCGTTGACC TGCAGGTCGA  
9721 C

## (2) INFORMATION FOR SEQ ID NO:2513:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2513:

1 ACAACCTTT TCGAGGCAAA AGGCAAAAAA GGCTGCTCTG GGATTCTCTT CAGCCAATCT  
61 TCAATGCTCA AGTGTCTGAA GCAGCCATGG CAGAAGTACC TAAGCTCGCC AGTGAAATGA  
121 TGGCTTATTA CAGTGGCAAT GAGGATGACT TGTCTTTTGA AGCTGATGGC CCTAAACAGA  
181 TGAAGTGCTC CTTCCAGGAC CTGGACCTCT GCCCTCTGGA TGGCGGCATC CAGCTACGAA  
241 TCTCCGACCA CCACTACAGC AAGGGCTTCA GGCAGGCCGC GTCAGTTGTT GTGGCCATGG  
301 ACAAGCTGAG GAAGATGCTG GTTCCCTGCC CACAGACCTT CCAGGAGAAT GACCTGAGCA  
361 CCTTCTTTCC CTTTCATCTT GAAGAAGAAC CTATCTTCTT CGACACATGG GATAACGAGG  
421 CTTATGTGCA CGATGCACCT GTACGATCAC TGAAGTGCAC GCTCCGGGAC TCACAGCAAA  
481 AAAGCTTGGT GATGTCTGGT GCATATGAAC TGAAAGCTCT CCACCTCCAG GGACAGGATA  
541 TGGAGCAACA AGTGGTGTTC TCCATGTCTT TTGTACAAGG AGAAGAAAGT AATGACAAAA  
601 TACCTGTGGC CTTGGGCCCTC AAGGAAAAGA ATCTGTACCT GTCCTGCGTG TTGAAAGATG  
661 ATAAGCCAC TCTACAGCTG GAGAGTGTAG ATCCCAAAAA TTACCCAAAG AAGAAGATGG  
721 AAAAGCGATT TGTCTTCAAC AAGATAGAAA TCAATAACAA GCTGGAATTT GAGTCTGCCC  
781 AGTTCCCCAA CTGGTACATC AGCACCTCTC AAGCAGAAAA CATGCCCGTC TTCTGGGAG  
841 GGACCAAGG CGGCCAGGAT ATAAGTACTG TCACCATGCA ATTTGTGTCT TCCTAAAGAG  
901 AGCTGTACCC AGAGAGTCTT GTGCTGAATG TGGACTCAAT CCCTAGGGCT GCAGAAAGG  
961 GAACAGAAAG GTTTTTGAGT ACGGCTATAG CCTGGACTTT CCTGTTGTCT ACACCAATGC  
1021 CCAACTGCCT GCCTTAGGGT AGTGCTAAGA GGATCTCCTG TCCATCAGCC AGGACAGTCA  
1081 GCTCTCTCCT TTCAGGGCCA ATCCAGCCC TTTTGTGAG CCAGGCCCTC CTCACCTCTC  
1141 CTAACACTT AAAGCCCGCC TGACAGAAAC CAGGCCACAT TTTGGTCTA AGAAACCTC  
1201 CTCTGTCAAT CGCTCCACA TTCTGATGAG CAACCGCTTC CCTATTATT TATTATTG  
1261 TTTGTTTGTG TTGATTCATT GGTCTAATTT ATTCAAAGGG GGCAAGAAGT AGCAGTGTCT  
1321 GTAAAGAGC CTAGTTTTTA ATAGCTATGG AATCAATTCA ATTTGGACTG GTGTGCTCTC  
1381 TTTAAATCAA GTCCTTTAAT TAAGACTGAA AATATATAAG CTCAGATTAT TTAAATGGGA  
1441 ATATTATATA ATGAGCAAAT ATCATACTGT TCAATGGTTC TCAATAAAC TTCACT

## (2) INFORMATION FOR SEQ ID NO:2514:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2514:

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1 CTGGCAGGAG TAGCAGCTGC CCCTTGGCGC GACTGCTGGA GCCGCGAACT AGAGAAACAC
61 AGACACGCCT CATAGAGCAA CGGCGTCTCT CGGAGCGTGG AGCCCGCCAA GCTCGAGCTG
121 AGCTTTCGCT TGCCGTCCAC CACTGCCAC ACTGTGTTT GCTGCCATCG CAGACCTGCT
181 GCTGACTTCC ATCCCTCTGG ATCCGGCAAAG GGCCTGCGAT TTGACAATG TCAAGATTTA
241 CCGTATATCC CTGTTTGTGTT GGATACACCA GTGACGTCCA CTTCTAGAAG ACAAGTTAT
301 ATTACTTAAA CAACCAAAGA TATGAACTA TCCATGAAGA ACAATATTAT CAATACACAG
361 CAGTCTTTTG TAACCATGCC CAATGTGATT GTACCAGATA TTGAAAAGGA AATACGAAGG
421 ATGGAAAATG GAGCATGCAG CTCCTTTTCT GAGGATGATG ACAGTGCCTC TACATCTGAA
481 GAATCAGAGA ATGAAAACCC TCATGCAAGG GGTTCCTTTA GTTATAAGTC ACTCAGAAAG
541 GGAGGACCAT CACAGAGGGA GCAGTACCTG CCTGGTGCCA TTGCCATTTT TAATGTGAAC
601 AACAGCGACA ATAAGGACCA GGAACCAGAA GAAAAAAGA AAAAGAAAAA AGAAAAGAAG
661 AGCAAGTCAG ATGATAAAAA CGAAAATAAA AACGACCCAA AGAAGAAGAT GGAAAAGCGA

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(2) INFORMATION FOR SEQ ID NO:2515:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2002 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2515:

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1 atggccaaag ttccagacat gtttgaagac ctgaagaact gttacagtga aaatgaagaa
61 gacagttcct ccattgatca tctgtctctg aatcagaaat ctttctatca tgtaagctat
121 ggccactccc atgaaggctg catggatcaa tctgtgtctc tgagtatctc tgaaacctct
181 aaaacatcca agcttacctt caaggagagc atggtggtag tagcaaccaa cgggaagggtt
241 ctgaagaaga gacggttgag ttttaagcaa tccatcactg atgatgacct ggaggccatc
301 gccaatgact cagaggaaga aatcatcgaag cctaggctcag cacccttttag cttcctgagc
361 aatgtgaaat acaactttat gaggatcatc aaatacgaat tcatcctgaa tgacgccttc
421 aatcaaagta taattcgagc caatgatcag tacctcacgg ctgctgcatt acataatctg
481 gatgaagcag tgaaatttga catgggtgct tataagtcac caaaggatga tgctaaaatt
541 accgtgattc taagaatctc aaaaactcaa ttgtatgtga ctgcccaga tgaagacca
601 ccagtgtctg tgaaggagat gcctgagata cccaaaacca tcacaggtag tgagaccaac
661 ctctctttct tctgggaaac tcacggcact aagaactatt tcacatcagt tgcccattca
721 aacttgttta ttgccacaaa gcaagactac tgggtgtgct tggcaggggg gccaccctct
781 atcactgact ttcagatact ggaaaaccag gcgtaggtct ggagtctcac ttgtctcact
841 tgtgcagtgt tgacagttca tatgtaccat gtacatgaag aagctaaatc ctttactgtt
901 agtcatttgc tgagcatgta ctgagccttg taattctaaa tgaatgttta cactctttgt
961 aagagtggaa ccaacactaa catataatgt tgttatttaa agaaccacct atattttgca
1021 tagtaccaat cattttaatt attattcttc ataacaattt taggaggacc agagctactg
1081 actatggcta ccaaaaagac tctaccata ttacagatgg gcaaattaa gcataagaaa
1141 actaagaaat atgcacaata gcagttgaaa caagaagcca cagacctagg atttcatgat
1201 ttcatctcaa ctggtttgct tctgctttta agttgctgat gaactcttaa tcaaatagca
1261 taagtttctg ggacctcagt tttatcattt tcaaaatgga gggaataata cctaagcctt
1321 cctgccgcaa cagtttttta tgctaactcag ggaggtcatt ttggtaaaat acttctcgaa
1381 gccgagcctc aagatgaagg caaagcacga aatgttattt ttttaattat atttatatat
1441 gtatttataa atatatatta gataattata atatactata tttatgggaa ccccttcac
1501 ctctgagtgt gaccaggcat cctccacaat agcagacagt gttttctggg ataagtaagt
1561 ttgatttcat taatacaggg catttttggtc caagttgtgc ttatcccata gccaggaaac
1621 tctgcattct agtacttggg agacctgtaa tcatataata aatgtacatt aattaccttg
1681 agccagtaat tgggtccgac tttgactctt ttgccattaa acttacctgg gcattcttgt
1741 ttcattcaat tccacctgca atcaagtcct acaagctaaa attagatgaa ctcaactttg
1801 acaaccatag accactgtta tcaaaacttt cttttctgga atgtaataaa tgtttctctt
1861 aggttctaaa aattgtgatc agaccataat gttacattat tatcaacaat agtgattgat
1921 agagtgttat cagtcataac taaataaagc ttgcaagtga gggagtcatt tcattggcgt
1981 ttgagtcagc aaagaagtca ag

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(2) INFORMATION FOR SEQ ID NO:2516:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2027 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2516:

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1 AGCTGCCAGC CAGAGAGGGA GTCATTTTAT TGGCGTTTGA GTCAGCAAAG AAGTCAAGAT
61 GGCCAAAGTT CCAGACATGT TTGAAGACCT GAAGAACTGT TACAGTGAAG ATGAAGAAGA
121 CAGTTCCTCC ATTGATCATC TGTCTCTGAA TCAGAAATCC TTCTATCATG TAAGCTATGG
181 CCCACTCCAT GAAGGCTGCA TGGATCAATC TGTGTCTCTG AGTATCTCTG AAACCTCTAA
241 AACATCCAAG CTTACCTTCA AGGAGAGCAT GGTGGTAGTA GCAACCAACG GGAAGGTTCT

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301 GAAG      A CGGTTGAGTT TAAGCCAATC CATCACTGAT GAGCCATGG AGGCCATCGC
361 CAATGACTCA GAGGAAGAAA TCATCAAGCC TAGGTCATCA CCTTTTAGCT TCCTGAGCAA
421 TGTGAAATAC AACTTTATGA GGATCATCAA ATACGAATTC ATCCTGAATG ACGCCTCAA
481 TCAAAGTATA ATTCGAGCCA ATGATCAGTA CCTCACGGCT GCTGCATTAC ATAATCTGGA
541 TGAAGCAGTG AAATTTGACA TGGGTGCTTA TAAGTCATCA AAGGATGATG CTAAATTTAC
601 CGTGATTCTA AGAATCTCAA AAACCTCAATT GTATGTGACT GCCCAAGATG AAGACCAACC
661 AGTGCTGCTG AAGGAGATGC CTGAGATACC CAAAACCATC ACAGGTAGTG AGACCAACCT
721 CCTCTTCTTC TGGGAAACTC ACGGCACTAA GAACTATTTT ACATCAGTTG CCCATCCAAA
781 CTTGTTTATT GCCACAAAGC AAGACTACTG GGTGTGCTTG GCAGGGGGGC CACCCTCTAT
841 CACTGACTTT CAGATACTGG AAAACCAGGC GTAGGTCTGG AGTCTCACTT GTCTCACTTG
901 TGCAGTGTTG ACAGTTCATA TGTACCATGT ACATGAAGAA GCTAAATCCTT TTAAGTTAG
961 TCATTTGCTG AGCATGTACT GAGCCTTGTA ATTCTAAATG AATGTTTACA CTCTTTGTAA
1021 GAGTGAACCC AACACTAACA TATAATGTTG TTATTTAAAG AACACCCTAT ATTTTGACATA
1081 GTACCAATCA TTTTAATTAT TATTTCTCAT AACAAATTTA GGAGGACCAG AGCTACTGAC
1141 TATGGCTACC AAAAAGACTC TACCCATATT ACAGATGGGC AAATTAAGGC ATAAGAAAAC
1201 TAAGAAATAT GCACAATAGC AGTCGAAACA AGAAGCCACA GACCTAGGAT TTCATGATTT
1261 CATTCAACT GTTTGCCTTC TGCTTTTAAG TTGCTGATGA ACTCTTAATC AAATAGCATA
1321 AGTTTCTGGG ACCTCAGTTT TATCATTTC AAAATGGAGG GAATAATACC TAAGCCTTCC
1381 TGCCGCAACA GTTTTTTATG CTAATCAGGG AGGTCATTTT GGTAAAATAC TTCTCGAAGC
1441 CGAGCCTCAA GATGAAGGCA AAGCAGGAAA TGTTATTTT TAATTATTAT TTATATATGT
1501 ATTTATAAAT ATATTTAAGA TAATTATAAT ATACTATATT TATGGGAACC CCTCATCCTT
1561 CTGAGTGTGA CCAGGCATCC TCCACAATAG CAGACAGTGT TTTCTGGGAT AAGTAAGTTT
1621 GATTTCATTA ATACAGGGCA TTTTGGTCCA AGTTGTGCTT ATCCCATAGC CAGGAAACTC
1681 TGCATTCTAG TACTTGGGAG ACCTGTAATC ATATAATAAA TGTACATTAA TTACCTTGAG
1741 CCAGTAATTG GTCCGATCTT TGACTCTTTT GCCATTAAAC TTACCTGGGC ATTCTGTGTT
1801 CATTCAATTC CACCTGCAAT CAAGTCCTAC AAGCTAAAAT TAGATGAAC TCACTTTGAC
1861 AACCATGAGA CCACTGTTAT CAAAACCTTC TTTTCTGGAA TGTAATCAAT GTTTCTTCTA
1921 GGTCTATAAA ATTGTGATCA GACCATAATG TTACATTATT ATCAACAATA GTGATTGATA
1981 GAGTGTTATC AGTCATAACT AAATAAGCT TGAACAAAA TTCTCTG

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## (2) INFORMATION FOR SEQ ID NO:2517:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs
- (B) TYPE: 29433 nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2517:

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1 AAGCTTCTAC CCTAGTCTGG TGCTACACTT ACATTGCTTA CATCCAAGTG TGGTTATTTT
61 TGTGGCTCCT GTTATAACTA TTATAGCACC AGGTCTATGA CCAGGAGAAT TAGACTGGCA
121 TTAATCAGA ATAAGAGATT TTGCACCTGC AATAGACCTT ATGACACCTA ACCAACCCCA
181 TTATTTACAA TTAAACAGGA ACAGAGGGAA TACTTTATCC AACTCACACA AGCTGTTTTT
241 CTCCAGATC CATGCTTTTT TGCGTTTATT ATTTTTTAGA GATGGGGGCT TCACTATGTT
301 GCCCACTG GACTAAACT CTGGGCTCA AGTGATTGTC CTGCCTCAGC CTCCTGAATA
361 GCTGGGACTA CAGGGGCATG CCATCACACC TAGTTCATTT CCTCTATTTA AAATATACAT
421 GGCTTAACT CCAACTGGGA ACCCAAACA TTCATTTGCT AAGAGTCTGG TGTTCTACCA
481 CCTGAAC TAGTGGCCACA GGAATTATAA AAGCTGAGAA ATTCTTTAAT AATAGTAACC
541 ATGCCAATC ATTGAAGGCT CATATGTAAA AATCCATGCC TTCCTTTCTC CCAATCTCCA
601 TTCCCAACT TAGCCACTGG TTCTGGCTGA GGCCTTACGC ATACCTCCCG GGGCTTGCAC
661 ACACCTTCTT CTACAGAAGA CACACCTTGG GCATATCCTA CAGAAGACCA GGCTTCTCTC
721 TGGTCCTTGG TAGAGGGCTA CTTTACTGTA ACAGGGCCAG GGTGGAGAGT TCTCTCCTGA
781 AGCTCCATCC CCTCTATAGG AAATGTGTTG ACAATATTCA GAAGAGTAAG AGGATCAAGA
841 CTCTTTTGTG CTCAAATACC ACTGTCTCT TCTCTACCCT GCCCTAACCA GGAGCTTGTC
901 ACCCCAACT CTGAGGTGAT TTATGCCTTA ATCAAGCAA CTTCCTCTCT CAGAAAAGAT
961 GGCTCATTTT CCTCAAAG TGCCAGGAG CTGCCAAGTA TTCTGCCAAT TCACCCTGGA
1021 GCACAATCAA CAAATTCAGC CAGAACACAA CTACAGCTAC TATTAGAACT ATTATTATTA
1081 ATAAATTCCT CTCAAATCT AGCCCTTGA CTTGCGATT CACGATTTCT CCCTTCCTCC
1141 TAGAACTTG ATAAGTTTCC CGCGCTTCCC TTTTCTAAG ACTACATGTT TGTCACTTTA
1201 TAAAGCAAAG GGTGAATAA ATGAACCAA TCAATAACT CTGGAATATC TGCAACAAC
1261 AATAATATCA GCTATGCCAT CTTTCACTAT TTAGCCAGT ATCGAGTTGA ATGAACATAG
1321 AAAAATACAA AACTGAATTC TTCCCTGTAA ATCCCGGT TTGACGACGC ACTTGAGCC
1381 ACGTAGCCAC GCCTACTTAA GACAATTACA AAAGGCGAAG AAGACTGACT CAGGCTTAAG
1441 CTGGCAGCCA GAGAGGGAGT CATTTCATTG CGGTTTGAGT CAGCAAAGGT ATTGTCTCA
1501 CATCTCTGGC TATTAAAGTA TTTTCTGTTG TTGTTTTTCT CTTTGGCTGT TTTCTCTCAC
1561 ATTGCCTTCT CTAAAGCTAC AGTCTCTCT TCTTTTCTT GTCCCTCCCT GGTGTTGTTT
1621 GTGACCTAGA ATTACAGTCA GATTTCAGAA AATGATTCTC TCATTTTGCT GATAAGGACT
1681 GATTGTTTT ACTGAGGGAC GGCAGAACTA GTTTCCTATG AGGGCATGGG TGAATACAAC
1741 TGAGGCTTCT CATGGGAGGG AATCTCTACT ATCCAAATTT ATTAGGAGAA AATTGAAAT
1801 TTCAAATCT GTCTCTCTCT TACCTCTGTG TAAGGCAAAT ACCTTATTCT TGTGGTGTGTT
1861 TTGTAACCTC TTCAAATTT CATTGATTGA ATGCCTGTTT TGGCAATACA TTAGGTTGGG

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1921 CACATAAGGA ATACCAACAT AAATAAAACA TTCTAAAAGA AGTTTACGAT CTAATAAAGG  
1981 AGACAGGTAC ATAGCAAAC TTTTCAGGAA GCACAAAGAG GAGGGGCTCC CCTCACAGAT  
2041 GACTAAGTCA TTCAACAAAG TTTTCAGGAA GCACAAAGAG GAGGGGCTCC CCTCACAGAT  
2101 ATCTGGATTA GAGGCTGGCT GAGCTGATGG TGGCTGGTGT TCTCTGTTGC AGAAGTCAAG  
2161 ATGGCCAAAG TTCCAGACAT GTTTGAAGAC CTGAAGAAC GTTACAGGTA AGGAATAAGA  
2221 TTTATCTCTT GTGATTTAAT GAGGGTTTCA AGGCTCACCA GAATCCAGCT AGGCATAACA  
2281 GTGGCCAGCA TGGGGGCAGG CCGGCAGAGG TTGTAGAGAT GTGTACTAGT CCTGAAGTCA  
2341 GAGCAGGTTT AGAGAAGACC CAGAAAAACT AAGCATTGAG CATGTTAAAC TGAGATTACA  
2401 TTGGCAGGGA GACCGCCATT TTAGAAAAAT TATTTTGTAG GTCTGCTGAG CCCTACATGA  
2461 ATATCAGCAT CAACTTAGAC ACAGCCTCTG TTGAGATCAC ATGCCCTGAT ATAAGAAATGG  
2521 GTTTTACTGG TCCATTCTCA GGAAAACTG ATCTCATTCA GGAACAGGAA ATGGCTCCAC  
2581 AGCAAGCTGG GCATGTGAAC TCACATATGC AGGCAAATCT CACTCAGATG TAGAAGAAAG  
2641 GTAAATGAAC ACAAAGATAA AATTACGGAA CATATTAAAC TAACATGATG TTTCCATTAT  
2701 CTGTAGTAAA TACTAACACA AACTAGGCTG TCAAAATTTT GCCTGGATAT TTTACTAAGT  
2761 ATAAATTATG AAATCTGTTT TAGTGAATAC ATGAAAGTAA TGTGTAACAT ATAATCTATT  
2821 TGGTTAAAAT AAAAAGGAAG TGCTTCAAAA CCTTCTTTTT CTCTAAAGGA GCTTAACATT  
2881 CTTCCCTGAA CTTCAATTAA AGCTCTTCAA TTTGTTAGCC AAGTCCAATT TTTACAGATA  
2941 AAGCACAGGT AAAGCTCAAA GCCTGTCTTG ATGACTACTA ATTCCAGATT AGTAAGATAT  
3001 GAATTACTCT ACCTATGTGT ATGTGTAGAA GTCCTTAAAT TTCAAAGATG ACAGTAATGG  
3061 CCATGTGTAT GTGTGTGACC CACAACATC ATGGTCATTA AAGTACATTG GCCAGAGACC  
3121 ACATGAAATA ACAACAATTA CATTCTCATC ATCTTATTTT GACAGTGAAA ATGAAGAAGA  
3181 CAGTTCCTCC ATTGATCATC TGTCTCTGAA TCAGGTAAGC AAATGACTGT AATTCTCATG  
3241 GGAAGTCTAT TCTTACACAG TGGTTTCTTC ATCCAAAGAG AACAGCAATG ACTTGAATCT  
3301 TAAATACTTT TGTTTTACCC TCACTAGAGA TCCAGAGACC TGTCTTTCAT TATAAGTGAG  
3361 ACCAGCTGCC TCTCTAAACT AATAGTTGAT GTGCATTGGC TTCTCCGAGA ACAGAGCAGA  
3421 ACTATCCCAA ATCCCTGAGA ACTGGAGTCT CCTGGGGCAG GCTTCATCAG GATGTTAGTT  
3481 ATGCCATCCT GAGAAAGCCC CGCAGGCCGC TTCACCAGGT GTCTGTCTCC TAACGTGATG  
3541 TGTGTGGTGT GTCTTCTCTG ACACCAGCAT CAGAGGTTAG AGAAAGTCTC CAAACATGAA  
3601 GCTGAGAGAG AGGAAGCAAG CCAGCTGAAA GTGAGAAGTC TACAGCCCAT CATCAATCTG  
3661 TGTATTGTG TTTGGAGACC ACAAATAGAC ACTATAAGTA CTGCCTAGTA TGTCTTCAGT  
3721 ACTGCTTTA AAAGCTGTCC CCAAAGGAGT ATTTCTAAAA TATTTTGAGC ATTGTTAAGC  
3781 AGATTTTTAA CCTCCTGAGA GGGAACTAAT TGGAAAGCTA CCACTACTA CAATCATTGT  
3841 TAACCTATTT AGTTACAACA TCTCATTTTT GAGCATGCAA ATAAATGAAA AAGTCTTCCT  
3901 AAAAAAATCA TCTTTTATC CTGGAAGGAG GAAGGAAGGT GAGACAAAAG GGAGAGAGGG  
3961 AGGGAAGCCT AATGAAACAC CAGTTACCTA AGACCAGAA GTGAGATCCTC CTCCTACCT  
4021 CTGTTGAATA CAGCACCTAC TGAAAGAAGT TTTCTTCCCT GACCATGAAC AGCCTCTCAG  
4081 CTTCTGTTTT CCTTCTCAC AGAAATCCTT CTATCATGTA AGCTATGGCC CACTCCATGA  
4141 AGGCTGCATG GATCAATCTG TGTCTCTGAG TATCTCTGAA ACCTCTAAAA CATCCAAGCT  
4201 TACCTTCAAG GAGAGCATGG TGGTAGTAGC AACCACCGGG AAGGTTCTGA AGAAGAGACG  
4261 GTTGAAGTTA AGCCAATCCA TCACTGATGA TGACCTGGAG GCCATCGCCA ATGACTCAGA  
4321 GGAAGGTAAG GGGTCAAGCA CAATAATATC TTTCTTTTAC AGTTTAAAGC AAGTAGGGAC  
4381 AGTAGAATTT AGGGGAAAT TAAACGTGGA GTCAGAATAA CAAGAAGACA ACCAAGCATT  
4441 AGTCTGGTAA CTATACAGAG GAAAATTAAT TTTTATCCTT CTCCAGGAGG GAGAAATGAG  
4501 CAGTGGCCTG AATCGAGAAT ACTTGCTCAC AGCCATTATT TCTTAGCCAT ATTGTAAAGG  
4561 TCGTGTGACT TTTAGCCTTT CAGGAGAAAG CAGTAATAAG ACCACTACG AGCTATGTTT  
4621 CTCTCATACT AACTATGCCT CCTTGGTCAT GTTACATAAT CTTTTCGTGA TTCAGTTTCC  
4681 TCTACTGTAA AATGGAGATA ATCAGAATCC CCCACTCATT GGATTGTTGT AAAGATTAAAG  
4741 AGTCTCAGGC TTTACAGACT GAGCTAGCTG GGCCCTCCTG ACTGTTATAA AGATTAAATG  
4801 AGTCAACATC CCCTAACTTC TGGACTAGAA TAATGTCTGG TACAAAGTAA GCACCCAATA  
4861 AATGTTAGCT ATTACTATCA TTATTATTAT TATTTTATTT TTTTATTTT AGATGGAGTC  
4921 TGGCTCTGTC ACCCAGGCTG GAGTGCAGTG GCACAATCTC GGCTCACTGC AAGCTCTGCC  
4981 TCCTGGGTTT ATGCCATTCT CCTGCCTCAG CCTCCGAGT AAGCTGGGAA TACAGGCACC  
5041 CGCCACTGTT CCCGGCTAAT TTTTGTATT TTTAGTAGAG ACGGAGTTT ACCGTGGTCT  
5101 CCATCTCCTC GTGATCCACC CACCTTGGCC TCCCAAAGTG CCGGATTAC AGGCGTGAGC  
5161 CACCGCGCCC GGCCTATTAT TATTATTATT ACTACTACTA CTACCTATAT GAATACTACC  
5221 AGCAATACTA ATTTATTAAT GACTGGATTA TGTCTAAACC TCACAAGAA CCTACCTTCT  
5281 CATTTTACAT AAAAGGAAAC TAAGTCAATT GAGTAGGTA AACTGCCCCA TGGCATAGAT  
5341 CTGTAAGTGG GAGAGCCTCA AATCTAATTC AGTTCTACCT GAGTAAAAAA ATCATGTTTT  
5401 CTCTCCATC CCTTTACTGT ACAAGCCTCC ACATGAAC TAACCCCAAT ATTCTGTTTT  
5461 TTAAGATAAT ACCTAAGCAA TAACGCATGT TCACCTAGAA GGTTTTAAAA TGTAACAAAA  
5521 TATAAGAAAA TAAAAATCAC TCATATCGTC AGTGAGAGTT TACTACTGCC AGCACTATGG  
5581 TATGTTTCCT TAAAAATCTT GCTATACACA TACCTACATG TGAACAAATA TGTCTAACAT  
5641 CAAGACCACA CTATTTACAA CTTTATATCC AGCTTTTCTT ACTTAGCAAT GTATTGAGGA  
5701 CATTTTAGAG TGCCCGTTTT TCACCATTAT AAGCAATGCA ACAATGAACA TCTGTATAAA  
5761 TAAATATTCA TTTCTCTCAC CCTTTATTTT CTGAGAATAT ATTCTAGAA GTAGAATTTT  
5821 CCAGAGCCAT GAGGATTTGT GACGCTATTG ATATGTGCCA CTTTGCACTC TCTGTGACAT  
5881 ATATAATTAT TTTTAATGCA TTCATTTTTT TCTCAGAGTG CATTCGTTTG AAAACATAGA  
5941 CGGGAAATAC TGGTAGTCTT CCTTGTCTAG TAGAAACACC CAAACAATGA AAAATGAAAA



6001 AGTTGAA ATAGTCTCTA AAAACAATGA AACTATTGCC TCGAAATG AAGTTTAAAA  
6061 AGAAGCACAT AAGCAACAC AAGGATAATC CTAGAAAACC AGTTCTGCTG ACTGGGTGAT  
6121 TTCACTTCTC TTTGCTTCTC CATCTGGATT GGAATATTCC TAATACCCCC TCCAGAACTA  
6181 TTTTCCCTGT TTGTACTAGA CTGTGTATAT CATCTGTGTT TGTACATAGA CATTAATCTG  
6241 CACTTGTGAT CATGGTTTGA GAAATCATCA AGCCTAGGTC ATCACCTTTT AGCTTCCCTGA  
6301 GCAATGTGAA ATACAACCTT ATGAGGATCA TCAAATACGA ATTCATCCTG AATGACGCCC  
6361 TCAATCAAAG TATAATTGGA GCCAATGATC AGTACCTCAC GGCTGCTGCA TTACATAATC  
6421 TGGATGAAGC AGGTACATTA AAATGGCACC AGACATTCT GTCATCTCTC CCTCCTTTCA  
6481 TTTACTTATT TATTTATTTC AATCTTTCTG CTGCAAAAA ACATACCTCT TCAGAGTTCT  
6541 GGGTTGCACA ATTCTTCCAG AATAGCTTGA AGCACAGCAC CCCATAAAAA ATCCCAAGCC  
6601 AGGGCAGAAG GTTCAACTAA ATCTGGAAGT TCCACAAGAG AGAAGTTTCC TATCTTTGAG  
6661 AGTAAAGGGT TGTGCACAAA GCTAGCTGAT GTACTACCTC TTTGGTTCTT TCAGACATTC  
6721 TTACCCTCAA TTTTAAACT GAGGAACTG TCAGACATAT TAAATGATTT ACTCAGATTT  
6781 ACCCAGAAGC CAATGAAGAA CAATCACTCT CCTTTAAAAA GTCTGTTGAT CAAACTCACA  
6841 AGTAACACCA AACCAGGAAG ATCTTTATTA TCTCTGATAA CATATTTGTG AGGCAAAACC  
6901 TCCAATAAGC TACAAATATG GCTTAAAGGA TGAAGTTAG TGTCCAAAAA CTTTATCAC  
6961 ACACATCCAA TTTTCATGGC GGACATGTTT TAGTTTCAAC AGTATACATA TTTTCAAAGG  
7021 TCCAGAGAGG CAATTTTGCA ATAAACAAGC AAGACTTTTT CTGATTGGAT GCACTTCAGC  
7081 TAACATGCTT TCAACTCTAC ATTTACAAAT TATTTTGTGT TCTATTTTTC TACTTAATAT  
7141 TATTTCTGCA ATTTTCCCAA TATTGACATC GTGTATGTAT TTGCCATTTT TAATATCACT  
7201 AGACAATTCA ATCAGGTTGC TACGTTGGTC CCTTGGGTTT ACTCTAAATA GCTTGATTGC  
7261 AAATATCTTT GTATATATTA TTGTTTTTTC TCCTATCTTG TAATTTCTTT GAGCACATCC  
7321 CAAAGAGGAA TGCCTAGATC AATGGGCACA AATAATTGTA CAGCTCTTAT TAAACATTAT  
7381 TCTGTAAGTA AAAACTGAAC TACTTTTCAG TATCACTAGC AACATATGAG TGTATCAGCT  
7441 TCCTAAACCC CTCCATGTTA GGTCATTATG AACTTATGAT CTAACAAATT ACAGGGTCTT  
7501 ATCCCACATA TGAAATTATA AGAGATTCAA CACTTATTCA GCCCCGAAGG ATTCATTCAA  
7561 CGTAGAAAAT TCTAAGAACTA TTAACCAAGT ATTTACCTGC CTAGTGAGTG TGAAGACAT  
7621 TGTGAAGGAC ACAAAGATGT ATAGAATTCC ATTCCTGACT TCCAGGTATT TACACCATAG  
7681 GTGGGGACCT AACTACACAC ACACACACAC ACACACACAC ACACACACAC ACCATGCACA  
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8521 TCAGCTCTCT CTTTTCAGGG CCAATCCCCA GCCCTTTTGT TGAGCCAGGC CTCTCTCACC  
8581 TCTCCTACTC ACTTAAAGCC CGCCTGACAG AAACCACGGC CACATTTGGT TCTAAGAAAC  
8641 CCTCTGTCT TCGTCCCACT ATTCTGATGA GCAACCGCTT CCTATTAT TATTATTAT  
8701 GTTTGTTTGT TTTGATTCAT TGGTCTAATT TATTCAAAGG GGGCAAGAAG TAGCAGTGTC  
8761 TGTAAGAGAG CCTAGTTTTT AATAGCTATG GAATCAATTC AATTTGGACT GGTGTGCTCT

8821 CTTTAAATCA AGTCCTTTAA TTAAGACTGA AAATATATAA GCTCAGATTA TTTAAATGGG  
8881 AATATTTATA AATGAGCAAA TATCATACTG TTCAATGGTT CTGAAATAAA CTTCAGTGAA  
8941 GAAAAAATAA AAAGGGTCTC TCCTGATCAT TGAAGTCTG GATTGACACT GACAGTAAGC  
9001 AAACAGGCTG TGAGAGTTCT TGGGACTAAG CCCACTCCTC ATTGCTGAGT GCTGCAAGTA  
9061 CCTAGAAATA TCCTTGGCCA CCGAAGACTA TCCTCCTCAC CCATCCCCTT TATTTTCGTTG  
9121 TTCAACAGAA GGATATTGAG TGCACATCTG GAACAGGATC AGCTGAAGCA CTGCAGGGAG  
9181 TCAGGACTGG TAGTAACAGC TACCATGATT TATCTATCAA TGCACCAAAC ATCTGTTGAG  
9241 CAAGCGCTAT GTACTAGGAG CTGGGAGTAC AGAGATGAGA ACAGTCACAA GTCCCTCCTC  
9301 AGATAGGAGA GGCAGCTAGT TATAAGCAGA ACAAGGTAAC ATGACAAGTA GAGTAAGATA  
9361 GAAGAACGAA GAGGAGTAGC CAGGAAGGAG GGAGGAGAAC GACATAAGAA TCAAGCCTAA  
9421 AGGGATAAAC AGAAGATTTC CACACATGGG CTGGGCCAAT TGGGTGTCTG TTACGCCTGT  
9481 AATCCCAGCA CTTTGGGTGG CAGGGGCAGA AAGATCGCTT GAGCCCAGGA GTTCAAGACC  
9541 AGCCTGGGCA ACATAGTGAG ACTCCCATCT CTACAAAAA TAAATAAATA AATAAACAA  
9601 TCAGCCAGGC ATGCTGGCAT GCACCTGTAG TCCTAGCTAC TTGGGAAGCT GACACTGGAG  
9661 GATTGCTTGA GCCCAGAAGT TCAAGACTGC AGTGAGCTTA TCCGTTGACC TGCAGGTGGA  
9721 C

1 ACAAACTTT TCGAGGCAAA AGGCAAAAAA GGCTGCTCTG GGATTCTCTT CAGCCAATCT  
61 TCAATGCTCA AGTGTCTGAA GCAGCCATGG CAGAAGTACC TAAGCTCGCC AGTGAAATGA  
121 TGGCTTATTA CAGTGGCAAT GAGGATGACT TGTTCCTTGA AGCTGATGGC CCTAAACAGA  
181 TGAAGTGCTC CTTCCAGGAC CTGGACCTCT GCCCTCTGGA TGGCGGCATC CAGCTACGAA  
241 TCTCCGACCA CCACTACAGC AAGGGCTTCA GGCAGGCGC GTCAAGTTGT GTGGCCATGG  
301 ACAAGCTGAG GAAGATGCTG GTTCCCTGCC CACAGACCTT CCAGGAGAAT GACCTGAGCA  
361 CTTCTTTTCC CTTTCTCTTT GAAGAAGAAC CTATCTTCTT CGACACATGG GATAACGAGG  
421 CTTATGTGCA CGATGCACCT GTACGATCAC TGAATGCAC GCTCCGGGAC TCACAGCAAA  
481 AAAGCTTGGT GATGTCTGGT CCATATGAAC TGAAAGCTCT CCACCTCCAG GGACAGGATA  
541 TGGAGCAACA AGTGGTGTTC TCCATGTCCT TTGTACAAGG AGAAGAAAGT AATGACAAAA  
601 TACCTGTGGC CTTGGGCCTC AAGGAAAAGA ATCTGTACCT GTCCTGCGTG TTGAAAGATG  
661 ATAAGCCAC TCTACAGCTG GAGAGTGTAG ATCCCAAAAA TTACCCAAAG AAGAAGATGG  
721 AAAAGCGATT TGTCTTCAAC AAGATAGAAA TCAATAACAA GCTGGAATTT GAGTCTGCCC  
781 AGTTCCCCAA CTGGTACATC AGCACCTCTC AAGCAGAAAA CATGCCCGTC TTCTGGGAG  
841 GGACCAAGG CGGCCAGGAT ATAAGTACT TCACCATGCA ATTTGTGTCT TCCTAAAGAG  
901 AGCTGTACCC AGAGAGTCTT GTGCTGAATG TGGACTCAAT CCCTAGGGCT GGCAGAAAGG  
961 GAACAGAAAG GTTTTTGAGT ACGGCTATAG CCTGGACTTT CCGTGTGTCT ACACCAATGC  
1021 CCAATGCTCT GCCTTAGGGT AGTGCTAAGA GGATCTCCTG TCCATCAGCC AGGACAGTCA  
1081 GCTCTCTCCT TTCAGGGCCA ATCCAGCCCC TTTTGTGAG CCAGGCCTCT CTCACCTCTC  
1141 CTAATCACTT AAAGCCCGCC TGACAGAAAC CAGGCCACAT TTTGGTTCTA AGAAACCCTC  
1201 CTCTGTCAAT CGCTCCACA TTCTGATGAG CAACCGCTTC CCTATTTATT TATTTATTTG  
1261 TTTGTTTGTG TTGATTCAAT GGTCTAATTT ATTCAAAGG GGAAGAAGT AGCAGTGTCT  
1321 GTAAAGAGC CTAGTTTTTA ATAGCTATGG AATCAATTCA ATTTGGACTG GTGTGCTCTC  
1381 TTTAAATCAA GTCCTTTAAT TAAGACTGAA AATATATAAG CTCAGATTAT TTAATGGGA  
1441 ATATTTATAA ATGAGCAAAT ATCATACTGT TCAATGGTTC TCAATAAAC TTCACT  
1 CTGGCAGGAG TAGCAGCTGC CCCTTGGCGC GACTGCTGGA GCCGCGAAT AGAGAAACAC  
61 AGACACGCT CATAGAGCAA CGGCGTCTCT CGGAGCGTGG AGCCCCGCAA GCTCGAGCTG  
121 AGCTTTCGCT TGCCGTCCAC CACTGCCAC ACTGTCTGTT GCTGCCATCG CAGACCTGCT  
181 GCTGACTTCC ATCCCTCTGG ATCCGGCAAG GGCCTGCGAT TTTGACAATG TCAAGATTTA  
241 CCGTATATCC CTGTTTGTGTT GGATACACCA GTGACGTCCA CTTCTAGAAG ACAAGTTAT  
301 ATTACTTAAA CAACCAAGA TATGAACTA TCCATGAAGA ACAATATTAT CAATACACAG  
361 CAGTCTTTTG TAACCATGCC CAATGTGATT GTACAGATA TTGAAAAGGA AATACGAAGG  
421 ATGGAAAATG GAGCATGCAG CTCCTTTTCT GAGGATGATG ACAGTGCCTC TACATCTGAA  
481 GAATCAGAGA ATGAAAACCC TCATGCAAGG GGTTCCTTTA GTTATAAGTC ACTCAGAAAG  
541 GGAGGACCAT CACAGAGGGA GCAGTACCTG CCTGGTGCCA TTGCCATTTT TAATGTGAAC  
601 AACAGCGACA ATAAGGACCA GGAACAGAA GAAAAAAGA AAAAGAAAA AGAAAAGAG  
661 AGCAAGTCAG ATGATAAAAA CGAAATAA AAGCAACCAA AGAAGAAGAT GGAAGCGA  
1 ATGGCCAAAG TTCCAGACAT GTTGAAGAC CTGAAGAACT GTTACAGTGA AAATGAAGAA  
61 GACAGTTCCT CCATTGATCA TCTGTCTCTG AATCAGAAAT CCTTCTATCA TGTAAGCTAT  
121 GGCCCACTCC ATGAAGGCTG CATGGATCAA TCTGTCTCTC TGAGTATCTC TGAAACCTCT  
181 AAAACATCCA AGCTTACCTT CAAGGAGAGC ATGGTGGTAG TAGCAACCAA CGGAAGGTT  
241 CTGAAGAAGA GACGGTTGAG TTTAAGCCAA TCCATCACTG ATGATGACCT GGAGGCCATC  
301 GCCAATGACT CAGAGGAAGA AATCATCAAG CCTAGGTCAG CACCTTTTAG CTTCTGAGC  
361 AATGTGAAAT ACAACTTTAT GAGGATCATC AAATACGAAT TCATCCTGAA TGACGCCCTC  
421 AATCAAAGTA TAATTCGAGC CAATGATCAG TACCTCACGG CTGCTGCATT ACATAATCTG  
481 GATGAAGCAG TGAAATTTGA CATGGGTGCT TATAAGTCAT CAAAGGATGA TGCTAAATTT  
541 ACCGTGATTC TAAGAATCTC AAAAATCAA TTGTATGTGA CTGCCAAGA TGAAGACCAA  
601 CCAAGTGTGC TGAAGGAGAT GCCTGAGATA CCAAAACCA TCACAGGTAG TGAGACCAAC  
661 CTCCTCTTCT TCTGGGAAAC TCACGGCACT AAGAATATT TCACATCAGT TGCCCATCCA  
721 AACTTGTGTTA TTGCCACAAA GCAAGACTAC TGGGTGTGCT TGGCAGGGG GCCACCTCT  
781 ATCACTGACT TTCAGATACT GGAAGACAG CCGTAGGTCT GGAGTCTCAC TTGTCTCACT  
841 TGTGCAAGT TGACAGTTCA TATGTACCAT GTACATGAAG AAGCTAAATC CTTTACTGTT

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901 AGTCATTTGC TGAGCATGTA CTGAGCCTTG TAATTCTAAA TGAATGTTTA CACTCTTTGT
961 AAGAGTGGAA CCAACACTAA CATATAATGT TGTTATTTAA AGAACACCCT ATATTTTGCA
1021 TAGTACCAAT CATTTTAATT ATTATTCTTC ATAACAATTT TAGGAGGACC AGAGCTACTG
1081 ACTATGGCTA CAAAAAGAC TCTACCCATA TTACAGATGG GCAAATTAAG GCATAAGAAA
1141 ACTAAGAAAT ATGCACAATA GCAGTTGAAA CAAGAAGCCA CAGACCTAGG ATTTTCATGAT
1201 TTCATTTCAA CTGTTTGCCT TCTGCTTTTA AGTTGCTGAT GAACCTTAA TCAAATAGCA
1261 TAAGTTTCTG GGACCTCAGT TTTATCATT TCAAAATGGA GGGATAATA CTAAGCCTT
1321 CCTGCCGCAA CAGTTTTTTA TGCTAATCAG GGAGGTCATT TTGGTAAAT ACTTCTCGAA
1381 GCCGAGCCTC AAGATGAAGG CAAAGCACGA AATGTTATTT TTTAATTATT ATTTATATAT
1441 GTATTTATAA ATATATTAA GATAATTATA ATATACTATA TTTATGGGAA CCCCTTCATC
1501 CTCTGAGTGT GACCAGGCAT CCTCCACAAT AGCAGACAGT GTTTTCTGGG ATAAGTAAGT
1561 TTGATTTTCA TAATACAGGG CATTTTGGTC CAAGTTGTGC TTATCCCAT GCCAGGAAAC
1621 TGTGCATTCT AGTACTTGGG AGACCTGTAA TCATATAATA AATGTACATT AATTACCTTG
1681 AGCCAGTAAT TGGTCCGATC TTTGACTCTT TTGCCATTAA ACTTACCTGG GCATTCTTGT
1741 TTCATTCAAT TCCACCTGCA ATCAAGTCCT ACAAGCTAAA ATTAGATGAA CTCACCTTG
1801 ACAACCATAG ACCACTGTTA TCAAACTTT CTTTTCTGGA ATGTAATCAA TGTTTCTTCT
1861 AGGTTCTAAA AATTGTGATC AGACCATAAT GTTACATTAT TATCAACAAT AGTGATTGAT
1921 AGAGTGTTAT CAGTCATAAC TAAATAAAGC TTGCAAGTGA GGGAGTCATT TCATTGGCGT
1981 TTGAGTCAGC AAAGAAGTCA AG
1 AGCTGCCAGC CAGAGAGGGA GTCATTTTCA TGGCGTTTGA GTCAGCAAAG AAGTCAAGAT
61 GGCCAAAGTT CCAGACATGT TTGAAGACCT GAAGAACTGT TACAGTGAAA ATGAAGAAGA
121 CAGTTCCTCC ATTGATCATC TGCTCTGAA TCAGAAATCC TTCTATCATG TAAGCTATGG
181 CCCACTCCAT GAAGGCTGCA TGGATCAATC TGTGTCTCTG AGTATCTCTG AAACCTCTAA
241 AACATCCAAG CTTACCTTCA AGGAGAGCAT GGTGGTAGTA GCAACCAACG GGAAGGTTCT
301 GAAGAAGAGA CGGTTGAGTT TAAGCCAATC CATCACTGAT GATGACCTGG AGGCCATCGC
361 CAATGACTCA GAGGAAGAAA TCATCAAGCC TAGGTCATCA CCTTTTAGCT TCCTGAGCAA
421 TGTGAAATAC AACTTTATGA GGATCATCAA ATACGAATTC ATCCTGAATG ACGCCCTCAA
481 TCAAAGTATA ATTCGAGCCA ATGATCAGTA CCTCACGGCT GCTGCATTAC ATAATCTGGA
541 TGAAGCAGTG AAATTTGACA TGGGTGCTTA TAAGTCATCA AAGGATGATG CTAAATTAC
601 CGTGATTCTA AGAATCTCAA AAATCAATT GTATGTGACT GCCCAAGATG AAGACCAACC
661 AGTGCTGCTG AAGGAGATGC CTGAGATACC CAAAACCATC ACAGGTAGTG AGACCAACCT
721 CCTCTTCTTC TGGGAACTC ACGGCACTAA GAACTATTTT ACATCAGTTG CCCATCCAAA
781 CTTGTTTTATT GCCACAAAGC AAGACTACTG GGTGTGCTTG GCAGGGGGGG CACCCTCTAT
841 CACTGACTTT CAGATACTGG AAAACCAGGC GTAGGTCTGG AGTCTCACTT GTCTCACTTG
901 TGCAGTGTG ACAGTTCATA TGTACCATGT ACATGAAGAA GCTAAATCCT TTAGTGTAG
961 TCATTTGCTG AGCATGTACT GAGCCTTGTA ATTCTAAATG AATGTTTACA CTCTTTGTAA
1021 GAGTGAACC AACACTAACA TATAATGTTG TTATTTAAAG AACACCTAT ATTTTGATA
1081 GTACCAATCA TTTTAATTAT TATTCTTCAT AACAAATTTA GGAGGACCAG AGCTACTGAC
1141 TATGGCTACC AAAAGACTC TACCCATATT ACAGATGGGC AAATTAAGGC ATAAGAAAAC
1201 TAAGAAATAT GCACAATAGC AGTCGAAACA AGAAGCCACA GACCTAGGAT TTCATGATTT
1261 CATTTCAACT GTTTGCCTTC TGCTTTTAAG TTGCTGATGA ACTCTTAATC AAATAGCATA
1321 AGTTTCTGGG ACCTCAGTTT TATCATTTTC AAAATGGAGG GAATAATACC TAAGCCTTCC
1381 TGCCGCAACA GTTTTTATG CTAATCAGG AGGTCATTTT GGTAAATACC TTCTCGAAGC
1441 CGAGCCTCAA GATGAAGGCA AAGCACGAAA TGTATTTTTT TAATTATTAT TTATATATGT
1501 ATTTATAAAT ATATTTAAGA TAATTATAAT ATACTATATT TATGGGAACC CCTTCATCCT
1561 CTGAGTGTGA CCAGGCATCC TCCACAATAG CAGACAGTGT TTTCTGGGAT AAGTAAGTTT
1621 GATTTTCATTA ATACAGGGCA TTTTGGTCCA AGTTGTGCTT ATCCCATAGC CAGGAACTC
1681 TGCATTCTAG TACTTGGGAG ACCTGTAATC ATATAATAAA TGTACATTAA TTACCTTGAG
1741 CCAGTAATTG GTCCGATCTT TGACTCTTTT GCCATTAAAC TTACCTGGGC ATTCTTGTTT
1801 CATTCAATTC CACCTGCAAT CAAGTCTTAC AAGCTAAAT TAGATGAAT CAACCTTGAC
1861 AACCATGAGA CCACGTGTAT CAAAACCTTC TTTTCTGGAA TGTAATCAAT GTTCTTCTA
1921 GGTTCTAAAA ATTGTGATCA GACCATAATG TTACATTATT ATCAACAATA GTGATTGATA
1981 GAGTGTATC AGTCATAACT AAATAAAGCT TGCAACAAA TTCTCTG

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## (2) INFORMATION FOR SEQ ID NO:2518:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2518:

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1 GCCACGTGCT GCTGGGTCTC AGTCCTCCAC TTCCCGTGTC CTCTGGAAGT TGTGAGGAGC
61 AATGTTGCGC TTGTACGTGT TGGTAATGGG AGTTTCTGCC TTCACCCTTC AGCCTGCGGC
121 ACACACAGGG GCTGCCAGAA GCTGCCGTT TCGTGGGAGG CATTACAAGC GGGAGTTCAG
181 GCTGGAAGGG GAGCCTGTAG CCCTGAGGTG CCCCAGGTG CCCTACTGGT TGTGGGCTC
241 TGTGAGCCCC CGCATCAACC TGACATGGCA TAAAAATGAC TCTGCTAGGA CGGTCCCAGG
301 AGAAGAAGAG ACACGGATGT GGGCCCAGGA CGGTGCTCTG TGCTTCTGTC CAGCCTTGCA
361 GGAGGACTCT GGCACCTACG TCTGCACTAC TAGAAATGCT TCTTACTGTG ACAAATGTC
421 CATTGAGCTC AGAGTTTTTG AGAATACAGA TGCTTTCCTG CCGTTCATCT CATACCCGCA

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481 AATTTTAACC TTGTCAACCT CTGGGGTATT AGTATGCCCT GACCTGAGTG AATTCACCCG
541 TGACAAAACCT GACGTGAAGA TTCAATGGTA CAAGGATTCT CTTCTTTTGG ATAAAGACAA
601 TGAGAAATTT CTAAGTGTGA GGGGGACCAC TCACTTACTC GTACACGATG TGGCCCTGGA
661 AGATGCTGGC TATTACCGCT GTGTCTGAC ATTTGCCCAT GAAGGCCAGC AATACAACAT
721 CACTAGGAGT ATTGAGCTAC GCATCAAGAA AAAAAAAGAA GAGACCATTC CTGTGATCAT
781 TTCCCCCCTC AAGACCATAT CAGCTTCTCT GGGGTCAAGA CTGACAATCC CGTGTAAAGT
841 GTTTCTGGGA ACCGGCACAC CCTTAACCAC CATGCTGTGG TGGACGGCCA ATGACACCCA
901 CATAGAGAGC GCCTACCCGG GAGGCCGCGT GACCGAGGGG CCACGCCAGG AATATTGAGA
961 AAATAATGAG AACTACATTG AAGTGCCATT GATTTTTGAT CCTGTCACAA GAGAGGATTT
1021 GCACATGGAT TTAAATGTG TTGTCCATAA TACCCTGAGT TTTCAGACAC TACGCACCAC
1081 AGTCAAGGAA GCCTCCTCCA CGTTCTCCTG GGGCATTGTG CTGGCCCCAC TTTCACTGGC
1141 CTTCTTGGTT TTGGGGGGAA TATTGATGCA CAGACGGTGC AAACACAGAA CTGAAAAAGC
1201 AGATGGTCTG ACTGTGCTAT GGCCTCATCA TCAAGACTTT CAATCCTATC CCAAGTGAAA
1261 TAAATGGAAT GAAATAATTC AAACACAAAA AAAAAAAAAA AAAAAAAA

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## (2) INFORMATION FOR SEQ ID NO:2519:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2156 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2519:

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1 GCCGGAGCCG ACTCGGAGCG CGCGCGCGCG CCGGGAGGAG CCGAGCGCGC CGGGCGCGGC
61 GTGGGGGGCG CGGCTGCCCG GCGCGCCCGAG GGAGCGGCAG GAATGTGACA ATCGCGCGCC
121 CGCACCCTAG CACTCCTCGC TCGGCTCCTA GGGCTCTCGC CCTCTGAGCT GAGCCGGGTT
181 CCGCCCGGGC TGGGATCCCA TCACCCTCCA CGGCCGTCCG TCCAGGTAGA CGCACCCTCT
241 GAAGATGGTG ACTCCCTCCT GAGAAGCTGG ACCCCTTGGT AAAAGACAAG GCCTTCTCCA
301 AGAAGAATAT GAAAGTGTTA CTCAGACTTA TTTGTTTCAT AGCTCTACTG ATTCTTCTC
361 TGGAGGCTGA TAAATGCAAG GAACGTGAAG AAAAAATAAT TTTAGTGTC TCTGCAAATG
421 AAATTGATGT TCGTCCCTGT CCTCTTAACC CAAATGAACA CAAAGGCACT ATAACCTGGT
481 ATAAAGATGA CAGCAAGACA CCTGTATCTA CAGAACAAGC CTCAGGATT CATCAACACA
541 AAGAGAAACT TTGGTTTGTT CCTGCTAAGG TGGAGGATTC AGGACATTAC TATTGCGTGG
601 TAAGAAATTC ATCTTACTGC CTCAGAATTA AAATAAGTGC AAAATTTGTG GAGAATGAGC
661 CTAACCTATG TTATAATGCA CAAGCCATAT TTAAGCAGAA ACTACCCGTT GCAGGAGACG
721 GAGGACTTGT GTGCCCTTAT ATGGAGTTTT TTAATAATGA AAATAATGAG TTACCTAAAT
781 TACAGTGGTA TAAGGATTGC AAACCTCTAC TTCTTGACAA TATACACTTT AGTGGAGTCA
841 AAGATAGGCT CATCGTGATG AATGTGGCTG AAAAGCATAG AGGGAACAT ACTTGTCTATG
901 CATCCTACAC ATACTTGGGC AAGCAATATC CTATTACCCG GGTAATAGAA TTTATTACTC
961 TAGAGGAAAA CAAACCCACA AGGCCTGTGA TTGTGAGCCC AGCTAATGAG ACAATGGAAG
1021 TAGACTTGGG ATCCCAGATA CAATTGATCT GTAATGTCAC CGGCCAGTTG AGTGACATTG
1081 CTTACTGGAA GTGGAATGGG TCAGTAATTG ATGAAGATGA CCCAGTGCTA GGGGAAGACT
1141 ATTACAGTGT GGAAATCCTT GCAAACAAAA GAAGGAGTAC CCTCATCACA GTGCTTAATA
1201 TATCGGAAAT TGAAAGTAGA TTTTATAAAC ATCCATTTAC CTGTTTTGCC AAGAATACAC
1261 ATGGTATAGA TGCAGCATAT ATCCAGTTAA TATATCCAGT CACTAATTTT CAGAAGCACA
1321 TGATTGGTAT ATGTGTCACG TTGACATCA TAATTGTGTG TTCTGTTTTT ATCTATAAAA
1381 TCTTCAAGAT TGACATTGTG CTTTGGTACA GGGATTCTCG CTATGATTTT CTCCCAATAA
1441 AAGCTTCAGA TGGAAAGACC TATGACGCAT ATATACTGTA TCCAAAGACT GTTGGGGAAG
1501 GGTCTACCTC TGAATGTGAT ATTTTGTGT TTAAGTCTT GCCTGAGGTC TTGGAAAAAC
1561 AGTGTGATA TAAGCTGTTT ATTTATGGAA GGGATGACTA CGTTGGGGAA GACATTGTTG
1621 AGGTCAATTA TGAAACGTA AAGAAAAGCA GAAGACTGAT TATCATTTTA GTCAGAGAAA
1681 CATCAGGCTT CAGCTGGCTG GGTGGTTCAT CTGAAGAGCA AATAGCCATG TATAATGCTC
1741 TTGTTTCAAG TGAATTAATA GTTGCTCTGC TTGAGCTGGA GAAATCCAA GACTATGAGA
1801 AAATGCCAGA ATCGATTAAA TTCATTAAAG AGAAACATGG GGCTATCCCG TGGTCAGGGG
1861 ACTTTACACA GGGACCACAG TCTGCAAGA CAAGGTCTCG GAAGAATGTC AGGTACCACA
1921 TGCCAGTCCA GCGACGGTCA CCTTCATCTA AACACCAGTT ACTGTCACCA GCCACTAAGG
1981 AGAACTGCA AAGAGAGGCT CAGTGCCTC TCGGGTAGCA TGGAGAAGTT GCCAAGAGTT
2041 CTTTAGGTGC CTCTGTCTT ATGGCGTTGC AGGCCAGGTT ATGCCTCATG CTGACTTGCA
2101 GAGTTCATGG AATGTAATA TATCATCCTT TATCCCTGAG GTCACCAGGA ATCAGG

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## (2) INFORMATION FOR SEQ ID NO:2520:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2520:

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1 GCCACGTGCT GCTGGGTCTC AGTCCTCCAC TTCCCGTGTC CTCTGGAAGT TGTCAGGAGC
61 AATGTTGCGC TTGTACGTGT TGGTAATGGG AGTTTCTGCC TTCACCCTTC AGCCTGCGGC
121 ACACACAGGG GCTGCCAGAA GCTGCCGGTT TCGTGGGAGG CATTACAAGC GGGAGTTCAG

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181 GCTGGAAGGG GAGCCTGTAG CCCTGAGGTG CCCCAGGTG CCCTACTGGT TGTGGGCCTC
241 TGTCAGCCCC CGCATCAACC TGACATGGCA TAAAAATGAC TCTGCTAGGA CGGTCCCAGG
301 AGAAGAAGAG ACACGGATGT GGGCCCAGGA CGGTGCTCTG TGGCTTCTGC CAGCCTTGCA
361 GGAGGACTCT GGCACCTACG TCTGCACTAC TAGAAATGCT TCTTACTGTG ACAAATGTCT
421 CATTGAGCTC AGAGTTTTTG AGAATACAGA TGCTTTCCTG CCGTTCATCT CATACCCGCA
481 AATTTTAAAC TTGTCAACCT CTGGGGTATT AGTATGCCCT GACCTGAGTG AATTCACCCG
541 TGACAAAAC TACGTGAAGA TTCAATGGTA CAAGGATTCT CTTCTTTTGG ATAAAGACAA
601 TGAGAAATTT CTAAGTGTGA GGGGGACCAC TCACTTACTC GTACACGATG TGGCCCTGGA
661 AGATGCTGGC TATTACCGCT GTGTCCTGAC ATTTGCCCAT GAAGGCCAGC AATACAACAT
721 CACTAGGAGT ATTGAGCTAC GCATCAAGAA AAAAAAAGAA GAGACCATTG CTGTGATCAT
781 TTCCCCCTC AAGACCATAT CAGCTTCTCT GGGGTCAAGA CTGACAATCC CGTGTAAGGT
841 GTTTCTGGGA ACCGGCACAC CCTTAACCAC CATGCTGTGG TGGACGGCCA ATGACACCCA
901 CATAGAGAGC GCCTACCCGG GAGGCCGGGT GACCGAGGGG CCACGCCAGG AATATTGAGA
961 AAATAATGAG AACTACATTG AAGTGCCATT GATTTTTGAT CCTGTCAAA GAGAGGATTT
1021 GCACATGGAT TTTAAATGTG TTGTCCATAA TACCCTGAGT TTTAGACAC TACGCACCAC
1081 AGTCAAGGAA GCCTCCTCCA CGTCTCCTG GGGCATTGTG CTGGCCCCAC TTTCACTGGC
1141 CTTCTTGGTT TTGGGGGAA TATGGATGCA CAGACGGTGC AAACACAGAA CTGGAAAAGC
1201 AGATGGTCTG ACTGTGCTAT GGCCTCATCA TCAAGACTTT CAATCCTATC CCAAGTGAAG
1261 TAAATGGAAT GAAATAATTC AAACACAAA AAAAAA AAAAAA
1 GCGGGAGCCG ACTCGGAGCG CGCGGCGCGG CCGGGAGGAG CCGAGCGCGC CGGGCGCGGC
61 GTGGGGGCGC CGGCTGCCCG GCGCGCCAG GGAGCGGCAG GAATGTGACA ATCGCGCGCC
121 CGCACCCTAG CACTCCTCGC TCGGCTCCTA GGGCTCTCGC CCTCTGAGCT GAGCCGGGTT
181 CCGCCCGGGC TGGGATCCCA TCACCCTCCA CGGCCGTCG TCCAGGTAGA CGCACCCTCT
241 GAAGATGGTG ACTCCTCCT GAGAAGCTGG ACCCCTGGT AAAAGACAAG GCCTTCTCCA
301 AGAAGAATAT GAAAGTGTTA CTCAGACTTA TTTGTTTCAT AGCTCTACTG ATTTCTCTCT
361 TGGAGGCTGA TAAATGCAAG GAACGTGAAG AAAAAATAAT TTAGTGTGCA TCTGCAATG
421 AAATTGATGT TCGTCCCTGT CCTCTTAACC CAAATGAACA CAAAGGCACT ATAATTGGT
481 ATAAAGATGA CAGCAAGACA CCTGTATCTA CAGAACAGC CTCCAGGATT CATCAACACA
541 AAGAGAAACT TTGGTTTGTT TGGAGGATTG AGGACATTAC TATTGCGTGG
601 TAAGAAATTC ATCTTACTGC CTCAGAATTA AAATAAGTGC AAAATTTGTG GAGAATGAGC
661 CTAATTATG TTATAATGCA CAAGCCATAT TTAAGCAGAA ACTACCCGTT GCAGGAGACG
721 GAGGACTTGT GTGCCCTTAT ATGGAGTTT TTAATAATGA AAATAATGAG TTACCTAAAT
781 TACAGTGGTA TAAGGATTGC AAACCTCTAC TTCTTGACAA TATACACTTT AGTGGAGTCA
841 AAGATAGGCT CATCGTGATG AATGTGGCTG AAAAGCATAG AGGGAACAT ACTTGTCTATG
901 CATCCTACAC ATACTTGGGC AAGCAATATC CTATTACCCG GGTAATAGAA TTTATTACTC
961 TAGAGGAAAA CAAACCCACA AGGCCTGTGA TTGTGAGCCC AGCTAATGAG ACAATGGAAG
1021 TAGACTTGGG ATCCAGATA CAATTGATCT GTAATGTCAC CGGCCAGTTG AGTGACATTG
1081 CTTACTGGAA GTGGAATGGG TCAGTAATTG ATGAAGATGA CCCAGTGCTA GGGGAAGACT
1141 ATTACAGTGT GGAAATCCT GCAAACAAA GAAGGAGTAC CCTCATCACA GTGCTTAATA
1201 TATCGGAAAT TGAAAGTAGA TTTTATAAAC ATCCATTAC CTGTTTGGCC AAGAATACAC
1261 ATGGTATAGA TGCAGCATAT ATCCAGTTAA TATATCCAGT CACTAATTTT CAGAAGCACA
1321 TGATTGGTAT ATGTGTCACG TTGACAGTCA TAATTGTGTG TTCTGTTTTT ATCTATAAAA
1381 TCTTCAAGAT TGACATTGTG CTTTGGTACA GGGATTCTCT CTATGATTTT CTCCCAATAA
1441 AAGCTTCAGA TGGAAAGACC TATGACGCAT ATATACTGTA TCCAAAGACT GTTGGGAAG
1501 GGTCTACCTC TGACTGTGAT ATTTTGTGTG TTAAGTCTT GCCTGAGGTC TTGGAAGAAC
1561 AGTGTGGATA TAAGCTGTTC ATTTATGGAA GGGATGACTA CGTTGGGGAA GACATTGTTG
1621 AGGTCATTAA TGAAAACGTA AAGAAAAGCA GAAGACTGAT TATCATTTTA GTCAGAGAAA
1681 CATCAGGCTT CAGCTGGCTG GGTGGTTCAT CTGAAGAGCA AATAGCCATG TATAATGCTC
1741 TTGTTTCAAG TGAATTAAA GTTGTCCTGC TTGAGCTGGA GAAATCCAA GACTATGAGA
1801 AAATGCCAGA ATCGATTAAA TTCATTAAGC AGAAACATGG GGCTATCCG TGGTCAGGGG
1861 ACTTTACACA GGGACCACAG TCTGCAAAGA CAAGGTTCTG GAAGAAATG AGGTACCACA
1921 TGCCAGTCCA GCGACGGTCA CCTTCATCTA AACACCAGTT ACTGTACCA GCCACTAAGG
1981 AGAAACTGCA AAGAGAGGCT CACGTGCCTC TCGGGTAGCA TGGAGAAGTT GCCAAGAGTT
2041 CTTAGGTGCT CTCCTGTCTT ATGGCGTTGC AGGCCAGGTT ATGCCTCATG CTGACTTGCA
2101 GAGTTCATGG AATGTAAC TAATCATCCT TATCCCTGAG GTCACCAGGA ATCAGG

```

## (2) INFORMATION FOR SEQ ID NO:2521:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2521:

```

1 GCTCAGGGCA CATGCCTCCC CTCCCAGGC CGCGGCCAG CTGACCCTCG GGGCTCCCCC
61 GGAGCGGAC AGGGAAGGGT TAAAGCCCC CGGCTCCCTG CCCCTGCCG TGGGGAACCC
121 CTGGCCCTGT GGGGACATGA ACTGTGTTTG CCGCTGGTCT CTGGTCGTGC TGAGCCTGTG
181 GCCAGATACA GCTGTCGCCC CTGGGCCACC ACCTGGCCCC CCTCGAGTTT CCCAGACCC
241 TCGGGCCGAG CTGGACAGCA CCGTGCTCCT GACCCGCTCT CTCTGGCGG ACACGCGGCA
301 GCTGGCTGCA CAGCTGAGGG ACAAATCCC AGCTGACGGG GACCACAACC TGGATTCCCT

```



361 GCCCACCCTG GCCATGAGTG CGGGGGCACT GGGAGCTCTA CAGCTCCCAG GTGTGCTGAC  
421 AAGGCTGCGA GCGGACCTAC TGTCTACCT GCGGACGTG CAGTGGCTGC GCCGGGCAGG  
481 TGGCTCTTCC CTGAAGACCC TGGAGCCCGA GCTGGGCACC CTGCAGGCCC GACTGGACCG  
541 GCTGCTGCGC CGGCTGCAGC TCCTGATGTC CCGCCTGGCC CTGCCCCAGC CACCCCCGGA  
601 CCCGCCGCGC CCCCCGCTGG CGCCCCCTC CTCAGCCTGG GGGGGCATCA GGGCCGCCCA  
661 CGCCATCCTG GGGGGGCTGC ACCTGACACT TGA CTGGGCC GTGAGGGGAC TGCTGTGCT  
721 GAAGACTCGG CTGTGACCG GGGCCCAAAG CCACCACCGT CCTTCCAAAG CCAGATCTTA  
781 TTTATTTATT TATTTAGTA CTGGGGGCGA AACAGCCAGG TGATCCCCC GCCATTATCT  
841 CCCCTAGTT AGAGACA TCCTCCGTGAG GCCTGGGGGA CATCTGTGCC TTATTATATAC  
901 TTATTTATTT CAGGAGCAGG GGTGGGAGGC AGGTGGACTC CTGGGTCCCC GAGGAGGAGG  
961 GGA CTGGGGT CCCGGATTCT TGGGTCTCCA AGAAGTCTGT CCACAGACTT CTGCCCTGGC  
1021 TCTTCCCAT CTAGGCTG GCGAGAACAT ATATTATTTA TTTAAGCAAT TACTTTTCAT  
1081 GTTGGGGTGG GGACGGAGGG GAAAGGGAAG CCTGGGTTTT TGTACAAAAA TGTGAGAAAC  
1141 CTTTGTGAGA CAGAGAACAG GGAATTAAAT GTGCATACA TATCC

## (2) INFORMATION FOR SEQ ID NO:2522:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6870 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2522:

1 CAGCTGCGGC ATCCTCTGTC TCAGAGTCTT GGTGTCTCTG TTCCTTTCCC CTCGGGGTCT  
61 CCTGGGTCT CCCAAGTCC CTCCTGCTGT CTTCTCCCG CTCTCTGATC TCTGACTCCC  
121 AGAACCTCTC CCTCTGTCTC CAGGGCTGCC CCTCTGATCC TCTTTGCTTC TCTGGTGTGT  
181 CTCTCTGGCT GCCTCCATCT CTGTGGATCT CCGTCTCCCT GTCTCTGTCT CAGTCTGTCC  
241 TTCACTCTGT GTGTGTGTGT GTCTCTCTCT CTCTCTCTCC TTCCCTTCCA CTCCCTCTTC  
301 CTCCTGCCTC CACCTCTCCA GGCCCTGTG TTGTCCCTCC GTCCGGCCTT TCTCTGCCTT  
361 TCCGTCTCTC TGCCTCCCCA TCTCTCTCTG CTAGTCCCTGT CCAGCCGGAC CCCACCCAC  
421 AGTCGGGCCC CAGCGCTTGA GCCTGAGTGT CTGCTCCGGC CCGTGGAGGT GGAGGGAGGG  
481 GACGCCAATG ACCTCACCAG CCCCTCTCCG ACCACCCCCC CTTTCCCTT TTCAACTTTT  
541 CCAACTTTTC CTTCCGTGCC CTCCTCCGAG CGCGGCGGCG TGAGCCCTGC AAGGCAGCCG  
601 CTCCGTCTGA ATGGAAAAGG CAGGCAGGGA GGGTGAGTCA GGATGTGTCA GGCCGGCCCT  
661 CCCCTGCCGC CTGCCCCCG CCCGCCCGCC CCAGGCCCCC TATATAACCC CCCAGGCGTC  
721 CACACTCCCT CACTGCCGCG GGCCCTGCTG CTCAGGGCAC ATGCCTCCCC TCCCCAGCCG  
781 CGGGCCAGC TGACCTCGG GGCTCCCCG CGAGCGGACA GGAAGGGTT AAAGGCCCCC  
841 GGCTCCCTGC CCCCTGCCCT GGGGAACCCC TGGCCCTGTG GGGACATGAA CTGTAAGTTG  
901 GTTCATGGG AGGGTGGAG GGACAGGGAG GCAGGGAGGA GAGGGACCCA CGGCGGGGT  
961 GGGAGCAGAC CCCGTGAGT CGACAGAGA GGGACCCGGA GACAGGCAGC CGGGGAGGAG  
1021 AGCAGCTTCG GAGACAGGAG GCGCGGAGG AGATGGCAG AGAGAGACAC AGACAGGAGC  
1081 GGATGGAGGC AGCCAATCAG AGGCGCCGCA GGAGGACGG GCCAGACAGG GCCCGAGAGG  
1141 AGCGAGAGCG GAGACGAGC AGGGGACGGG ACGCAGGGAC TGGTGCCGGG AGGGAGGTGA  
1201 CCCCCATCGA CCCAGGCCCG AGGGAGCCCG CGGGGACCGG GAGACTCCCT GGGATTCCGG  
1261 CAGAGAGGCT CCGGAGGGAA ACTGAGGCAG GGTCCGCGGA GAGCGGAGCA AGCCAGGGAG  
1321 TAGCGACCCC AGCCGGGGG AGGAGAGAGA CTGGGCGCCG GGGGAAAGCG GGGAGAGCCG  
1381 GGCAGATGCG GCCGACGGAG GCGCGGACAG ACCGACGGCT GCGGGGCCG GGGGCGGGC  
1441 TGGGGGTGTG CGAGGCGCGG GCGGCGGGG AGCGCTGATT GGCTGGCGGG TGGCCGGGTG  
1501 GCGGGGGCGG CCGGGGTGGG CTGCGGGGAG CGAGCTCCGG ACCCCCGCGC CCCGCGGCC  
1561 CCCCAGGCC CCCGCGCCA GCTCTCCGC TCCCGCGCC CGGCCGGCC ATGGCTCTGC  
1621 CCCTCTCCG CCAGGTGCG TGCGGCCGG GCTTCTGCC CCCACCCGGC GGCTCCTGG  
1681 GAGGGCGTCT AAGGGGTCTC CCGTGGGAGA GGTCCGTGT TCCCGGACTC CGTCTGGG  
1741 TTTTGGCTCC TTCCCTGCT CCCAGCCAGC TCGGGCTCCC GCGGCCGGG GAGGGGCGAG  
1801 GTTCTGGCCT TGCTCTCCC CACCATCCG GCCCCGGGC CCAGATTCCG GCGTCCGGG  
1861 GCGGACGGGA GACGCCCCG CCGCTCTGC TCCGACGGG GGGGCAGCCA GAGCCAGGGA  
1921 GGGAGAGGGA AGCCCGCTG GCCCTGCGAC CTGCCCGCG GCGTTCCACC CTGGGACTTA  
1981 AGACCTCCAG CTCCATCTC CCTAAGGCCG GGAGTCCAG CCCCAGACC TCCTCCCCGA  
2041 GACCCAGGAG TCCAGACCC AGGCCCTCT CCTCAGACC TAGGAGTCCA GGGCCCCAGC  
2101 CTCTCTCCC TCAGACCCAG GAGGAGTCCA GACCCAGTT CCTCTCTCT CAGACCCGGG  
2161 AGTCCAGCCC AGGCCCTCT CTCTCAGACC CGGAGTCCAG CCTGAGCTCT CTGCCTTATC  
2221 CTGCCCCCAG GTGTTTGCCG CTTGGTCTG GTCGTGTGA GCCTGTGGCC AGATACAGCT  
2281 GTCGCCCCCT GGCACACC TGGCCCCCT CGAGTTTCCC CAGACCCTCG GCGCGAGCTG  
2341 GACAGCACCG TGCTCCTGAC CCGCTCTCT CTGGCGGACA CGCGGCAGCT GGCTGCACAG  
2401 CTGGTAGGAG AGACTGGGCT GGGGCCAGCA CAGGAGTGA AGGCAGAGAG GAACGGAGAG  
2461 GAGTCTGCGG GCAGCCACTT GGAGGGGTTT TGGGCTCTCA GGTGGCAGAG TGAGGGAGGG  
2521 GAAGAGTTGG GGGCCTGGCG TGGGGATGG AGGGAGCCCC GAGGCTGGG AGGGGCCACC  
2581 TCACAGCTTT TTTCCCTGCC AGAGGGACAA ATTCCAGCT GACGGGGACC ACAACCTGGA  
2641 TTCCCTGCCC ACCCTGGCCA TGAGTGCAGG GGCAGTGGGA GCTCTACAG TAAGGGCAAG  
2701 GGAGTGGGCT GGGGACAAGG TGGGAGGCG CAGTGAAGG GGGCGGGGAG GATGAGGGGC  
2761 ACTGGTCCGG TGTTCTCTGA TGTCCCGCT CTATCCCCAG CTCCAGGTG TGCTGACAG

2821 GCTGCGAGCG GACCTACTGT CCTACCTGCG GCACGTGCAG TGGCTGCGCC GGGCAGGTGG  
2881 CTCTTCCCTG AAGACCCTGG AGCCCCGAGT GGGCACCCTG CAGGCCCCGAC TGGACC GGCT  
2941 GCTGCGCCGG CTGCAGCTCC TGGTATGTCC TGGCCCCAAG ACCTGACACC CCAGACCCCG  
3001 ACCCCTGGCC CCAAATCCT GTGGCCTGAG TCCTTGAAGC CTGAGACCCC AGACCCGAGT  
3061 GCAACAGCCC CGCTCTGAGA CCCTGACACC CTAACAGCCC GCTCTGAGAC CCTGACACCG  
3121 TAACAGCCCC GCTCTGAGAC CCTGACCCTA ACAGTCCTGC TCTGAGACCC TGACCCCTGCA  
3181 GTCCCAAGAT CCTGTGGCCC TGAGACCCCTG AGGCCCTAGA CCCCCAATC CTGCCAGAA  
3241 ACTTCAAATT CTCACCCAAG ACCCTGAGAC TCCATCATCC ATGACCTCAA AGTCCCCAGA  
3301 TCCCAGCCCC TAAGACCCAA GACCCCATCC TGAAGCCCAA AGCCTTGAGA ATTCAAATCC  
3361 TCACCTCAAG ACTTGGAGAC CCTGGCCCCA TGACATTGAA AACCATGGAC CTGGCCAGGC  
3421 GTGGTGGCTC ACGCCTGTAA TCCCAGCACT TTGGGAGGCC GAGGCAAGTG GATCACTGA  
3481 GGTGGGAGT TCAAGACCAG CCAGACCAAC ATGGTGAAAC CCTGTCTCTA CTAATAATAC  
3541 AAAATTAGCC AGGCGTGGTG GTGCATGCCT GTAATCCCAG CTAATTGGGA GGCTGAGGCA  
3601 GGAGATCGC TTGAACCTGG GAGGCGGAGG TTGCAGTGAG CCGAGATCGC ACCATTACAC  
3661 TCCAGCCTGG GCAACAAGAG CAAAACCTCC TCTCTCTCAA AAAAAAATAA AAAAAAATAA  
3721 AAGAAGGAAA AGAAAACCAT GGACCTCCAG ACCCTGAGAC CCCAGGCCCC AGCCCTGAGA  
3781 TCCTGACATC TTAAGATACC CAGGCCCTAA GATACAAGAC CTTGACCCAA AGCCAGCCTT  
3841 GGGACCCTGG CTGTACAAAC CCAAGACCTC CAGGACCTAG ACCCCGAGCC CTGAGGCCCT  
3901 ATGTCTCACT CCCAACATCG AAAACCCCTGA CACCTCAGAT CCTGAGCCTG CGCCTGTACG  
3961 ACTCCAAGAC CCTCACTTCC AAAGCCAGGC CCAAAGCCCT GAGACCAGAA GACTTCAAAC  
4021 CCTGGTTCTT GGGCCTAACT CCAAAGACCC TGGATCTCAA ATTCCAATT CTAGCTCTGA  
4081 GACTCCAGCC CTACCCATG AGTTCTTGAA CTTGAACCCA GAGACCCCAT CTCTAAGACT  
4141 TCAGCCTTGA GATCCAGGCC CTGACCCTAG ACTCGAGCCC ACAGACCTCA GATACTGTCT  
4201 GTAAAACCCC AGCTCTGGTG GGGAGCAGTG GCTCACTCCT GTAATCCCAA GGCAGGGGAG  
4261 GCCAAGGCAG AAGGACCTCT TGAGGCCATG AGTTTGAGAC AGCCTGGGCA GCATAGCAAG  
4321 ACTCTGTTTC TTAATTATTA TTATTATTAT TATTTTTTGG AGACAGAGTC TCGCGCTCTG  
4381 TTGCCAGGC TAGAGTGCAA TGGTGCCATT TCGGCTTGCT GGAACCTCCG CCTCTGGGC  
4441 TCAAGCGATT CTCCTGCCTC AGCCTCCTGA GTAGCTGGGA CTTCAAGTGC ACACCTGCCAC  
4501 ACCCGATAA TTTTTTGTG TTTTAGTAGA CACAGGGTTT CACCGTGTG CCCAGGCTGG  
4561 TCACAAACTC CTGAGCTCAG GCCATCCGCC CGCCTCGGCC TCCCAAAGCC CTGGGATAAC  
4621 AGGCGTGACG CCGCGCCTGG CTTCTTAATT GTTCTAACAG CAGCGACAAC AACAAAAACC  
4681 CAGCTCTGAG ATTCCAGCCC CGGCGACTCT AACAGTCCCA GGCCCGATCC CTCACCTAGA  
4741 ACCGAGATGC CAGCCCTGAC TCCACAGACT TCACCCCAA CCCCCACACT CAGCTCTGGA  
4801 AGCCCGTCTT GACTCCAGCC TCCATTTTCG GAACCCACA GCCTGAAGAG CTCGCCGCTT  
4861 AAACACTTCA CCCCACGCGC CACAGTCCCC CTGTGAATAT GCAGCCCCGA TTCAGCTGCA  
4921 GCTCCACAGC ACCCCTGCCC TGCACCCCCG CTGCACCCCC TACCTGTGAC TCACCTCTCT  
4981 CCTCTCCCCA CAGATGTCCC GCCTGGCCCT GCCCCAGCCA CCCCAGGACC CGCCGGCGCC  
5041 CCCGCTGGCG CCCCCCTCCT CAGCCTGGGG GGGCATCAGG GCGGCCACG CCATCCTGGG  
5101 GGGGCTGCAC CTGACACTTG ACTGGGCCGT GAGGGGACTG CTGCTGCTGA AGACTCGGCT  
5161 GTGACCCGGG GCCCAAAGCC ACCACCGTCC TTCCAAAGCC AGATCTTATT TATTTATTTA  
5221 TTTCAGTACT GGGGGCGAAA CAGCCAGGTG ATCCCCCGC CATTATCTCC CCCTAGTTAG  
5281 AGACAGTCTT TCCGTGAGGC CTGGGGGGCA TCTGTGCTT ATTTATACTT ATTTATTTCA  
5341 GGAGCAGGGG TGGGAGGCAG GTGGACTCCT GGGTCCCCGA GGAGGAGGGG ACTGGGGTCC  
5401 CGGATTCTTG GGTCTCCAAG AAGTCTGTCC ACAGACTTCT GCCCTGGCTC TTCCCCATCT  
5461 AGGCCTGGGC AGGAACATAT ATTTATTTATT TAAGCAATTA CTTTTCATGT TGGGGTGGGG  
5521 ACGGAGGGGA AAGGGAAGCC TGGGTTTTTG TACAAAAATG TGAGAAACCT TTGTGAGACA  
5581 GAGAACAGGG AATTAAATGT GTCATACATA TCCACTTGAG GGCAGATTGT CTGAGAGCTG  
5641 GGGCTGGATG CTTGGGTAAC TGGGGCAGGG CAGGTGGAGG GGAGACCTCC ATTCAGGTGG  
5701 AGGTCCCAG TGGGCGGGGC AGCGACTGGG AGATGGGTG GTACCCAGA CAGCTCTGTG  
5761 GAGGCAGGGT CTGAGCCTTG CCTGGGGCCC CGCACTGCAT AGGGCCGTTT GTTTGTTTTT  
5821 TGAGATGGAG TCTCGCTCTG TTGCCTAGGC TGGAGTGCAG TGAGGCAATC TAAGGTCACT  
5881 GCAACCTCCA CCTCCCGGT TCAAGCAATT CTCCTGCCCT AGCCTCCGA TTAGCTGGGA  
5941 TCACAGGTGT GCACCACCAT GCCAGCTAA TTATTTATTT CTTTGTATT TTTAGTAGAG  
6001 ACAGGGTTTC ACCATGTTGG CCAGGCTGGT TTCGAACCTC TGACCTCAGG TGATCCTCCT  
6061 GCCTCGGCCCT CCCAAAGTGC TGGGATTACA GGTGTGAGCC ACCACACCTG ACCCATAGGT  
6121 CTTCAATAAA TATTTAATGG AAGGTTCCAC AAGTCACCT GTGATCAACA GTACCCGTAT  
6181 GGGACAAAGC TGCAAGGTCA AGATGGTTCA TTATGGCTGT GTTCACCATA GCAAACTGGA  
6241 AACAACTAG ATATCCAACA GTGAGGGTTA AGCAACATGG TGCATCTGTG GATAGAACGC  
6301 CACCCAGCCG CCGGAGCAG GACTGTCTAT TCAGGGAGGC TAAGGAGAGA GGCTTGCTTG  
6361 GGATATAGAA AGATATCCTG ACATTGGCCA GGCATGGTG CTCACGCTG TAATCCTGGC  
6421 ACTTTGGGAG GACGAAGCGA GTGGATCACT GAAGTCCAAG AGTTTGAGAC CGGCCTGCGA  
6481 GACATGGCAA AACCCTGTCT CAAAAAGAA AGAATGATGT CCTGACATGA AACAGCAGGC  
6541 TACAAAACCA CTGCATGCTG TGATCCCAAT TTTGTGTTTT TCTTTCTATA TATGGATTAA  
6601 AACAAAATC CTAAAGGGAA ATACGCCAAA ATGTTGACAA TGACTGTCTC CAGGTCAAAG  
6661 GAGAGAGGTG GGATTGTGGG TGACTTTTAA TGTGTATGAT TGTCTGTATT TTACAGAATT  
6721 TCTGCCATGA CTGTGATTTT TGCATGACAC ATTTTAAAAA TAATAACAC TATTTTGA  
6781 ATAACAGAA ATCAGCCTCC TCTCTCCAA AAATAAGCCC TCAGGAGGGG ACAAAGTTGA  
6841 CCGCTGATTG AGCCTGTCAG GGCTGTGCAC

## (2) INFORMATION FOR SEQ ID NO:2523:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8055 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2523:

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1 GCTCAGGGCA CATGCCTCCC CTCCCCAGGC CGCGGCCCCAG CTGACCCTCG GGGCTCCCCC
61 GGCAGCGGAC AGGGAAGGGT TAAAGGCCCC CGGCTCCCTG CCCCCTGCCC TGGGGAACCC
121 CTGGCCCTGT GGGGACATGA ACTGTGTTTG CCGCTGGTTC CTGGTCGTGC TGAGCCTGTG
181 GCCAGATACA GCTGTGCCCC CTGGGCCACC ACCTGGCCCC CCTCGAGTTT CCCAGACCC
241 TCGGGCCGAG CTGGACAGCA CCGTGCTCCT GACCCGCTCT CTCCTGSCGG ACACGCGGCA
301 GCTGGCTGCA CAGCTGAGGG ACAAATTCCC AGCTGACGGG GACCACAACC TGGATTCCCT
361 GCCACCCCTG GCCATGAGTG CGGGGGCACT GGGAGCTCTA CAGCTCCAG GTGTGCTGAC
421 AAGGCTGCGA GCGGACCTAC TGTCTACCT GCGGCACGTG CAGTGGCTGC GCCGGGCAGG
481 TGGCTCTTCC CTGAAGACCC TGGAGCCCGA GCTGGGCACC CTGCAGGCC GACTGGACCG
541 GCTGCTGCGC CGGCTGCAGC TCCTGATGTC CCGCTGGCC CTGCCCCAGC CACCCCGGA
601 CCGGCCGCGC CCCCCTGCG CGCCCCCTC CTCAGCCTGG GGGGCGATCA GGGCCGCCCA
661 CGCCATCCTG GGGGGGCTGC ACCTGACACT TGACTGGGCC GTGAGGGGAC TGCTGCTGCT
721 GAAGACTCGG CTGTGACCCG GGGCCCAAAG CCACCACCGT CCTTCCAAAG CCAGATCTTA
781 TTTATTATT TATTTCAGTA CTGGGGCGCA AACAGCCAGG TGATCCCCC GCCATTATCT
841 CCCCTAGTT AGAGACAGTC CTTCCGTGAG GCCTGGGGGA CATCTGTGCC TTATTATATC
901 TTATTATTT CAGGAGCAGG GGTGGGAGGC AGGTGGACTC CTGGGTCCCC GAGGAGGAGG
961 GGAAGTGGGT CCCGATTCT TGGGTCTCCA AGAAGTCTGT CCACAGACTT CTGCCCTGGC
1021 TCTTCCCAT CTAGGCTGG GCAGGAACAT ATATTATTTA TTTAAGCAAT TACTTTTCAT
1081 GTTGGGTGG GACGGAGGG GAAAGGGAAG CCTGGGTTT TGTACAAAA TGTGAGAAAC
1141 CTTGTGAGA CAGAGAACAG GGAATTAAAT GTGTACATA TATCC
1 CAGCTGCGGC ATCCTCTGTC TCAGAGTCTT GGTGTCTCTG TTCCTTCCC CTCGGGTCT
61 CCCTGGGTCT CCCCAAGTCC CTCTGCTGT CTTCTCCCG CTCTCTGATC TCTGACTCCC
121 AGAACCTCT CCTCTGTCTC CAGGGTGGCC CCTCTGATCC TCTTTGCTTC TCTGGTGTG
181 CTCTCTGGCT GCCTCCATCT CTGTGGATCT CCGTCTCCCT GTCTCTGTCT CAGTCTGTCC
241 TCACTCTGT GTGTGTGTGT GTCTCTCTCT CTCTCTCTCC TTCCCTTCCA CTCCTCTTC
301 CTCCTGCCTC CACCTCTCCA GGCCCCGTCT TGTCTCTCTC GTCCGGCCTT TCTCTGCCTT
361 TCCGTCTCTC TGCTTCCCA TCTCTCTCTG CTAGTCTCTG CCAGCCGAC CCCACCCAC
421 AGTGGGGCCC CAGCGCTTGA GCCTGAGTGT CTGCTCCGGC CCGTGGAGGT GGAGGGAGGG
481 GACGCCAATG ACCTCACCAG CCCCTCTCCG ACCACCCCCC CCTTTCCTT TCAACTTTT
541 CCAACTTTT CTCTCGTCCC CTCTCTCCAG CGCGGCGCG TGAGCCCTGC AAGGCAGCCG
601 CTCCGTCTGA ATGGAAGAG CAGGCAGGGA GGGTGAATCA GGATGTGTCA GGCCTGGCCT
661 CCCCTGCCGC CTGCCCCCG CCCGCCGCG CCAGGCCCCC TATATAACCC CCCAGGCTC
721 CACACTCCCT CACTGCCGCG GGCCCTGCTG CTCAGGGCAC ATGCCTCCCC TCCCAGCCG
781 CGGGCCAGC TGACCCTCGG GGCTCCCCG GCAGCGGACA GGGAAGGTT AAAGCCCCC
841 GGCTCCCTGC CCCCTGCCCT GGGGAACCCC TGGCCCTGTG GGGACATGAA CTGTAAAGTT
901 GTTCATGGG AGGGTGGAGG GGACAGGGAG GCAGGGAGGA GAGGGACCCA CGGCGGGGT
961 GGGAGCAGAC CCCGCTGAGT CGCACAGAGA GGGACCCGGA GACAGGCAGC CGGGGAGGAG
1021 AGCAGCTTCG GAGACAGGAG GCGGCGGAG AGATGGGAG AGAGAGACAC AGACAGGAGC
1081 GGATGGAGGC AGCCAATCAG AGGCGCCGCA GGAGGGACGG GCCAGACAGG GCCCGAGAGG
1141 AGCGAGACGC GAGACCGAGC AGGGGAGGG ACAGCAGGAC TGGTCCCGG AGGGAGGTGA
1201 CCCCCATCGA CCCAGGCCCC AGGGAGCCCG CGGGGACCGG GAGACTCCCT GGGATTCCGG
1261 CAGAGAGGCT CCGGAGGGA ACTGAGGAG GGTCCGCGGA GAGCGGAGCA AGCCAGGAG
1321 TAGCGACCCC AGCCGGGGG AGGAGAGAGA CTGGGCGCG GGGGAAAGCG GGGAGAGCCG
1381 GGCAGATGCG GCCGACGGAG GCGCGGACAG ACCGACGGCT GCGGGGCCG GGGGGCGGGC
1441 TGGGGGTGTG CGAGGCGCG CTGCGGGGAG CCGCTGATT GGCTGGCGGG TGCCCGGGT
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1561 CCCCAGCGCC CCGCGGCCA GCTCTCCCG TCCCGGCGC CGGCCGGGC ATGGCTCTGC
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1741 TTTTGGCTCC TTCCCTGCT CCCAGCCAGC TCGGGCTCCC GCGGCCCGG GAGGGGGCAG
1801 GTTCTGGCCT GTGCTTCCC CACCATCCGC GCCCGGGGC CCAGATTCCG GCGTCCGGG
1861 GCGGACGGGA GACGCCGGG CCGCTCTGC TCCGACGGG GGGGAGCCA GAGCCAGGGA
1921 GGGAGAGGGA AGCCCGCTG GCCCTGCGAC CTGCCCCGG GCGTCCACC CTGGGACTTA
1981 AGACCTCCAG CTCCATCTC CTAAGGCCG GGAGTCCAG CCCAGACCC TCCTCCCCGA
2041 GACCAGGAG TCCAGACCCC AGGCCTTCT CCCTCAGACC TAGGAGTCCA GGGCCCCAGC
2101 CTCTCTCCC TCAGACCCAG GAGGAGTCCA GACCCAGTT CCTCTCCCT CAGACCCGG
2161 AGTCCAGCCC AGGCCCTCT CTCTCAGACC CGGAGTCCAG CCTGAGCTCT CTGCTTATC
2221 CTGCCCCCAG GTGTTTGGC CTTGGTCTG GTCGTGCTGA GCCTGTGGC AGATACAGCT
2281 GTCGCCCCG GGCACACC TGGCCCCCT CGAGTTTCC CAGACCTCG GCGGAGCTG
2341 GACAGACCG TGCTCTGAC CCGCTCTCT CTGGCGGACA CGCGGACGT GGCTGCACAG
2401 CTGGTAGGAG AGACTGGGCT GGGGCCAGCA CAGGAGTGAG AGGCAGAGAG GAACGGAGAG
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2461 GAGTCTGGG GCAGCCACTT GGAGGGGTTT TGGGCTCTCA GGTGSCAGAG TGAGGGAGGG  
2521 GAAGAGTTGG GGGCCTGGCG TGGGGGATGG AGGGAGCCCC GAGGCTGGGC AGGGGCCACC  
2581 TCACAGCTTT TTTCCCTGCC AGAGGGACAA ATTCCCAGCT GACGGGGACC ACAACCTGGA  
2641 TTCCCTGCCC ACCCTGGCCA TGAGTGCAGG GGCAGTGGGA GCTCTACAGG TAAGGGCAAG  
2701 GGAGTGGGCT GGGGACAAGG TGGGAGGCAG GCAGTGAAGG GGGCGGGGAG GATGAGGGGC  
2761 ACTGGTCGGG TGTTCTCTGA TGTCCTGGCT CTATCCCCAG CTCCAGGTG TGCTGACAAG  
2821 GCTGCGAGCG GACCTACTGT CCTACCTGCG GCACGTGCAG TGGCTGCGCC GGGCAGGTGG  
2881 CTCTTCCCTG AAGACCCTGG AGCCCGAGCT GGGCACCCTG CAGGCCCCAG TGGACCGGT  
2941 GCTGCGCCGG CTGCACTCC TGSTATGTCC TGGCCCCAAG ACCTGACACC CCAGACCCCC  
3001 ACCCTGGGCC CCAAAATCCT GTGGCCTGAG TCCTTGAAGC CTGAGACCCC AGACCCGAGT  
3061 GCAACAGCCC CGCTCTGAGA CCCTGACACC CTAACAGCCC GCTCTGAGAC CCTGACACCG  
3121 TAACAGCCCC GCTCTGAGAC CCTGACCCTA ACAGTCTGCT TCTGAGACCC TGACCCTGCA  
3181 GTCCCAAGAT CCTGTGGCCC TGAGACCCTG AGGCCCTAGA CCCCCAAATC CTGCCCAGAA  
3241 ACTTCAAATT CTCACCCAAG ACCCTGAGAC TCCATCATCC ATGACCTCAA AGTCCCCAGA  
3301 TCCCAGCCCC TAAGACCCAA GACCCCATCC TGAAGCCCAA AGCCTTGAGA ATTCAAATCC  
3361 TCACCTCAAG ACTTGAGAC CCTGGCCCCA TGACATTGAA AACCATGGAC CTGGCCAGGC  
3421 GTGGTGGCTC ACGCCTGTAA TCCAGCACT TGGGAGGCC GAGGCAAGTG GATCACCTGA  
3481 GGTGCGGAGT TCAAGACCAG CCAGACCAAC ATGGTGAAAC CCTGTCTCTA CTAAAAATAC  
3541 AAAATTAGCC AGGCGTGGTG GTGCATGCCT GTAATCCCAG CTACTTGGGA GGCTGAGGCA  
3601 GGAGAATCGC TTGAACCTGG GAGGCGGAGG TTGCAGTGAG CCGAGATCGC ACCATTACAC  
3661 TCCAGCCTGG GCAACAAGAG CAAACTCCC TCTCTCTCAA AAAAAAAAAA AAAAAAAAAA  
3721 AAGAAGGAAA AGAAAACCAT GGACCTCCAG ACCCTGAGAC CCCAGGCCCC AGCCTGAGA  
3781 TCCTGACATC TTAAAGATCC CAGGCCCTAA GATACAAGAC CTTGACCCAA AGCCAGCCTT  
3841 GGGACCCCTG CTGTACAAAC CCAAGACCTC CAGGACCTAG ACCCCGAGCC CTGAGGCCCT  
3901 ATGTCTCACT CCCAACATCG AAAACCCCTG CACCTCAGAT CCTGAGCCTG CGCCTGTACG  
3961 ACTCCAAGAC CCTCACTTCC AAAGCCAGGC CCAAAGCCCT GAGACCAGAA GACTTCAAAC  
4021 CCTGGTTCTT GGGCCTAACT CCAAAGACCC TGGATCTCAA ATTCCAATT CTAGCTCTGA  
4081 GACTCCAGCC CTCACCCATG AGTTCCTGAA CTTGAACCCA GAGACCCCAT CTCTAAGACT  
4141 TCAGCCTTGA GATCCAGGGC CTGACCCTAG ACTCGAGCCC ACAGACCTCA GATACTGTCT  
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4261 GCCAAGGCAG AAGGACCTCT TGAGGCCATG AGTTTGAGAC AGCCTGGGCA GCATAGCAAG  
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4381 TTGCCCAGGC TAGAGTGCAA TGGTGCCATT TCGGCTTGCT GGAACCTCCG CCTCCTGGGC  
4441 TCAAGCGATT CTCCTGCCTC AGCCTCCTGA GTAGCTGGGA CTTCAGGTGC ACACTGCCAC  
4501 ACCCGGATAA TTTTGTGTA TTTTAGTAGA CACAGGGTTT CACCGTGTG CCCAGGCTGG  
4561 TCACAAATC CTGAGCTCAG GCCATCCGCC CGCCTCGGCC TCCCAAAGCG CTGGGATAAC  
4621 AGGCGTGACG CCGCGCCTGG CTCTTAATT GTTCTAACAG CAGCGACAAC AACAAAAACC  
4681 CAGCTCTGAG ATTCCAGCCC CGGCGACTCT AACAGTCCCA GGCCCGATCC CTCACCTAGA  
4741 ACCGAGATGC CAGCCCTGAC TCCACAGACT TCACCCCAA CCCCCAAGT CAGCTCTGGA  
4801 AGCCCGTCTT GACTCCAGCC TCCATTTTCG GAACCCACA GCCTGAAGAG CTCCCGCCT  
4861 AAACACTTCA CCCCACGCGC CACAGTCCCC CTGTGAATAT GCAGCCCCGA TTCAGCTGCA  
4921 GCTCCACAGC ACCCCTGCCC TGCAACCCCG CTGCACCCCG TACCTGTGAC TCACCTCTCT  
4981 CCTCTCCCA CAGATGTCCC GCCTGGCCCT GCCCAGCCA CCCCCGACC CGCCGGCGCC  
5041 CCCGCTGGCG CCCCCTCCT CAGCCTGGGG GGGCATCAGG GCGGCCACG CCATCCTGGG  
5101 GGGGCTGCAC CTGACACTTG ACTGGGCCGT GAGGGGACTG CTGCTGCTGA AGACTCGGT  
5161 GTGACCCGGG GCCCAAAGCC ACCACCGTCC TTCAAAGCC AGATCTTATT TATTTATTTA  
5221 TTTTCACTACT GGGGGCGAAA CAGCCAGGTG ATCCCCCGC CATTATCTCC CCCTAGTTAG  
5281 AGACAGTCCT TCCGTGAGGC CTGGGGGGCA TCTGTGCCTT ATTTATCTT ATTTATTTCA  
5341 GGAGCAGGGG TGGGAGGCAG GTGGACTCCT GGGTCCCCGA GGAGGAGGGG ACTGGGGTCC  
5401 CGGATTCTTG GGTCTCCAAG AAGTCTGTCC ACAGACTTCT GCCCTGGCTC TTCCCATCT  
5461 AGGCTGGGC AGGAACATAT ATTATTTATT TAAGCAATTA CTTTTCATGT TGGGGTGGGG  
5521 ACGGAGGGGA AAGGGAAGCC TGGGTTTTTG TACAAAATG TGAGAAACCT TTGTGAGACA  
5581 GAGAACAGGG AATTAAATGT GTCATACATA TCCACTTGAG GCGGATTGT CTGAGAGCTG  
5641 GGGCTGGATG CTTGGGTAAC TGGGGCAGG CAGGTGGAGG GGAGACCTCC ATTCAGGTGG  
5701 AGGTCCCGAG TGGCGGGGGC AGCGACTGGG AGATGGGTCG GTCACCCAGA CAGCTCTGTG  
5761 GAGGCAGGGT CTGAGCCTTG CCTGGGGCCC CGCACTGCAT AGGGCCGTTT GTTTGTTTTT  
5821 TGAGATGGAG TCTCGCTCTG TTGCCTAGGC TGGAGTGCAG TGAGGCAATC TAAGGTCACT  
5881 GCAACCTCCA CCTCCGGGT TCAAGCAATT CTCCTGCCTC AGCCTCCGA TTAGCTGGGA  
5941 TCACAGGTGT GCACCACCAT GCCCAGCTAA TTATTTATTT CTTTGTATT TTAGTAGAG  
6001 ACAGGGTTTC ACCATGTTGG CCAGGCTGGT TTCGAATCC TGACCTCAGG TGATCCTCCT  
6061 GCCTCGGCCT CCCAAAGTGC TGGGATTACA GGTGTGAGCC ACCACACCTG ACCCATAGGT  
6121 CTTCAATAAA TATTTAATGG AAGGTTCCAC AAGTACCCT GTGATCAACA GTACCCGTAT  
6181 GGGACAAAGC TGCAAGGTCA AGATGGTTCA TTATGGCTGT GTTACCATA GCAAACCTGA  
6241 AACAATCTAG ATATCCAACA GTGAGGGTTA AGCAACATGG TGCATCTGTG GATAGAACC  
6301 CACCCAGCCG CCGGAGCAG GGAAGTGCAT TCAGGGAGGC TAAGGAGAGA GGCTTGCTTG  
6361 GGATATAGAA AGATATCCTG ACATTGGCCA GGCATGGTGG CTCACGCTG TAATCCTGGC  
6421 ACTTTGGGAG GACGAAGCGA GTGGATCACT GAAGTCCAAG AGTTTGAGAC CGCCTGCGA  
6481 GACATGGCAA AACCTGTCT CAAAAAGAA AGAATGATGT CCTGACATGA AACAGCAGGC

6541 TACAAAACCA CTGCATGCTG TGATCCCAAT TTTGTGTTTT TCTTTCTATA TATGGATTAA  
6601 AACAAAAATC CTAAGGGGAA ATACGCCAAA ATGTTGACAA TGACTGTCTC CAGGTCAAAG  
6661 GAGAGAGGTG GGATTGTGGG TGACTTTTAA TGTGTATGAT TGTCTGTATT TTACAGAATT  
6721 TCTGCCATGA CTGTGTATTT TGCATGACAC ATTTTAAAAA TAATAAACAC TATTTTGTAGA  
6781 ATAACAGAAT ATCAGCCTCC TCCTCTCCAA AAATAAGCCC TCAGGAGGGG ACAAAGTTGA  
6841 CCGCTGATTG AGCCTGTCAG GGCTGTGCAC

## (2) INFORMATION FOR SEQ ID NO:2524:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1681 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2524:

1 gctgtagctg gtgagaggaa gtcctagagg ctatggacac tctgtgtgtg ggatcaccga  
61 gatgagcagc agctgtctag ggctgagcag ggtcctgggt gccgtggcta cagccctggg  
121 gtctgcctcc tccccctgcc cccaggcctg gggcccccga ggggtccagt atgggcagcc  
181 agggaggtcc gtgaagctgt gttgtcctgg agtgactgcc ggggacccag tgtcctgggt  
241 tcgggatggg gagccaaagc tgctccaggg acctgactct gggctagggc atgaactggt  
301 cctggcccag gcagacagca ctgatgagg cacctacatc tgccagaccc tggatgggtg  
361 acttgggggc acagtgaccc tgcagctggg ctaccctcca gcccgccctg ttgtctctctg  
421 ccaagcagcc gactatgaga acttctcttg cacttggagt cccagccaga tcagcgggtt  
481 acccaccgcg tacctcacct cctacaggaa gaagacagtc ctaggagctg atagccagag  
541 gaggagtcca tccacagggc cctggccatg cccacaggat cccctagggg ctgcccgtg  
601 tgttggtcac ggggctgagt tctggagcca gtaccggatt aatgtgactg aggtgaaccc  
661 actgggtgcc agcacacgcc tctggatgtg gagcttgacg agcatcttgc gccctgaccc  
721 accccagggc ctgagggtag agtcagtacc aggttaccac cgacgcctgc gagccagctg  
781 gacataccct gcctcctggc cgtgccagcc ccacttctct ctcaagtccc gtttgagta  
841 ccgtccggcg cagcatccag cctgggtccac ggtggagcca gctggactgg aggaggtgat  
901 cacagatgct gtggctgggc tgccccatgc tgtacgagtc agtgcccggg actttctaga  
961 tgctggcacc tggagcacct ggagcccga ggcctgggga actccgagca ctgggaccat  
1021 accaaaaggag ataccagcat ggggccagct acacacgcag ccagagggtg agcctcaggt  
1081 ggacagccct gtcctccaa ggcctccct ccaaccacac cctcggtac ttgatcacag  
1141 ggactctgtg gagcaggtag ctgtgtggc gtctttggga atccttctt tccctgggact  
1201 ggtggctggg gccctggcac tggggtctct gctgaggctg agacgggggt ggaaggatgg  
1261 atcccaaaag cctgggttct tggcctcagt gattccagtg gacaggcgtc caggagctcc  
1321 aaactcttag aggacccagg agggcttcgg cagattccac ctataattct gtcttctgtg  
1381 tgtggataga aaccaggcag gacagtagat ccctatgggt ggatctcagc tgggaagttct  
1441 gtttggagcc catttctgtg agaccctgta tttcaaat tgcagtgaaa ggtgcttgta  
1501 cctctgattt caccacagag ttggagtctt gctcaaggaa cgtgtgtaat gtgtacatct  
1561 gtgtccatgt gtgacatgt gtctgtgaag gccagggaac atgtattcct ctgcatgcat  
1621 gtatgtaggt gcctgggagt gtgtgtggtc cttgtcttgg ccctttccct tgcaggggtg  
1681 tgcaggtgtg aataaa

## (2) INFORMATION FOR SEQ ID NO:2525:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1681 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2525:

1 ggaagatgag cagcagctgc tcagggtga gcagggtcct ggtggccgtg gctacagccc  
61 tgggtgtctg ctctccccc tgccccagg cctggggccc cccaggggtc cagtatgggc  
121 agccaggcag gtccgtgaag ctgtgtgtc ctggagtac tgccggggac ccagtgtcct  
181 ggtttcggga tggggagcca aagctgtcc agggaccta ctctgggcta gggcatgaac  
241 tggctcctgg ccaggcagac agcactgat agggcaccta catctgccag accctggatg  
301 gtgcacttgg gggcacagt accctgcagc tgggctaccc tccagcccgc cctgtgtct  
361 cctggcaagc agccgactat gagaacttct ctgcaactg gactcccagc cagatcagcg  
421 gtttaccac ccgtacctc acctcctaca ggaagaagac agtccatgga gctgatagcc  
481 agaggaggag tccatccaca gggccctggc catgccaca ggatccccta ggggtgccc  
541 gctgtgttgt ccacggggt gagttctgga gccagtaccg gattaatgtg actgaggtga  
601 acccactggg tgccagcaca cgcctgctgg atgtgagctt gcagagcatc ttgcgccctg  
661 acccaccaca gggcctgcgg gtagagtcag taccagggtta ccccgacgc ctgcgagcca  
721 gctggacata cctgcctcc tggcctgccc agccccactt cctgctcaag ttccgtttgc  
781 agtaccgtcc ggccgagcat ccagcctggg ccaggtgga gccagctgga ctggaggagg  
841 tgatcacaga tgctgtggct gggctgcccc atgctgtacg agtcagtgcc cgggactttc  
901 tagatgctgg cacctggagc acctggagcc cggaggcctg ggaactccg agcactggga  
961 ccataccaaa ggagatacca gcatggggcc agctacacac gcagccagag gtggagcctc  
1021 aggtggacag cctgtctct ccaaggccct ccctccaacc acaccctcgg ctacttgatc

1081 acaggggactc tgtggagcag gtagctgtgc tggcgtcttt gggaaatcctt tctttcctgg  
 1141 gactgggtggc tggggccctg gcaactggggc tctggctgag gctgagacgg ggtgggaagg  
 1201 atgcatcccc aaagcctggg ttcttggcct cagtgtattcc agtggacagg cgtccaggag  
 1261 ctccaaacct gtagaggacc caggagggtc tcggcagatt ccacctaataa ttctgtcttg  
 1321 ctgggtgtgga tagaaaccag gcaggacagt agatccctat ggttggatct cagctggaag  
 1381 ttctgttttg agcccatttc tgtgagaccc tgtatttcaa atttgcagct gaaaggtgct  
 1441 tctacctctg atttcacccc agagtgtggag ttctgtctcaa ggaacgtgtg taatgtgtac  
 1501 atctgtgtcc atgtgtgacc atgtgtctgt gaggcaggga acatgtattc tctgcatgca  
 1561 tgtatgtagg tgcctgggga gtgtgtgtgg gtccttggct cttggccttt ccttgcaggg  
 1621 gttgtgcagg tgtgaataaa gagaataagg aagttcttgg agattatact cagaaaaaaa  
 1681 aa

## (2) INFORMATION FOR SEQ ID NO:2526:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2526:

1 tctgtggagc aggtagctgt gctggcgtct ttgggaatcc tttctttcct gggactgggtg  
 61 gctggggccc tggcactggg gctctggtaa gtgactgcca ttgggtccctc agcctctgat  
 121 cctcacacat gctctgatgc ccatagacca cattcatctc cacccttcat gactgcctgc  
 181 tgaacctgtc tgattctgga actacctccc catacctcca tcccctatgc cccacttgat  
 241 tttaactgat tcctctcctg accctttact aataaaccct ttggcggaga ctgagataac  
 301 ccacattggt ggagagacag ctgcctttct atgccccagg ctgaggctga gacggggtgg  
 361 gaaggatgga tccccaagc ctgggttctt ggcctcagtg attccagtg aca

## (2) INFORMATION FOR SEQ ID NO:2527:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: - base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2527:

1 gctgtagctg gtgagaggaa gtcctagagg ctatggacac tctgctgctg ggatcacccga  
 61 gatgagcagc agctgtcag ggctgagcag ggtcctgggt gccgtggcta cagccctggt  
 121 gtctgcctcc tccccctgcc cccaggcctg gggcccccca ggggtccagt atgggcagcc  
 181 agggaggtcc gtgaagctgt gttgtcctgg agtgactgcc ggggacccag tgtcctgggt  
 241 tcgggatggg gagccaaagc tgctccaggg acctgactct gggctagggc atgaactggt  
 301 cctggcccag gcagacagca ctgatgaggg caccacacac tgccagaccc tggatgggtg  
 361 acttgggggc acagtgaccc tgcagctggg ctaccctcca gcccgcctg ttgtctcctg  
 421 ccaagcagcc gactatgaga acttctcttg cacttggagt cccagccaga tcagcgggtt  
 481 acccaccgca tacctcacct cctacaggaa gaagacagtc ctaggagctg atagccagag  
 541 gaggagtcca tccacagggc cctggccatg cccacaggat cccctagggt ctgcccgctg  
 601 tgtgtccac ggggctgagt tctggagcca gtaccggatt aatgtgactg aggtgaaccc  
 661 actgggtgcc agcacacgcc tgctggatgt gagcttgag agcatcttgc gccctgaccc  
 721 acccagggc ctgctgggtg agtcagtacc aggttaccct cgacgcctgc gagccagctg  
 781 gacataacct gcctcctggc cgtgccagcc caacttctct ctcaagttcc gtttgcagta  
 841 ccgtccggcg cagcatccag cctggtccac ggtggagcca gctggactgg aggaggtgat  
 901 cacagatgct gtggctgggc tgccccatgc tgtacgagtc agtgcccggg actttctaga  
 961 tgctggcacc tggagcacct ggagcccggg ggcctgggga actccgagca ctgggacct  
 1021 accaaaggag ataccagcat ggggcccagc acacacgcag ccagagggtg agcctcaggt  
 1081 ggacagccct gtcctcccaa ggcctccct ccaaccacac cctcggtac ttgatcacag  
 1141 ggactctgtg gagcaggtag ctgtgctggc gtctttggga atccttctt tcttgggact  
 1201 ggtggctggg gccctggcac tggggtctct gctgaggctg agacgggggt ggaaggatgg  
 1261 atcccaaaag cctgggttct tggcctcagt gattccagt gacaggcgct caggagctcc  
 1321 aaacctgtag aggacccagg agggcttcgg cagattccac ctataattct gtcttctggt  
 1381 tgtggataga aaccaggcag gacagttagt ccctatggtt ggatctcagc tggaaagtct  
 1441 gtttggagcc catttctgtg agaccctgta tttcaaattt gcagctgaaa ggtgcttgta  
 1501 cctctgattt caccacagag ttggagtctt gctcaaggaa cgtgtgtaat gtgtacatct  
 1561 gtgtccatgt gtgaccatgt gtctgtgaag gccagggaac atgtattcct ctgcatgcat  
 1621 gtatgtaggt gcctgggagt gtgtgtggtc ctgtctctgg cccttccct tgcagggttg  
 1681 tgcaggtgtg aataaa  
 1 ggaagatgag cagcagctgc tcagggtcga gcagggtcct ggtggccgtg gctacagccc  
 61 tgggtgtctgc ctctccccc tgcctccagg cctggggccc cccagggggt cagtatgggc  
 121 agccaggcag gtccgtgaag ctgtgttctc ctggagtac tgccgggac ccagtgtcct  
 181 ggtttcggga tggggagcca aagctgtctc agggacctga ctctgggcta gggcatgaac  
 241 tggctcctgg ccaggcagac agcactgatg agggcaccta catctgccag accctggatg  
 301 gtgcacttgg gggcacagt accctgcagc tgggtaccc tccagccgc cctgttgtct

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361 cctgccaaagc agccgactat gagaacttct cttgcacttg gaggcccagc cagatcagcg
421 gtttaccacac ccgtacctc acctcctaca ggaagaagac agtcctagga gctgatagcc
481 agaggaggag tccatccaca gggccctggc catgccaca ggatccccta ggggctgccc
541 gctgtgttgt ccacggggct gatttctgga gccagtaccg gattaatgtg actgaggtga
601 acccactggg tgccagcaca cgctgtctgg atgtgagctt gcagagcatc ttgcgcctg
661 acccacccca gggcctgcgg gtagagtcag taccagggtta ccccgacgc ctgcgagcca
721 gctggacata ccctgcctcc tggccgtgcc agccccactt cctgctcaag ttccgtttgc
781 agtaccgtcc ggcgcagcat ccagcctggt ccacgggtga gccagctgga ctggaggagg
841 tgatcacaga tgctgtggct gggctgcccc atgtgttacg agtcagtgcc cgggactttc
901 tagatgctgg cacctggagc acctggagcc cggaggcctg gggaactccg agcactggga
961 ccataccaaa ggagatacca gcatggggcc agctacacac gcagccagag gtggagcctc
1021 aggtggacag ccctgctctt ccaaggccct ccctccaacc acaccctcgg ctacttgatc
1081 acagggactc tgtggagcag gtagctgtgc tggcgtcttt gggaatcctt tcttctctgg
1141 gactggtggc tggggccctg gcaactgggc tctggctgag gctgagacgg ggtgggaagg
1201 atggatcccc aaagcctggg ttcttggcct cagtgtattc agtggacagg cgtccaggag
1261 ctccaaacct gtagaggacc caggagggtt tcggcagatt ccacctataa ttctgtcttg
1321 ctggtgtgga tagaaaccag gcaggacagt agatccctat ggttggatct cagctggaag
1381 ttctgtttgg agcccatttc tgtgagaccc tgtatttcaa atttgagct gaaaggtgct
1441 tctacctctg atttcacccc agagttggag ttctgtctaa ggaacgtgtg taatgtgtac
1501 atctgtgtcc atgtgtgacc atgtgtctgt gaggcaggga acatgtattc tctgcatgca
1561 tgtatgtagg tgccctggga gtgtgtgtgg gtccttggct cttggccttt ccttgagggg
1621 gttgtgcagg tgtgaataaa gagaataagg aagttcttgg agattatact cagaaaaaaa
1681 aa
1 tctgtggagc aggtagctgt gctggcgtct ttgggaatcc tttcttctct gggactgggtg
61 gctggggccc tggcactggg gctctggtta gtgactgcca ttggtccctc agcctctgat
121 cctcacacat gctctgatgc ccatagacca cattcatctc cacccttcat gactgcctgc
181 tgaacctgtc tgattctgga actacctccc catacctcca tcccctatgc cccacttgat
241 tttaactgat tctctcctg accctttact aataaacctt ttggcggaga ctgagataac
301 ccacattggt ggagagacag ctgcctttct atgccccagg ctgaggctga gacggggtgg
361 gaaggatgga tccccaaagc ctgggttctt ggcctcagtg attccagtgg aca

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## (2) INFORMATION FOR SEQ ID NO:2528

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 901 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2528:

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1 cttcaactca ataagcattt taagtattct aatcttagta tttctctagc tgacatgtaa
61 gaagcaatct atcttattgt atgcaattag ctctattgtg ggataaaaag gtaaaaccat
121 tctgaaacag gaaaccaata cacttctgtt ttaatcaaca aatctaaaca tttattcttt
181 tcatctgttt actcttgctc ttgtccacca caatatgcta ttcacatgtt cagtgtagtt
241 ttatgacaaa gaaaattttc tgagttactt ttgtatcccc acccccttaa agaaaggagg
301 aaaaactggt tcatacagaa ggcgttaatt gcatgaatta gagctatcac ctaagtgtgg
361 gctaattgta caaagaggga ttccacctac atccattcag tcagtctttg ggggtttaa
421 gaaattccaa agagtcacat gaagaggaaa aatgaaggta atgttttttc agacaggtaa
481 agtctttgaa aatatgtgta atatgtaaaa cattttgaca cccccataat atttttccag
541 aattaacagt ataaattgca tctctgttcc aagagttccc tatcactctc tttaatcact
601 actcacagta acctcaactc ctgccacaat gtacaggatg caactcctgt cttgcattgc
661 actaagtctt gcactgtgca caaacagtgc acctacttca agttctacaa agaaaacaca
721 gctacaactg gagcatttac ttctggattt acagatgatt ttgaatggaa ttaatgtaag
781 tatatttctt ttcttactaa aattattaca tttagtaatc tagctggaga tcatttctta
841 taacaatgca ttatactttc ttagaattac aagaatccca aactcaccag gatgctcaca
901 tttaagtttt acatgcccac gaaggtaagt acaatatttt

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## (2) INFORMATION FOR SEQ ID NO:2529:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2529:



421 ggttcttcca gcatgcagct tgagatctga gaatggacag actgcctcct caagtgggtc  
481 cctgaccccc gagtaacct actgggaggg accccaagta ggggcagact gacacctcag  
541 atggctgggt actcctctga gaaaaaactt ccagaggaac gatcaggcag caacatttgc  
601 tggtcaccac tatccactgt tctgcagcct cctgtgctaa taccacaggca aatgggtctg  
661 gagaggacct ccagcaagct ccaacagacc tacagctgag ggtcctgact gttagaagga  
721 aaactaacaa acagaaaagg catccacacc aaaaccctat ctgtacggca ccatcatcaa  
781 agaccaaagg tagataaaac cacaagatg gggaaaaaaa cacagcagaa aaactggtaa  
841 ctctaaaaat tagagcgctt ctctcctcct aaaggaacgc agctcctcac cagcaatgga  
901 accaagctgg acagagaatg actttgacga gttgagagaa gaaggcttca gatgatcaaa  
961 ctactctgag ctaaaaggag aagttcgaac ccacggcaaa gaagttaaaa accttgaaaa  
1021 aaattagatg aatggctaac tagaataaac aatgcagaga agtccttaaa ggacctgatg  
1081 gagctgaaaa ccatggcaca agaactacat gacaaatgca caagcctcag tagctgattc  
1141 gatcaactgg aagaaagggt atcagtgatg gaagatcaaa tgaatgaaat gaagcaagaa  
1201 gagaagttta gagaaaaaag aaaaaaaga aatgaacaaa gcctccaaga aatatgggac  
1261 tatgtgaaaa gaccaaactt acgtctgatt ggtgtacctg aaagtgatgg ggagaatgga  
1321 accaagctgg aaaacactct gcaggatatt atccaagaga acttcccaa tctagcaagg  
1381 caggctgaca ttcaaatca ggaaatacag agaacgccac aaataaatc ctcgagaaga  
1441 gcaactccaa gacacataat tgtagattc actaaagttg aaatgaagga aaaaatgtta  
1501 agggcagcca gagagaaagg tcagcttacc cacaagggaa agcccatcag attaacagct  
1561 gatctctcgg cagaaactct acaagccaga agagagtggg ggccaatatt caacattctt  
1621 aaagaaaaga attttcaacc cagaatttca tatccagcca aactatgctt cataagttaa  
1681 ggagaaataa aatatagaca agtgaacgat gaaagatttt gtcaccacca ggcctgcctt  
1741 acaagagctc ctgaagggaag cactaaacat ggaaagggaac aaccgggtacc agccactgca  
1801 aaaacatgcc aaattgtaaa caccattgag gccaggaaga aactgcatca actaacgagc  
1861 aaaataacca gctaacatca tcatgacagg atcaaatca cacataacaa tattaacctt  
1921 aaatgtaaat aggtctaatg ctccaattaa aagacacaga ctggcaaaact ggataaagag  
1981 tcaagaccca tcagtgtgct gtattcagga aacctatctc acgtgcagag acacacatag  
2041 gctcaaaata aagggatgga ggaagatcta ccaaacaac ggaaaacaaa aaaaggcagg  
2101 ggttgcaatc ctagtctctg ataaaacaga ctttaaacca acaaatgata aaagagacac  
2161 agaaggccat tacataatgg taaagggatc aattcaacaa gaagagttaa ctatcctaaa  
2221 tatatatgca cccaatacag gagcacctag attcataaag caagtcctta gagacctaca  
2281 aatagactta gactcccaca caataataat gggagacttt aacaccccac tgtaacattt  
2341 agacagatca atgagacaga aaattaacaa ggatatccag gaattgaact caactctgca  
2401 ccaagcggac ctaatagaca tctacagaac tctccacccc aatatcaacag aatatacatt  
2461 cttttcggca ccacaccaca ccgattccaa aattgaacac atagttggaa gtaaaagcact  
2521 cctcagcaaa tgtaaaagaa cagaaagtac aacaaactgt ctctcagacc acagtgcaat  
2581 caaactaaaa ctcaggatta agaaactcac tcaaaaccgc tcaactacat ggaaactgaa  
2641 caacctgctc ctgaatgact actgggtaca taacgaatg aaggcagaag taaagatggt  
2701 ctttgaacc aacgagaaca aagacacaac ataccagaat ctctgggaca cattcaaagc  
2761 agtctgtaga ggaataattt tagcactaaa tgcccacaag agaaagcagg aaagatctaa  
2821 aattgacagc ctaacatcac aattaaaaga actagagaaa caagagcaaa cacattcaaa  
2881 agctagcaga aggcaagaaa taactacaat cagagcagaa ctgaaggaga tagagacata  
2941 caaaaaaccc ttcaaaaaat caatgaatcc aggagctggt tttttgaaaa gatcaacaaa  
3001 attgatagac cactagcaaa actaatacag aagagagaag aatcaaatag acacaataaa  
3061 aaatgataaa cgggatatca ccactgatcc cacagaaata caaactacca tcaagaataa  
3121 ctataaacac ctctatgcaa ataaactaga aaatctagaa gaaatggata aattcctcga  
3181 cacatacacc ctccaagacc taaaccagga agaagctgaa tctctgaata gaccaataac  
3241 aggtcttgaa attgaggcaa caattaacac cttaccaacc aataaaagtc caggaccaga  
3301 tggattcaca gccaaattct accagaggta caaggaggag ctggtacgat tccttctgaa  
3361 actattccaa tcaatagaaa aagagggaa cctccctaac tcattttatg aggccagcat  
3421 catcctgata ccaaagcctg gcagagacac aacaaaaaaa gagaatttca gaccaatatt  
3481 cctgatgaac atcgatgcaa aaatttttaa taaaatactg gcaaactgaa tccagcagca  
3541 catcacaagg cttatccacc atgatcaagc tggcttcatt cctgggatgc aaggctgggt  
3601 caacatacgg aaaatcaata aatgtaatcc agcatataaa cagaaccaac aacacacaac  
3661 acatgattat ctcaacagat gcagaaaagg cctttgacaa aattcaacag cccttcagtc  
3721 taaaaactct caataaatta ggtactgatg ggacgtatct caaaataata agcgctatct  
3781 atgaccaacc cacagccaat atcatactgg atgggcaaaa actggaagca ttccctttga  
3841 aaactggcac aagacaggga tgccctctct caccactcct attcaacaca gtgttcgaag  
3901 ttctggcagg gcaatcaggc aggagaaaga aataaagggt attcaattag gaaaagagga  
3961 ggtcaaatg tccctgtttg cagatgacat gattgtatat atagaaaacc ccattgtctc  
4021 agcccaaaat ctcccttaagc tgataagcaa cttcagcaaa gtctcaggat caaaatcaat  
4081 gtgcaaaaat cacaagcatt cttatacacc aataacagac aaacagagag ccaactcaca  
4141 agtgaactcc cattcacaat tgcttcaagg agaataaaat acctaggaat ccaactcaca  
4201 agggatgtga gagacctctt caaggagaac tataaaccac tgctcaatga aatgagagga  
4261 tacagataaa tggaagaaca ttccatgctc atgggttaga agaatacaata tcgtgaaaat  
4321 ggccatactg cccaaggtaa ttttatagat tcaatgccat ccccatcaag ctaccaatga  
4381 ctttcttcac agaattggaa aaaactactt taaagttcat atggaaccaa aaaagagccc  
4441 gcattgccaa gtcaatccta agccaaaaga acaaaagctag aggcatacaca ctacctgact



4501 tcaaaactata ctacaaggct acagtaacca aaacagcatg gtactgggtac caaagcagag  
4561 atatatagacca atggaacaaa acagtgcctt cagaaataat actgcatatc tacaaccatc  
4621 tgatcttttga caaacctgac aaaaacaagc aatggggaaa ggattcccta tttataaata  
4681 ggtgctggga aaactggcta gccatatgta gaaagctgaa attggatccc ttccttacac  
4741 cttgtacaaa aattaattca agatggatta cagacttaaa tgttagacct aaaccataa  
4801 aaaccctaga agaaaaccta ggcaatacca ttcaggacat aggcattggg aagaacttca  
4861 tgtctagaac accaaaagta atggcaacaa aagccaaaat tgacaaatgg gtctaattaa  
4921 actaaagagc ttctgcacag caaaagaaac taccatcaga gtgaaggagg aacctacaga  
4981 atggggagaaa atttttgcaa tctgacaaaa gggctaattt ttgcatctga caaagggtta  
5041 atattccagaa tctacaatga actcaaacaa atttacaaga aaaaaacaaa tttacaagaa  
5101 aaaaacaaaa tttacaagaa aaaaacaaat ttacaagaaa aaaacaaaca accccatcaa  
5161 aaagtgggca aaggataaga acagtcaact ctcaaaagaa gacattttatg cagccaaaag  
5221 acacatgaaa aaattctcat catcactggc catcagagaa atgcaaatca aaaccacaat  
5281 gagatcccat ctcacaccag ttagaatggc gatcattaaa aagtcaagaa acaacagggtg  
5341 ctggagagga tgtggagaaa taggaacact tttacactgt tagtggggc gttaactagt  
5401 tcaacattgt ggaaatcagt atggcgattc ctcagggtac tagaactaga aataccattt  
5461 gaccagacca tcccattact gggatatata ccaaaggatt ataaatcatg ctgctataaa  
5521 gacacttgca cacatatgtt tattgtggta ctattcaca tagcaaagac ttggaattaa  
5581 cccaaatgtc caacaatgat agactagatt aagaaaatgt ggcacatata cactatggaa  
5641 tactttgcag ccataaaaaa ggatgagttc atgtcctttg tagggacatg gatgaagctg  
5701 gaaaccatca tctcggcaa actatcgcaa ggtcaaaaaa ccaaacaccg catgttctca  
5761 ctcataagggt gtaactgaac aatgagaaca catggtcaca ggaaggggag catcacgcac  
5821 tggggcctgt tgtggggtgg ggggagtggt cagggtatagc attaggagac atacctaatg  
5881 ttaaatgacg atttaattggg tgcagcacac caacatggca catgtatata tatgtaacaa  
5941 acccacacgt tgtgcacatg tactctaaaa cttaaagtat aattaaaata aataaataaa  
6001 gtaaaaaaga aatcctaagg atactcaaat tgttgtttag gtgaagatgg atgatgcctt  
6061 ctttgaatca tcagctacca ccgacagagt gaagttagat ggaatagtg gcacaatctc  
6121 attcatccta ctctatgtag cctaattgggt ccagaattta tcatcactat tttacactgg  
6181 aaaaaagatg agattatgag ggtcaggga ggtttgagt tttgtctta acttcaccac  
6241 taattaagaa tgtgatcttg ggtgaagccac ttttaacctt gtaaatgtca aatttcttat  
6301 cagtaaaatg tgactatata agacaataaa tttgaaaata ctttgcaaaa ttgaaagtac  
6361 catggaaata attcttcaat cccaaaaggt tatgaacatt attaaaattt gccacatgga  
6421 agagcacaca ccacagagac ataactgtga tcataaacag atttacaataa gtggtgtttc  
6481 attatggagg gccatagggc tgataaagac aaatgcacat ccaagctatg tccgagctca  
6541 ttcagatttt tacaggaaac acagagcttc tagctgaatt atctctggat ggtgtggaaa  
6601 ttgtccaaca cgttcctaatt ttcaaagaaa cagaactgaa tcttgaaaac ccaagaggcc  
6661 tttacagaaa ctgacaagag atgaattaat atagggtatca agctacagac caaattaaag  
6721 ttttacaata ctttgaaaga gggtcagaaa gaagaaactt atgggaagca gagtcttgga  
6781 aagttagctt tgatggagtg acaatatgtg caacacagtg agcaatctct taggtaggca  
6841 gcttcaggga tgggggttgc cctttgaaag gacttgggac actcttgagt ctaaggagct  
6901 aagtcacaaa caatgctaag caactaaaaa tagcttcttg ttttaatagta aaattctgca  
6961 tagtaaaagg agaagcaggg ggtatgacac acgtggtagt tagcagctca ctagtactt  
7021 tactgccaca accagaaaag ccagctgagt tgtcagacgt gagaaagcga aagtatgtca  
7081 cagcgaatgt agcttttcca cacgtatttc aagaaagaaa tgaaaaaggc caactctat  
7141 aatgggtgct actgtgcatt aacagagata aactaggggt ctaagaatc agttttctac  
7201 aggttcccag aagtatagcc atatatgcc ccattctcta atggaaatag ccagagaaat  
7261 agaaatatca agactggaga acatcaaata cctcattgga aaagcccca cataggaaaa  
7321 tgtgtgggct tgaattcttc cattctggaa gggtaaaggc ctgagttagt atgctgggat  
7381 tagacactga aactctttag agaagcaaaa caagtataat aaagctgtac tttattatat  
7441 taaaataata acacacagac taccaaatag cctgccctt ataacagcgt taatgtgatt  
7501 ttgatctgaa atgtatagag acattttgca ttttttcggt ataaaaagtt catgagattt  
7561 ggcctaatac tggacctttt cttcattttt ttttctactt gagggactat aatctttatt  
7621 tttaaatttg ttttatattc tccgaacatt acctaacgca tagaaaactc ttttgaacc  
7681 atttttctct gttctttgta aaatattaca tttgactgtt ccttagactg ctttaatcat  
7741 tcctgcctat gcaccctcct caaaatccag tttaaattaa ttgttcctta ttcaagattc  
7801 cttatatcca cctcccttgg ggcagcaatc acctatcacc caggactaca cttgtgtatg  
7861 tacatatctt ccttattaca aatcaggttc tttgaaaaaa tacaattggg aagagagtgg  
7921 atttttggag tcagtacatt ctcttttcaa atccttcttc tgccccttac tggcaataag  
7981 ggctgagtga cctagagcaa attacttaac ttctctgagc ctcagttttc taatctgcaa  
8041 aataggagcc atcacttcac aagtctgtaa gacttatatt agactaagtg cctgctgtga  
8101 cactgttctc ttttctctct ttctatatac ctgaaggcat tataggtgct agatgtctgt  
8161 ttaaagacca gacaatattg tcttaaaaaa acaaacaaaa acacagacaa taccatcttt  
8221 aaaaaaaaaa aaaagtcag gtaagaaata aataaggcca tagaatggaa gctttacaag  
8281 gactctctgt gagacaggat ctctcaagt gtccccaggt taaattagaa gtatatatcc  
8341 gtacaattgt tcagccagtt tgtgactgt actgaggatg aatgaacacc tatcctaata  
8401 atcctagtct tctgactaaa aacaagatca tatttcataa cgattattgt tacattcata  
8461 gtgtcccagg tgatttagag gataaataaa aatccattaa agaggtaaag acataaaaaac  
8521 gagaaacatg gactgtttaa cacataacac atacaaagtc tattataaaa ctagcatcag

8581 tatccgaa tgcaaacctt tttctgagta ttttaacaatc gcaaccttta aaaaatgtac  
8641 aatagacatt aagagactta aacagatata taatcatttt aaattaaaat agcgtaaag  
8701 agtacctcaa gctcaataag cattttaagt attctaattct tagtatttct ctgctgaca  
8761 tgtaagaagc aatctatctt attgtatgca attagctcat tgtgtggata aaaaggtaaa  
8821 accattctga aacaggaaac caatacactt cctgtttaat caacaaatct aaacatttat  
8881 tcttttctac tgtttactct tgctgtgtgc caccacaata tgctattcac atgttcagtg  
8941 tagttttatg acaaagaaaa ttttctgagt tacttttgta tccccacccc cttaaagaaa  
9001 ggaggaaaaa ctgtttcata cagaaggcgt taattgcatg aattagagct atcacctaag  
9061 tgtgggctaa tgtaacaaaag agggatttca cctacatcca ttcagtcagt ctttgggggt  
9121 ttaaagaaat tccaaagagt catcagaaga ggaaaaatga aggtaatgtt ttttcagaca  
9181 ggtaaaagtct tggaaaatat gtgtaatatg taaaacattt tgacaccccc ataattttt  
9241 tccagaatta acagtataaa ttgcatctct tgttcaagag ttccttatca ctctctttaa  
9301 tcaactactca cagtaacctc aactcctgcc acaatgtac

## (2) INFORMATION FOR SEQ ID NO:2530:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5701 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2530:

1 ttaatcaaca aatctaaaca tttattcttt tcatctgttt actcttgtct ttgttcacca  
61 caatatgcta ttcacatgtt cagtgtagtt ttatgacaaa gaaaattttc tgagttactt  
121 ttgtatcccc acccccttaa agaaaggagg aaaaactgtt tcatacagaa ggcgttaatt  
181 gcatgaatta gagctatcac ctaagtgtgg gctaattgaa caaaggaggga ttccacctac  
241 atccattcag tcagtccttg ggggtttaa gaattccaaa gagtcatcag aaggaggaaa  
301 atgaaggtaa tgttttttca gacaggtaa gtctttgaaa atatgtgtaa tatgtaaaac  
361 attttgacac ccccataata tttttccaga attaacagta taaattgcac ctcttgttca  
421 agagttccct atcactctct ttaactacta ctcacagtaa cctcaactcc tgccacaatg  
481 tacaggatgc aactcctgtc ttgcattgca ctaagtcttg cacttgtcac aaacagtga  
541 cctacttcaa gttctacaaa gaaacacag ctacaactgg agcatttact gctggattta  
601 cagatgattt tgaatggaat taatgtaagt atatttcctt tcttactaaa attattacat  
661 ttagtaattc agctggagat catttcttaa taacaatgca ttatactttc ttagaattac  
721 aagaatccca aactcaccag gatgtcaca ttttaagttt acatgcccaa gaaggtaaagt  
781 acaatatttt atgttcaatt tctgttttaa taaaattcaa agtaatatga aaatttgac  
841 agatgggact aatagcagct catctgaggt aaagagtaac ttttaattgt tttttgaaa  
901 acccaagttt gataatgaag cctctattaa aacagtttta cctatatatt taatatatat  
961 ttgtgtgttg gtgggggttg gaagaaaaca taaaaataat attctcacct ttatcgataa  
1021 gacaattcta acaaaaaatg ttcatttatg gtttcattta aaaatgtaaa actctaaaat  
1081 atttgattat gtcattttag tatgtaaaat accaaaatct atttccaagg agcccacttt  
1141 taaaaatctt tcttgtttt aggaaagggt tctaagttag aggcagcata acactaatag  
1201 cacagagtct ggggccagat atctgaagtg aaatctcagc tctgccatgt cctagctttc  
1261 atgatctttg gcaaaattacc tactctgttt gtgattcagt ttcattgcta cttaaatgaa  
1321 taactgtata tacttaatat ggctttgtga gaattagtaa gttaaatgta aagcactcag  
1381 aaccgtgtct ggcataaggt aaataccata caagcattag ctattattag tagtattaaa  
1441 gataaaattt tcaactgagaa atacaaagta aaattttgga ctttatcttt ttaccaatag  
1501 aacttgagat ttataatgct atatgactta ttttccaaga taaaagctt cattaggttg  
1561 tttttggatt cagatagagc ataagcataa tcattccaagc tcctaggcta cattaggtgt  
1621 gtaagctac ctatgagttg tgccagttaa gagagaatga acaaaatctg gtgccagaaa  
1681 gagcttgtgc caggtggaat ccaagccag aaaaataatg gatttaaggg gacacagatg  
1741 caatcccatt gactcaaatt ctattaatc aagagaaatc tgcttctaac taccctctg  
1801 aaagatgtaa aggagacagc ttacagatgt tactctagtt taatcagagc cacataatgc  
1861 aactccagca acataaagat actagatgct gttttctgaa gaaaatttct ccacattggt  
1921 catgccaaaa acttaaacc gaattttagt aattttagt ggtgaattga aagcgcaata  
1981 gatggacata tcaggggatt ggtattgtct tgacctacct tccccactaa agagtgttag  
2041 aaagatgaga ttatgtgcat aatttagggg gtggtagaat tcatggaaat ctaagtttga  
2101 aaccaaaagt aatgataaac tctattcatt tgttcattta accctcattg cacatttaca  
2161 aaagatttta gaaactaata aaaatatttg attccaagga tgctatgta atgctataat  
2221 gagaaagaaa tgaatctaa ttctggctct acctacttat gtggtcaaat tctgagattt  
2281 agtgtgttta ttataaagt ggagatgata cttcactgcc tacttcaaaa gatgactgtg  
2341 agaagtaaat gggcctattt tggagaaaat tcttttaaat tgtaatatat catagaaata  
2401 tgaaatatta tatataatat agaatcaaga ggctgttcca aaagtcctcc caaagtatta  
2461 taatctttta tttcactggg acaaacattt ttaaaatgca tcttaatgta gtgattgtag  
2521 aaaagtaaaa ttaagacat atttaaaaaat gtgtcttct caaggctata ttgagagcca  
2581 ctactacatg attattgtta cctagtgtaa aatgttggga ttgtgataga tggcattcaa  
2641 gagttccttc tctctcaaca ttctgtgatt cttactctt agactatcaa atattataat  
2701 catagaatgt gatttttatg cttccacatt ctaactcatc tggttctaag gattttctat  
2761 gcagattgga aaagtaatca gcctgcatct gtgataggca cttacgatgc agaaagtcta  
2821 acattttgca aagccaaatt aagctaaaac cagttagtca actatcactt aacgctagtc

2881 atagggtactt gagccctagt tttccagtt ttataatgta aactctactg gtccattctt  
2941 tacagtgcaca ttgagaacag agagaatggt aaaaactaca tactgtactt ccaaataaaa  
3001 taaattggaa attaatctt gattctgacc tctatgtaaa ctgagctgat gataattatt  
3061 attctaggcc acagaactga aacatcttca gtgtctagaa gaagaactca aacctctgga  
3121 ggaagtgcata aatttagctc aaagcaaaaa ctttacttta agaccaggg acttaactag  
3181 caatatcaac gtaatagttc tggaactaaa ggtaaggcat tactttattt gctctcctgg  
3241 aaataaaaaa aaaaaagtc ggggaaaaag taccacattt taaagtgaac taacattttt  
3301 ggtatttgta agtaccatc gcatgtaatt agcctacatt ttaagtacac tgtgaacatg  
3361 aatcatttct aatgttaaat gattaactgg ggagtataag ctactgagtt tgcacctacc  
3421 atctactaat ggacaagcct catcccaaac tccatcacct ttcattataa cacaaaactg  
3481 ggagtgcagag aagggtactga gttgagtttc acagaagca ggcagatttt attatatatt  
3541 tttcgattct tcagatcatt tactgaaata gccaaactg attacctgaa aggcttttca  
3601 aatgggtgtt ccttatcatt tgatggaagg actaccata agagatttgt cttaaaaaaa  
3661 aaaactggag ccattaaaat ggccagtggg ctaaaacaa acaactctt tttagaggca  
3721 tccccacttt cagaacttta agtattttta aatgcacagg aagcataaaa tatgcaaggg  
3781 actcagtgta tgaataagag attcactttt gtctttttat atcccgcttc ctaaggata  
3841 aaattcatga gttaataggt atcctaata agcagcataa gtatagtagt aaaagacatt  
3901 cctaaaagta actccagttg tgtccaaatg aatcacttat tagtggactg tttcagttga  
3961 attaaaaaaa tacattgaga tcaatgtcat ctgacattg acagattcag ttccttatct  
4021 atggcaagag ttttactcta aaataattaa catcagaaaa ctcattctta actcttgata  
4081 caaatttaag acaaaacat gcaaaaatct gaaaactgtg tttcaaaagc caaacacttt  
4141 ttaaaataaa aaatcccaag atatgacaat atttaacaa ttatgcttaa gaggatacag  
4201 aacactgcaa cagtttttta aaagagaata cttattttaa gggaacactc tatctcacct  
4261 gcttttgctc ccagggtagg aatcacttca aatttgaaaa gctctctttt aaatctcact  
4321 atatatcaaa atatttctc cttagcttat caactagagg aagcgttaa atagctcctt  
4381 tcagcagaga agcctaattt ctaaaagcc agtccacaga acaaaatttc taatgtttaa  
4441 acttttaaaa gttggcaaat tcacctgcat tgatactatg atgggtagg gataggtgta  
4501 agtattttaga agatgttctt cacacaatt tatcccaaac ggaagcatgt cctagcttac  
4561 tctagttagt tctgttctg ctttgggaa aatataagga gattcactta agtagaaaaa  
4621 taggagactc taatcaagat ttagaaaaa agaaagtata atgtgcata caattcatac  
4681 atttaactta cacaaatata ggtgtacatt cagaggaaaa gcgatcaagt ttatttcaca  
4741 tccagcattt aatatttgc tagatctatt tttattttaa tctttatttg cacccaattt  
4801 agggaaaaaa ttttgtgtt cattgactga attaacaat gaggaaaatc tcagcttctg  
4861 tgttactatc atttggatc ataacaaaat atgtaatttt ggcattcatt ttgatcattt  
4921 caagaaaatg cgaataatta atatgttgg taagcttgaa aataaaggca acaggcctat  
4981 aagacttcaa ttgggaataa ctgtatataa ggtaactac tctgtacttt aaaaaattaa  
5041 catttttctt ttataggat ctgaaacaac attcatgtgt gaatatgctg atgagacagc  
5101 aaccattgta gaatttctga acagatggat taccttttgt caaagcatca tctcaacact  
5161 gacttgataa ttaagtgtt cccacttaaa acatatcagg ctttctattt atttaaatat  
5221 ttaaatttta tatttattgt tgaatgtatg gtttgctacc tattgttaact attattctta  
5281 atcttaaaac tataaatatg gatcttttat gattcttttt gtgccctagg ggccttaaaa  
5341 tggtttcact ttttatccc aaatatttta ttattatgtt gaattgttaa tatagtgtca  
5401 tgtagattgg ttagtaaaac ttttaataa atttgataaa tataaacaag cctggatatt  
5461 tgttattttg gaaacagcac agagtaagca tttaaatatt tcttagttac ttgtgtgaa  
5521 tgtaggatgg ttaaaatgct tacaaaagtc actctttctc tgaagaaata tgtagaacag  
5581 agatgtagac ttctcaaaag cccttgcttt gtcccttcaa gggctgatca gacccttagt  
5641 tctggcatct cttagcagat tatattttcc ttcttcttaa aatgccaaac acaaacactc  
5701 ttgaaactct tcatagattt ggtgtggcta tgaattc

## (2) INFORMATION FOR SEQ ID NO:2531:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5521 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2531:

1 cgaattcccc tatcacctaa gtgtgggcta atgtaacaaa gagggatttc acctacatcc  
61 attcagtcag tctttggggg tttaaagaaa ttccaaagag tcatcagaag aggaaaaatg  
121 aaggtaatgt ttttccagac tggtaaagtc tttgaaaata tgtgtaatat gtaaaacatt  
181 ttgacacccc cataatattt ttccagaatt aacagtataa attgcatctc ttgttcaaga  
241 gtccctatc actctttaat cactactcac agtaacctca actcctgcca caatgtacag  
301 gatgcaactc ctgtcttgca ttgactaag tcttgactt gtcacaaaca gtgcacctac  
361 ttcaagttct acaaaagaaa cacagctaca actggagcat ttactgctgg atttacagat  
421 gattttgaat ggaattaatg taagtataat tcctttctta ctaaaattat tacatttagt  
481 aatctagctg gagatcattt cttaataaca atgcattata ctttcttaga attacaagaa  
541 tcccaaacctc accaggatgc tcacatttaa gttttacatg cccaagaagg taagtacaat  
601 attttatgtt caatttctgt ttaataaaaa ttcaaagtaa tatgaaaatt tgcacagatg  
661 ggactaatag cagctcatct gaggtaaaaga gtaactttaa tttgtttttt tgaaaaccca  
721 agtttgataa tgaagcctct attaaaacag ttttacctat atttttaata tatatttgtg

781 tgttgggagg ggtgggagaa aacataaaaa taatattctc tctttatc gataagacaa  
841 ttctaaacaa aaatgttcat ttatggtttc atttaaaaat gtaaaactct aaaatatttg  
901 attatgtcat ttttagtatgt aaaataccaa aatctatttc caaggagccc acttttaaaa  
961 atcttttctt gttttaggaa aggttttctaa gtgagaggca gcataacact aatagcacag  
1021 agtctggggc cagatatctg aagtgaatc tcagctctgc catgtcctag ctttcatgat  
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1321 agatttataa tgctatatga cttattttcc aagattaaaa gcttcattag gttgtttttg  
1381 gattcagata gagcataagc ataatacctc aagctcctag gctacattag gtgtgtaaa  
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4021 agaacactgc aacagttttt taaaagagaa tacttattta aagggaacac tctatctcac  
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4321 tgtaagtatt tatgaagatg ttcatcaca caaatttacc caaacaggaa gcatgtccta  
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4681 tcagcttctg tgttactatc atttggatc ataacaaaat acgcaatttt ggcattcatt  
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4801 acaggcctat aagacttcaa ttgggaataa ctgtatataa ggtaaacctac tctgtacttt

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4861 aaaaaattaa catttttctt ttatagggat ctgaaacaac attcatgtgt gaatatgctg
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5401 atatgtagaa cagagatgta gacttctcaa aagcccttgc tttgtccctt caagggctga
5461 tcagaccctt agttctggca tctcttagca gatttatatt tccctcttct taaaatgcca
5521 aacacaaaca ctctgaaac tcttcataga tttgtgtgg c

```

## (2) INFORMATION FOR SEQ ID NO:2532:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 841 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2532:

```

1 ccccataata ttttccaga attaacagta taaattgcat ctcttggtca agagttccct
61 atcactctct ttaataacta ctcacagtaa cctcaactcc tgccacaatg tacaggatgc
121 aactcctgtc ttgcattgca ctaagtcttg cacttgctac aaacagtgc cctacttcaa
181 gttctacaaa gaaaacacag ctacaactgg agcatttact gctggattta cagatgattt
241 tgaattggaat taataattac aagaatccca aactcaccag gatgctcaca ttaagtttt
301 acatgcccaa gaaggccaca gaactgaaac atcttcagtg tctagaagaa gaactcaaac
361 ctctggagga agtgctaaat ttagctcaaa gcaaaaactt tcacttaaga cccagggact
421 taatcagcaa tatcaacgta atagtcttg aactaaagg atctgaaaca acattcatgt
481 gtgaatatgc tgatgagaca gcaaccattg tagaatttct gaacagatgg attacctttt
541 gtcaaaagcat catctcaaca ctgacttgat aattaagtgc ttcccactta aaacatatca
601 ggccttctat ttattttaa atttaaaatt tatatttatt gttgaatgta tggtttgcta
661 cctattgtaa ctattattct taatcttaaa actataaata tggatctttt atgattcttt
721 ttgtaagccc taggggctct aaaatgggtt cacttattta tcccaaaata ttattatta
781 tgttgaatgt taaatatagt atctatgtag attggttagt aaaactattt aataaatttg
841 ataa

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## (2) INFORMATION FOR SEQ ID NO:2533:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22265 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2533:

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1 cttcaactca ataagcattt taagtattct aatcttagta tttctctagc tgacatgtaa
61 gaagcaatct atcttattgt atgcaattag ctcatgtgt ggataaaaag gtaaaaccat
121 tctgaaacag gaaaccaata cacttctgt ttaatcaaca aatctaaaca tttattcttt
181 tcatctgttt actcttgctc ttgtccacca caatatgcta ttcacatgtt cagtgtagtt
241 ttatgacaaa gaaaattttc tgagttactt ttgtatcccc acccccttaa agaaaggagg
301 aaaaactggt tcatacagaa ggcgttaatt gcatgaatta gagctatcac ctaagtgttg
361 gctaattgaa caaagaggga tttcacctac atccattcag tcagcttttg ggggtttaa
421 gaaattccaa agagtcatca gaagaggaaa aatgaaggta atgttttttc agacaggtaa
481 agtctttgaa aatatgtgta atagttaaaa cattttgaca ccccataat attttccag
541 aattaacagt ataaattgca tctcttggtc aagagtccc tatcactctc tttaactact
601 actcacagta acctcaactc ctgccacaat gtacaggatg caactcctgt ctgcatgtc
661 actaagtctt gcacttgta caaacagtgc acctacttca agttctacaa agaaaacaca
721 gctacaactg gagcatttac ttctggattt acagatgatt ttgaatggaa ttaatgtaag
781 tatatttctt ttcttactaa aattattaca tttagtaatc tagctggaga tcatttctta
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421 ggttctccca gcatgcagct tgagatctga gaatggacag actgcctcct caagtgggtc
481 cctgaccccc gagtaaccta actgggaggc accccaagta ggggcagact gacacctcac
541 atggctgggt actcctctga gaaaaaactt ccagagggaac gatcaggcag caacatttgc

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601 tgttcaaa tatccactgt tctgcagcct cctgtgctaa taccaggga aatgggtctg  
661 gagaggacct ccagcaagct ccaacagacc tacagctgag ggtcctgact gttagaagga  
721 aaactaacia acagaaagga catccacacc aaaaccctat ctgtacggca ccatcatcaa  
781 agaccaaaag tagataaaac cacaagatg gggaaaaaaa cacagcagaa aaactggtaa  
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5401 atatgtagaa cagagatgta gacttctcaa aagcccttgc tttgtccttt caagggtctga  
5461 tcagaccctt agttctggca tctcttagca gattatattt tcttcttct taaaatgcc  
5521 aacacaaaca ctcttgaac tcttcataga tttggtgtgg c  
1 ccccataata tttttccaga attaacagta taaattgcat ctcttgttca agagttccct  
61 atcactctct ttaatcacta ctcacagtaa cctcaactcc tgccacaatg tacaggatgc  
121 aactcctgtc ttgcattgca ctaagtcttg cacttgtcac aaacagtga cctacttcaa  
181 gttctacaaa gaaaacacag ctacaactgg agcatttact gctggattta cagatgattt  
241 tgaatggaat taataattac aagaatccca aactcaccag gatgctcaca ttttaagttt

301 acatgcccaa gaaggccaca gaactgaac atcttcagtg tctagaagaa gaactcaaac  
 361 ctctggagga agtgctaaat ttagctcaaa gcaaaaactt tcacttaaga cccagggact  
 421 taatcagcaa tatcaacgta atagtcttg aactaaaggg atctgaaaca acattcatgt  
 481 gtgaatatgc tgaatgagca gcaaccattg tagaatttct gaacagatgg attacctttt  
 541 gtcaaagcat catctcaaca ctgacttgat aattaagtgc ttcccactta aaacatatca  
 601 ggccttctat ttatttaaat atttaaatat tatatttatt gttgaatgta tggtttgcta  
 661 cctattgtaa ctattattct taatcttaaa actataaata tggatctttt atgattcttt  
 721 ttgtaagccc taggggctct aaaatggttt cacttattta tcccaaaata ttattatta  
 781 tgttgaatgt caaatatagt atctatgtag attgggtagt aaaactattt aataaatttg  
 841 ataa

## (2) INFORMATION FOR SEQ ID NO:2534:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 901 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2534:

1 aggccagtt gaaaccagg agttgctctc ctttctctc ccttgacctc acccctcaga  
 61 ccattgccaat tctgcctcct aaacctccca ggccagcccc tccccagct cccagtgcga  
 121 gtgtcctcag gtacctgagc tcagctctcg gtgctaccag agggactgca gggctgcaga  
 181 ggctgagtc caccagcgag gaacagccat gccactgcta gcagaccagt aagagaatgg  
 241 ccacctgggg cctgagcgcc ctgcccctc caccagaaac aaagtgtcaa ggagaagctg  
 301 cccgaagccc atgggacaaa ccactgggga ctggaacacc agtaattctg tattgggaag  
 361 cggcaccaag agatgtgctt ctgagagcct gaggtgaac gtggatgttt agcagcgtga  
 421 ccggctacca gacaaactct catctgttcc agtggcctc tggccacca ccaggacca  
 481 gcagggcggg cagcagagg ccagggtagt ccagggtgat gcagatgaga tcccactggg  
 541 caggaggcct cagtgaagtg agtcaggctt ccccttctc ccacaggggt cctctcacct  
 601 gctgcatgc ttcccctctc tcctctctc tgacaagatg aagtataacc gtttaagtaa  
 661 tcttttttct tgtttactg atcttgagta ctgaaagtc atggatgaat aattacgtct  
 721 gtggttttct atggaggttc catgtcagat aaagatcctt ccgacgctg cccacacca  
 781 ccacctcccc cgccttgccc ggggttgagg gcaccttgct gctgcacata taaggcgagg  
 841 gctgttgcca actcttcaga gcccacgaa ggaccagaac aagacagagt gcctcctgcc  
 901 gatccaaaca tgagccgc

## (2) INFORMATION FOR SEQ ID NO:2535:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 421 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2535:

1 gccaccacc aggaccaagc agggcgggca gcagagggc agggtagtcc aggtgatggc  
 61 agatgagatc cactgggca ggaggcctca gtgagctgag tcaggcttcc ccttctgccc  
 121 acaggggtcc tctcacctgc tgccatgctt cccatctctc atctccttg acaagatgaa  
 181 gtgataccgt ttaagtaac tttttcttg ttctactgat cttgagtact agaaagtcat  
 241 ggatgaataa ttacgtctgt ggtttctat ggaggttcca tgcagataa agatccttcc  
 301 gacgcctgcc ccacaccacc acctcccccc gccttgcccg gggttggtgg caccttgctg  
 361 ctgcacatat aaggcgagg gttgttgcca actcttcaga gcccacgaa ggaccagaac  
 421 aagacagagt gcctcctgcc gatccaaaca tg

## (2) INFORMATION FOR SEQ ID NO:2536:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2701 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2536:

1 gatccaggag accagtctcc tagtaccagg tctgcttgcc taaacttgga gtataagagc  
 61 catagacact gtctcttcga tcagtccttg cccccacccc ctgctgttgc acccttatct  
 121 ttcaccctat tgctcctgca ttgaagacag aagcaccagc ttcccctgc ctcagcataa  
 181 cttgctagcc ttcatttctt cgtgctggtc acatcacacc acaaccgac ccaaaccctg  
 241 gtttctctac catgcccctg ctcccctgca cccaggtct gtcacactca tcttctacca  
 301 aaactccagc tttgtgctgt ggcctgtcaa cctgtcccat ggaaaagggg gccaccccat  
 361 ccttcaggga ctgtcccctg gctctccaca ctcttggtt tgccacttct tctctagctg  
 421 tggtttctca ggtcctttga gaacttccca taactgtccc tgtttcctc ccacctctgt  
 481 aggcctgagc tgcaaacag ctcactctcc acccaggtc cagggccgac tgggatttag  
 541 atccctcaat atggctttcc ttcaggaggt agttctctt tctcctctg cctcccggc  
 601 tcaaacttgt ccattgccac tgctacaccg tctgcagct cccagtaact aacactattc

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661 tcaaggca cctttgtccc taggtcccta agcctaatta tctgttat cagaaggatg
721 gcctagtgtt tgcagtcata tctccatcaa gggttctgtc ctctagatgt gggccttagc
781 gcattgcctt actgcactga gactagacca gtgaaggagt gagctgaact ccatatccac
841 ctgcaaggaa taagggtcaa tgggaaggct gcctagaggg agagggagct ctagctacca
901 ggggccagag gactagccca cccatggacg ttaaccatg tgccagaatg cctaccatgt
961 tcaagtttgc cccagtgcac ctggtggccc actaatagt gtggcccaca gtcaggggca
1021 gatttgtaca agggatggt ggaagaggtt ccagtgcaca gaaaccccaa gctggctcgg
1081 agccaggcta cttctcccca ccactgttt ccactcggtc catctctatg acaaaggaa
1141 aagatggcct ttgaataagc agtctttctt cccatgtcga taattttgag tactagaaaa
1201 cgatgaataa gtctgtggtt tgctatggag gttccatgtc agataaagct gcttctgatg
1261 cctgcccttc ccccatgcc ctgcctgggg ccgccccgc cctctcgtat gaatatatat
1321 aagggtgaagg ctctgtggc ttcttcagaa ctcttggag gaccagaacg agacaatggt
1381 tcttgccagc tctaccacca gcctcctctg tatgtgtctc ccgtcctga tgctctcca
1441 ccagggactc cagatttcag acaggggctc agatgccac catttactca ggacgttga
1501 ttgcaggact attgccttgg agattttggt gaagctccca gtgagttagt ggctgaggtt
1561 agcctgggca ggctggcttc aacagggtgc tcggaccaat aagcctcatg attcttctt
1621 ttagtatcct caggtatctg gactcaataa tagtgacgac aaagccaatc tgagggttaag
1681 agcctgtctc ttgggcattc ttgggttcca tctgtctcct gcctgggtga ctttagccat
1741 gtcactgcac cctgctttgc ttccgttttc acatctatct cagtggggtt attaaggaaa
1801 tcatcagatg actctctgag cctcagtctg tgccacagcc agctgcaata atgaaagtgt
1861 cattttagga gatacaatgg agagagaact gtgagtgaac cctgccacag gcctctggct
1921 ccactttcag tggggatgcc atgggatgc catggaccag tgaacgagtt gccttctgtg
1981 actgtgtctt ttgcttttct tctcctcca aaactgagct tgtgttctcc acttccacca
2041 gcctaagaca ttaccatttg cagttatttt cccagctcta gttagatata atggttctgt
2101 ttctgtttta ttgtttgca agcgtgtctg gtgtctacgt ttcccctccc tagggacatg
2161 atgaagtctg taggattttc ttctagatat ctagaagttc ttaattaaat taaagcattg
2221 ggggttggga tttagctcag tggtagagtg cttgcctagc aagcgcaagg ccctgagttc
2281 attccccagc tccgaaaaaa agaaaaaaga aaaagaaaaa aaattaaagc attaaccttg
2341 gtgtttggca tcttgggcat aagtatttcc cttggccaac cttctgcctt ttctagagct
2401 tgtctggaga gatagttttc ctttaaaaac agacagatct gcttagagcc ttcacacagt
2461 ccacaggctg ccaggggtta agacctgtg ctcaggagaa acaggccctt gtctgggatg
2521 tgccctagct ttagccccag gataaggaaa ggaccaggag taaggctgtt caaagaaacc
2581 tctaacagca gtcacacctc ccagctctc acctccccag ctctcacctc cccagctctc
2641 acctctcccg ctctcacctc ccagctctc acctctccag ctctcacctc cccagttctc
2701 acctccccag ctctcacctc tccagctctc acctccccag ctctcacct

```

## (2) INFORMATION FOR SEQ ID NO:2537:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 901 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2537:

```

1 cagagcccca cgaaggacca gaacaagaca gagtgcctcc tgccgatcca aacatgagcc
61 gcctgcccgt cctgctcctg ctccaactcc tgggtccgcc cggactccaa gctcccatga
121 cccagacaac gcccttgaag acaagctggg ttaactgtct taacatgatc gatgaaatta
181 taacacactt aaagcagcca cctttgcctt tgctggactt caacaacctc aatggggaag
241 accaagacat tctgatgaa aataaccttc gaaggccaaa cctggaggca ttcaacaggg
301 ctgtcaggag ttacagaaac gcatacagaa ttgagagcat tcttaaaaat actctgccat
361 gtctgcccct ggccacggcc gcacccacgc gacatccaat ccatatcaag gacgtgact
421 ggaatgaatt ccggaggaaa ctgacgttct atctgaaaac ccttgagaat gcgcaggctc
481 aacagacgac tttgagcctc gcgatctttt agtccaacgt ccagctcgtt ctctgggctt
541 tctcaccaca gagcctcggg acatcaaaaa cagcagaact tctgaaacct ctgggtcatc
601 tctcacacat tccaggacca gaagcatttc accttttctt gcggcatcag atgaattggt
661 aattatctaa tttctgaaat gtgcagctcc catttggcct tgtgcggttg tgttctcatt
721 tttatcccat tgagactatt tatttatgta tgatgtatt tatttatata ttgcctggag
781 tgtgaactgt atttatatta gcagaggagc catgtcctgc tgcttctgca aaaaactcag
841 agtgggggtg ggagcatgtt catttgtacc tcgagtttta aactgggttc tagggatgtg
901 tgagaataaa ctgactctg aac

```

## (2) INFORMATION FOR SEQ ID NO:2538:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2538:

```

1 tgtgtaagta agtgcaagct acagagaaaa ccaagggaaga aaaaaattgc cagagatcca
61 ggttaaaaaa aaaaaaagaa aaagaaaaga aaaccaagga agcaatcatc ataaaaagaa

```

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121 ggtgagtggg ttacctctaa gggcgagcag tcacgattag aggacaaata tggggagagt
181 tttggagcgt tggcgatttt tttttgactt aagcatgggt aaatgggtga ttgcttataa
241 ttacttggtta aattagggtta attaggtttt atttacctgt tttatgctct tttctgcatg
301 catttggtct ctattttttt aattaaaaaa taaaataaag taaaactatg tttcttgca
361 ttaaaatact ggaaaaccaa agagaatctg aaaaactttt agaataaaga gagtttgga
421 agacggcaag aaccttgct ttttccactg ggcctttctt cctcccaccc tgagggtgct
481 ccattggaaaa tgcaaatcta cttaactgac tttcgcaaat gtcaaatgta gagtacgaat
541 tcaaggggga gcctggggct gtgccatctc ctgctgtgag ctacagtttt ccagcctcta
601 gagccatctt aacaagggtc ctgctgggtg tctactaccc cagtattgtc tccaaccctt
661 gcccaggcct cctagtgtga gagaggatat agacatggcc tctccatgga aacctccagg
721 gctggtatga caccttaaca aacaaaaagg gaggttgcc ggtacagcg agtcccgcag
781 gaggataggt gttgcttct aggtggtagg gaggtgaga gggccatcca gagtagggac
841 cacgaactgg ggtctcaaca tgaagagtcg ttcacatgat ct

```

## (2) INFORMATION FOR SEQ ID NO:2539:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2581 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2539:

```

1 agggccagtt gaaaccaggg agttgctctc ctttctcctc ccttgacctc acccctcaga
61 ccatgccaat tctgctcctt aaacctccca ggccagcccc tccccagct cccagtgcaga
121 gtgtcctcag gtacctgagc tcagctctcg gtgctaccag agggactgca ggggtgcaga
181 ggctgagtcc cacacgcagg gaacagccat gccactgcta gcagaccagt aagagaatgg
241 ccacctgggg cctgagcgcc ctgcggccatc caccagaaac aaagtgtcaa ggagaagctg
301 cccgaagccc atgggacaaa ccactgggga ctggaacacc agtaattctg tattgggaag
361 cggcaccaag agatgtgctt ctgagagcct gaggtgaac gtggatgttt agcagcgtga
421 ccggctacca gacaaactct catctgttcc agtggcctcc tggccacca ccaggacca
481 gcaggcgagg cagcagaggg ccagggtagt ccagggtatg gcagatgaga tcccactggg
541 caggaggcct cagtgaagct agtcaggctt ccccttctg ccacaggggt cctctcacct
601 gctgccatgc ttcccatctc tcatcctcct tgacaagatg aagtgatacc gtttaagtaa
661 tcttttttct tgtttcactg atcttgagta ctgaaaagtc atggatgaat aattacgtct
721 gtggttttct atggaggttc catgtcagat aaagatcctt ccgacgcctg cccacacca
781 ccacctcccc cgccttgccc ggggttggtg gcaccttgct gctgcacata taaggcggga
841 gctgttgcca actcttcaga gcccacgaa ggaccagaac aagacagagt gcctcctgcc
901 gatccaaaca tgagccgccc
1 gcccaccacc aggaccaagg agggcgggca gcagagggcc agggtagtcc aggtgatggc
61 agatgagatc ccactgggca ggaggcctca gtgagctgag tcaggcttcc ccttctctgc
121 acagggggtc tctcacctgc tgccatgctt cccatctctc atcctccttg acaagatgaa
181 gtgataccgt ttaagtaatc ttttttcttg tttcactgat cttgagtact agaaagtcat
241 ggatgaataa ttacgtctgt ggttttctat ggagggtcca tgtcagataa agatccttcc
301 gacgcctgcc ccacaccacc acctcccccc gccttgcccg ggggttggtg caccttgctg
361 ctgcacatat aaggcgggag gttgttgcca actcttcaga gcccacgaa ggaccagaac
421 aagacagagt gcctcctgcc gatccaaaca tg
1 gatccaggag accagtctcc tagtaccagg tctgcttgcc taaacttga gtataagagc
61 catagacact gtctcttcga tcagtccttg cccccacccc ctgctgttgc acccttatct
121 ttcaccctat tgctcctgca ttgaagacag aagcaccagc tttcccctgc ctcagcataa
181 cttgctagcc ttcatttctt cgtgctgggt acatcacacc acaaccgac ccaaaccctg
241 gtttctctac catgcccctg cttccctgca cccaggctt gtccactca tcttctacca
301 aaactccage tttgtgctgt ggctgtcaa cctgtcccat ggaaaagggg gccaccctat
361 ccttcagggg ctgtcccctg gctctccaca ctctggctt tgccacttct tctctagctg
421 tggtttctca ggtcctttga gaacttccca taactgtccc tgttctctt ccacctctgt
481 aggcctgagc tgcaaacacc ctcccactcc acccaggctc cagggccgac tgggatttag
541 atccctcaat atggctttcc ttcaggaggt agttctctt tctcctctt ccctcccggc
601 tcaaacttgt ccatgccacc tgctacaccg tctgcaagt cccagtaact aacactatct
661 tcaaggccca cctttgtccc taggtcccta agcctaatta tctgagttat cagaaggatg
721 gcctagtgtt tgcagtcata tctccatcaa ggggtctgtc ctctagatgt gggccttagc
781 gcattgcctt actgcactga gactagacca gtgaaggagt gagctgaact ccatatccac
841 ctgcaaggaa taagggtcaa tgggaaggct gcctagaggg agaggagct ctagtacca
901 gcggccagag gactagccca cccatggacg ttaaccatg tgccagaatg cctaccatgt
961 tcaagtttgc cccagtgaac ctggtggccc actaatagtg gtggccaca gtcaggggca
1021 gattttgtaca agggatggta ggaagaggtt ccagtgcaca gaaaccccaa gctggctcgg
1081 agccaggcta cttcctccca ccacctgttt cactcgggtc catctctatg acaagggaag
1141 aagatggcct ttgaataagc agtctttctt cccatgtcga taattttgag tactagaaaa
1201 cgatgaataa gtctgtggtt tgctatggag gttccatgtc agataaagct gcttctgatg
1261 cctgcccctt ccccctgccc ctgcccgggg cccgccccgc cctctctgat gaatatatat
1321 aagggtgaag ctctgtggc tcttctcaga ctctttggag gaccagaacg agacaatggt
1381 tcttgccagc tctaccacca gcctcctctg tatgctgtc cgcctctga tgctcttcca

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1441 ccagggtcc cagatttcag acaggggctc agatgcccac catcactca ggacgttgga  
1501 ttgcaggact attgccttgg agatttttgt gaagctccca gtgagtagct ggctgaggtt  
1561 agcctgggca ggctggcttc aacagggtgcc tcggaccaat aagcctcatg attctttctt  
1621 ttagtatcct caggtatctg gactcaataa tagtgacgac aaagccaatc tgagggttaag  
1681 agccctgctc ttggggcatc ttgggttcca tctgtctcct gcctgggtga ctttagccat  
1741 gtcactgcac cctgctttgc ttccgttttc acatctatct cagtgggggtt attaaggaaa  
1801 tcatcagatg actctctgag cctcagtcctg tgccacagcc agctgcaata atgaaagtgt  
1861 catttttagga gatacaatgg agagagaact gtgagtgaac cctgccacag gcctctggct  
1921 ccactttcag tggggatgcc atggggatgc catggaccag tgaacgagtt gcctctgtg  
1981 actgtgtctt ttgcttttct tctcctcca aaactgagct tgtgttctcc acttccacca  
2041 gcctaagaca ttaccatttg cagttatttt cccagctcta gttagatata atggttctgt  
2101 ttggttttta ttgttttga agcgtgctga gtgtctacgt tccccctccc tagggacatg  
2161 atgaagtctg taggattttc ttctagatat ctagaagtcc ttaattaaat taaagcattg  
2221 ggggttggga ttagctcag tggtagagtg cttgcctagc aagcgcaagg ccctgagttc  
2281 attccccagc tccgaaaaaa agaaaaaaga aaaagaaaaa aaattaaagc attaaccttg  
2341 gtgtttggca tcttggcat aagtatttcc cttggccaac cttctgcctt ttctagagct  
2401 tgtctggaga gatattttc ccttaaaaaa agacagatct gcttagagcc ttcacagct  
2461 ccacaggctg ccagggttga agacctggtg ctcaggagaa acaggccctt gtctgggtg  
2521 tgccctagct ttagccccag gataaggaaa ggaccaggag taaggctgtt caaagaaacc  
2581 tctaacagca gtcacacctc cccagctctc acctccccag ctctcacctc cccagctctc  
2641 acctctcccg ctctcacctc cccagctctc acctctccag ctctcacttc cccagttctc  
2701 acctccccag ctctcacctc tccagctctc acctccccag ctctcacct  
1 cagagcccca cgaaggacca gaacaagaca gagtgcctcc tgccgatcca aacatgagcc  
61 gcctgcccgt cctgtcctg ctccaactcc tgggtccgcc cggactccaa gctcccatga  
121 cccagacaac gcccttgaag acaagctggg ttaactgtc taacatgac gatgaaatta  
181 taacacactt aaagcagcca cctttgcctt tgcctggact caacaacctc aatggggaag  
241 accaagacat tctgatgaa aataaccttc gaaggccaaa cctggaggca ttcaacaggg  
301 ctgtcaagag ttacagaac gcatcagcaa ttgagagcat tcttaaaaat ctctgccat  
361 gtctgcccct ggccacggcc gcacccacgc gacatccaat ccatatcaag gacggtgact  
421 ggaatgaatt ccggaggaaa ctgacgttct atctgaaaac ccttgagaat gcgcaggctc  
481 aacagacgac tttgacctc gcgatctttt agtccaacgt ccagctcgtt ctctgggcct  
541 tctcaccaca gagcctcggg acatcaaaaa cagcagaact tctgaaacct ctgggtcatc  
601 tctcacacat tccaggacca gaagcatttc accttttctt gcggcatcag atgaattgtt  
661 aattatctaa tttctgaaat gtgcagctcc catttggcct tgtgagggtg tgttctcatt  
721 tttatcccct tgagactatt ttttatgta tgtatgtatt ttttatttta ttgctggag  
781 tgtgaactgt atttatttta gcagaggagc catgtcctgc tgcctctgca aaaaactcag  
841 agtgggggtg ggagcatgtt catttgtacc tgcagtttta aactggttcc tagggatgtg  
901 tgagaataaa ctgactctg aac  
1 tgtgtaagta agtgaagct acagagaaaa ccaagggaaga aaaaaattgc cagagatcca  
61 ggttaaaaaa aaaaaagaa aaagaaaaa aaaccaagga agcaatcatc ataaaagaca  
121 ggtgagtggg ttacctctaa gggcgagcag tcacgattag aggacaaata tggggagagt  
181 tttggagcgt tggcgatttt tttttgactt aagcatgggtt aaatgggtga ttgcttataa  
241 ttacttggtt aattaggtta attaggtttt atttcatgtt tttatgctct tttctgcatg  
301 catttgctg ctattttttt aattaaaaaa taaaaataag taaaactatg tttcttgac  
361 ttaaaatact ggaataccaa agagaatctg aaaaactttt agaatagaag gaggttggca  
421 agacggcaag aacccttgct tttccactg ggcctttctt cctcccacc tgagggtgct  
481 ccatggaaaa tgcaaatcta cttaactgac tttcgcaaat gtcaaatgta gattacgaat  
541 ttcaagggga gcctggggct gtgccatata ctgctgtgag ctacagtttt ccagcctcta  
601 gagcatctt aacaaggtgc ctgcctggtg tctactacc cagtatgtgc tccaaccctt  
661 gccaggcct ctagtgcta gagaggatat agacatggcc tctccatgga aacctccagg  
721 gctggtatga caccttaaca acaaaaaagg gaggattgcc ggtacagcgg agtcccgcag  
781 gaggataggt gttgccttct aggtggtagg gaggctgaga ggccatcca gaggtaggac  
841 cacgaactgg ggtctcaaca tgaagagtcg ttcacagat ct

## (2) INFORMATION FOR SEQ ID NO:2540:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2540:

1 gcacacggga agatatacaga aacatcctag gatcaggaca cccagatct tctcaactgg  
61 aaccacgaag gctgtttctt ccacacagca ctttgatctc catttaagca ggcacctctg  
121 tctgcgcttc cggagctgcg ttcccagatg tctcctttg gctcacgctg ctctgatcgt  
181 ccctgccctg tctcctgcaa acgaaggaa atccaaaccc accaatcacg aacctaaagga  
241 tgaagcaaaa ggctcagcag ttgacctggg accttaacag aaatgtgacc gatatcgagt  
301 gtgttaaaaa tgccgactat tctatgccgg cagtgaacaa tagctattgc cagtttggag  
361 caatttctct atgtgaagt accaactaca ccgtccgagt ggccaacca ccattctcca  
421 cgtggatcct cttccctgag aacagtgga agccttgggc aggtgcggag aatctgacct

```

481 gctggattca tgacgtggat ttcttgagct gcagctgggc ggtaggcccg ggggcccccg
541 cggacgtcca gtacgacctg tacttgaacg ttgccaacag gcgtcaacag tacgagtgtc
601 ttactataca aacggatgct cagggaaacac gtatcggggtg tcgtttcgtg gacatctctc
661 gactctccag cggttctcaa agttcccaca tcctgggtgcg gggcaggagc gcagccttcg
721 gtatcccctg cacagataag ttgtcgtct tttcacagat tgagatatta actccacca
781 acatgactgc aaagtgtaat aagacacatt cctttatgca ctggaaaatg agaagtcatt
841 tcaatcgcaa atttcgctat gagcttcaga tacaaaagag aatgcagcct gtaatcacag
901 aacaggtcag agacagaacc tccttcacgc tactcaatcc tggaacgtac acagtacaaa
961 taagagcccg ggaagagtg tatgaattct tgagcgctg gagcaccccc cagcgcttcg
1021 agtgcgacca ggaaggaggc gcaaacacac gtgcctggcg gacgtcgctg ctgacgcgc
1081 tggggacgct gctggccctg gtctgtgtct tcgtgatctg cagaaggtat ctggtgatgc
1141 agagactctt tccccgcatc cctcacatga aagaccccat cggtagacgc ttccaaaacg
1201 acaagctggg ggtctgggag gcgggcaag ccggcctgga ggagtgtctg gtgactgaag
1261 tacaggtcgt gcagaaaact tgagactggg gttcagggtg tgtgggggtc tgcctcaatc
1321 tccctggccg ggcagggcg ctgcacagac tggctgtctg acctgcgcac gcagcccagg
1381 aatggacatt cctaacgggt ggtgggcatg ggagatgcct gtgtaatttc gtccgaagct
1441 gccaggaaga agaacagaac

```

## (2) INFORMATION FOR SEQ ID NO:2541:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2541:

```

1 gatcgtagc ttctcctgat aaactaattg cctcacattg tcaactgaaa tcgacaccta
61 ttaatgggtc tcacctcca actgttccc cctctgttct tcctgtagc atgtgccggc
121 aactttgtcc acggacacaa gtgcgatatc accttacagg agatcatcaa aactttgaac
181 agcctcacag agcagaagac tctgtgcacc gagttgaccg taacagacat ctttgcgtgc
241 tccaagaaca caactgagaa ggaacacctc tgcagggctg cgactgtgct ccggcagttc
301 tacagccacc atgagaagga cactcgctgc ctgggtgcga ctgcacagca gtccacagc
361 cacaagcagc tgatccgatt cctgaaacgg ctgcacagga acctctgggg cctggcgggc
421 ttgaattcct gtcctgtgaa ggaagccaac cagagtacgt tggaaaactt cttggaaaag
481 ctaaagacga tcatgagaga gaaatattca aagtgttcga gctgaatatt ttaatttatg
541 agtttttgat agctttattt ttaagtatt tatatattta taactcatca taaaataaag
601 tatatataga atct

```

## (2) INFORMATION FOR SEQ ID NO:2542:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9841 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2542:

```

1 gaattcaata aaaaacaagc agggcgcggtg gtggggcact gactaggagg gctgatttgt
61 aagttggtaa gactgtagct ctttttcccta attagctgag gatgtgttta ggttccattc
121 aaaaagtggg cattcctggc caggcatggt ggctcacacc tgtaatctca gagctttggg
181 agactgaggt aggaggatca cttgagccca ggaatttgag atgagcctag gcaacatagt
241 gagactctta tctctatcaa aaaataaaaa taaaaatgag ccaggcatgg tgcggtggac
301 cagcacctta ctgctagggg ggtgaggtg ggaggatcat tgagcctggg aggttgaggc
361 tgcagtgatc cctgatcaaa cattgcattt cagcctgggt gacagagtga gacctgtct
421 cagaaaaaaa aaaaaaagt cattcctgaa acctcagaat agacctacct tgccaagggc
481 ttccttatgg gtaaggacct tatggacctg ctgggaccca aactaggcct cacctgatac
541 gacctgtcct tctcaaaaca ctaaacttgg gagaacattg tccccagtg ctggggtagg
601 agagtctgcc tgttattctg cctctatgca gagaaggagc cccagatcat ctttccatg
661 acaggacagt ttccaagatg ccacctgtac ttggaagaag ccagggtaaa atacttttca
721 agtaaaaactt tcttgatatt actctatctt tccccaggag gactgcatta caacaaattc
781 ggacacctgt ggcctctccc ttctatgcaa agcaaaaagc cagcagcagc cccaagctga
841 taagattaat ctaaagagca aattatgggt taatttcccta tgcagaaact ttgtagttaa
901 ttttttaaaa aggtttcatt ttctatttgg tctgatttca caggaacatt ttacctgttt
961 gtgaggcatt ttttctcctg gaagagaggt gctgattggc cccaagtgc tgacaatctg
1021 gtgtaacgaa aatttccaat gtaaacatcat tttccctcgg tttcagcaat tttaaatcta
1081 tatatagaga tatctttgtc agcattgcat cgtagcttc tcctgataaa ctaattgcct
1141 cacattgtca ctgcaaatcg acacctatta atgggtctca cctcccaact gcttccccct
1201 ctgttcttcc tgctagcatg tgccggcaac tttgtccacg gacacaagtg cgatatcacc
1261 ttacaggaga tcatcaaaac tttgaacagc ctacacagagc agaaggtgag tacctatctg
1321 gcaccatctc tccagatgtt ctggtgatgc tctcagtatt tctaggcatg aaaacgttaa
1381 cagctgctag agaagttgga actggtggtt ggtggcagtc cagggcacac agcgaggctt
1441 ctccctgcca ctcttttttc tgagggtttg taggaagttt cctcagttgg agggagttag

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1501 agctgctt caaggacttc tctgtccggt tggagggttaa ctc tct tgctctctca  
1561 tttctgcctg gaccaagact ctgtgaccg agttgaccgt aacagacatc tttgtgcct  
1621 ccaaggtaag aagccgtccc acggtctgtt ttagcaaatg gggagatcca tccccaaatg  
1681 tctgaacaag aaacttgtct aatggaaaac gagcggggccc aaattaactc taagggtgta  
1741 gatgttttca aagaacgaga agtctgatct ttactcttaa gcatgttttg gtctttctgg  
1801 tttcacttga tttagaagac atgtaataga aagcttacat gctgtagtcc tgactcagat  
1861 cctgggtcaaa gaaaagccct cttgggtttt acttagcttt ggcatagtgc ctggaacgta  
1921 ggaggcactc aataaatgcc tgttgaatga gagaattttt ctggcccata catttctgaa  
1981 aaaccaaata ctctcacaga aacagatatt gagatgacag gttgaggag ctttcatatt  
2041 gtctaagaga ctctctatgg caacagaaaa ggtatcgcca gagccctcc tcttcacag  
2101 cctggccacc taacagccct ctggttccgg ggctgccctc cagagctctc agcttgctct  
2161 ggccggccga actccctcc agctcgggtc ggaaccatcc tgctgggcag cgtccagcac  
2221 atccctgctt cgggctgctt gggcacctcg cctctctgcc tctgtgtgtg cctcaccctc  
2281 accctctat ctgtagtggg agggagatag atttgacagc tgatagtga ttttctctga  
2341 caaacacatg actacagcgg tatcaatagt tttgtgcatt tcagtctctg ttttcatgga  
2401 aacacacggc tgagaatgaa agcccaaaag cctcaatttc acagtgtgtc cctaactacc  
2461 tgctttccat gcaaactagg gagatgatag ggccaggagt gaagccctgt gtgttgggca  
2521 gggtcacact ccagcaccca gaccatagaa cagggcccat cctgcttcat gagggaaact  
2581 gctcttcggg ccttttagctg gactatctca tttcattagt tatcccgga gtccgataca  
2641 ggatgagatt ctgaaggga aatacacact ttttttttt ttttgagata gggctctgtt  
2701 ctgtcaccca ggctggagt cagtgggtgc atttcagctc atagcagct ccacctccca  
2761 ggctcaagct atcttctac ctacgctcc caagtagccg ggacgacagg tgtgcaccac  
2821 cagcctggc taatttttgt atttttttgt agagatggag tcttgccatt ttgcccaggc  
2881 ttgtctcgaa ctctctgggt caagcaatcc gtccacctcg gcctctcaa gtgctgggat  
2941 tagccactgc acctgggcaa cagtttatgt gtgtgtgtgt gtgtgtgtgt atatatgtgt  
3001 gtgtgtgtat atatatgtgt gtatgtatat atgtgtatgt atatgtgtgt gtgtgtgtgt  
3061 gtgtgtgtgt gtgtataaaa tctccaagtc catccaaccg agatggctcc tactagaagc  
3121 caagagtcca cggggttgag cactgggtct ctggaggcct gtcggactgc tgagaaggct  
3181 ctaacaaagc caagggaagg gccacctcac tagaagccag gcctggagga aggggtaggg  
3241 ctgagggtcg gaggtaaagc tgctgtggt tttagacca ggctctgcca ctgactagct  
3301 gtgtggctgg ccttcagaca tcttcacagc tctctgcacc tcagtttcca catgtgaaga  
3361 tatgaaagt attctgaagg tgattgcaag gttgattgga atccagctct tgagttagt  
3421 caaagtgtta ttgtgagatg atataaccac gattaaaaagc aagaacaggt gcagagaagc  
3481 gatgattcta agaaggagg gaccgggttg gaaaggatca aaccatccag gatgccagat  
3541 ctggggcaat ccactctggc tgtttctgga agacccctcg gtgcaggcca ggacactgtc  
3601 gccctccgt ccttaactcc cctcttact cagtcctcac tcacctccct ctcacacata  
3661 caaacatctc ctagaataat cccactgcc tgcccttact cttaccctgc tcatctgct  
3721 cccctgaact tcactctctt ggagttcacg atcttactct tctctttt cttccctcg  
3781 aagattcagc actgcttact tacatgttaa gatatttcag aacagtgaat tgttgcatt  
3841 ttcaaaaacc tacaaggtg gtatgcagag gaaaaggtac ttctttgtgt tcccaaagaa  
3901 aacatctttc caaaatccag cctattgatt ttatttctt gggggaacaa gaattttagt  
3961 atctctaagt tgggtagcat tctactcttg gcagttgtcg gaaagaaggc actggtctag  
4021 gtccctgggt tcacaggtaa cacctgtcag ggtgtctatg aagtcaaggc tgtctgagga  
4081 acagcaaaag ggggaagaagc aagctggctg gctgatgaag ggttcttggt gtggaagga  
4141 agttggagcg atttctatt taccaaagag agctaaagtt cataattcta cagagagttc  
4201 cataatgaac ctcaaatacc tctgtttttt gaaggagttt ctcatataca gcactagctg  
4261 actatcctgg gcaggatggg agataatgaa tgcagtgcca atcgggctgg atttatatgg  
4321 tcctagttag gctgggtcaag aaccgagtta gaactctcac agagtcactg cccacagaag  
4381 aaatctccca agtggctgtt tctgacatt cccgggaggc aggcctcctt ctgagtcact  
4441 ccctaagcag ttctgaactg tgaggtcagc caggctgtcc aagtgcactc cctgagccac  
4501 tggcagacac actcagcagc cagagctaga caggcaggtg gtaggagtc agggccacgg  
4561 cagggatgga gtgtcgcccc ctgctgcga taccagagca agtaaaacgt taaggccttg  
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4741 tttttctcta tactatgtgg ccataacagg gtcaaaaatta agtttaattt ccaggctcca  
4801 agccageggt tcagaaaaat ctaccaaggg tttgtggtaa aagaagcaaa gggctgactt  
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5221 tgaactgcat tcctagaatt tagctacat aaataagaga tgaacacaaa gatttctata  
5281 gtttactcac tgccgcttat ttacagaagc aaaaatctgc cacgataggg gcctgacaaa  
5341 tgacagtacc actgtgcaat gcgtttctac gcagctctca atccatggt ctctaatacc  
5401 accgaaggct taggaaatgc ttatgggtata tgtaaaagat aaagaagtta caaacagtat  
5461 cccagttga cccctattt aaaaagtatt tttgaaaagt gtgacgatat ttaccaaata  
5521 attaacgagc aatagttacc tctggctggt gggatgagt aatgtattt tgttgaatat



5581 atgttacctt tatagtaaat atatgttatt ttgatcatca gaaaaaaaaa tatgtaagaa  
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6061 cacagttgct ggcattccaa ggagattctc actccgcatc attggtccaa aaggccctt  
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6301 gggccaaagca gcagagttca ggccaaagga tgtgcaactca tttattcaac aggcattgcag  
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6601 ttctggggag aaggctgctg cgtttgcaat tgggagaggt tgttgacaga ggtttatgtc  
6661 tgtggcaagc agccttctct cagtggaaata cttgaagaca ggtctgtagt tgagcaaat  
6721 cactctcatt tgtctctctg gaaagaagaa atcaagagga aaaatctctc tccatcctc  
6781 caaatggagc tggcacattg ctatctgtgg catttgtctt tccagaacac aactgagaag  
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6961 ctgaaacggc tcgacaggaa cctctggggc ctggcgggct tggtaagctg cactgtattc  
7021 ctggcaagcc ggcgcgctgg ctctggtgg acagcagcct cacttctaaa cactccttag  
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7141 aagttccaca agtgctgggt gtggttctag gtgctgagga cgtgtcacta aagacagca  
7201 gccgagtcct tgttctcatg gaattgtteta atgggagagt tagaaaaaca aactgtaaa  
7261 atgatggcca gcagtgtatc gtgtacaaa gaaaaacata gaaataaaga acataagagt  
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7381 gggagcaggc cacatgacta actagggaga ccattccagg gagaaggagg aggtatgcaa  
7441 aggccttagg atggaatga actaacttcc tgtatttaaa gaccagtagg aaggccagt  
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7561 gattccacca cgagtatgga ggaacacctc gcagagcttt gggcaggaca aagactgtac  
7621 aatctgattt acgtgattta aaagggtcag tctggctact gtgtggtaaa taggtgaaa  
7681 gggggaaagc atagaagcaa gatggcctgt tgggaggcta ccacagtaaa ccaggctaga  
7741 gatgatggtg gcgtggacag aatgaagcaa gatggcctgt tgggaggcta ccacagtaaa  
7801 ccaggctaga gatgatggtg gcgtggacag aatgaagcaa gatggcctgt tgggaggcta  
7861 ccacagtaaa ccaggctaga gatgatggtg gcgtggacaa atggagcagt tgagggtaac  
7921 agatttggga tatgactaaa aataaaacca gaagatttgc tgacagatcg gttgtagggg  
7981 gtaagataca ggggaggaaa agatgacctc tttgttctg cccaaacccc tctggcgatc  
8041 gtcagtactg tttacagaga gatgaaagac tggcggaag gcagggtctg aggttcagca  
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8401 aagccggtga ggacactcaa ggaggggagg ttgactgtgt caaatgtact gaaaggacag  
8461 gtcagggtgag gaccaagaaa ggcctctggg tttggctgat ggaggccatg ggtgaggctg  
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8641 aaggctgcag agaaactgag cccacagctg cagggtggtt atggagttag ggaagctctt  
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8761 gaagaactga agagagcaga aagaggaaga atcattaggg ggcagaagtc cttgtagccc  
8821 agagtggatg ttatctaata tcgagtggag gaattaattg gcttttagagg agaacaagga  
8881 actgtatccc ctctctgggc ctatcacctt gtagacaatg ggataggta tgggatagga  
8941 acttggcaca acacatgttc tctcttttaa ttctctccat tatcttatga agcaggcaag  
9001 taggcaaaaa attgtcccaa ctttacaaaa gaaactgaag cttttataaa ttaagtagta  
9061 catcctaagc aatacaatta ataaatggta gagctgagat tcaaactgaa gcagtggcct  
9121 gggggtagca tctggaatcc ttcccacctt tagggctgct gtgctgcggt gctgctgttt  
9181 aatggcacag agggccagat gactgaatct ctctcagcag tccaggcagt catgcagaag  
9241 gccagtaga gcaccgggca ggtctgagcc agcatcttca agttccaccc tgtgagcaag  
9301 cacttagctg tgacacactt ctcgagagac tggactcccc ccgcgcaac ccacccaaaa  
9361 gcagataggt aatggtatag agtaaccatt tctagaagtg taagtagtat gcacccaaaa  
9421 taggcaaaac ctgctggcct agtgatagag acaactccca gtcaggctag actggaggcc  
9481 ttggttttat aagtgttcag gtgacaagtg ccacagtagg cttgatcaag tagacaggca  
9541 ggcaagacaa atgcttacca atgcaagcta atgaaatgtt tcttttgag aattcctgtc  
9601 ctgtgaagga agccaaccag agtacgttgg aaaacttctt ggaaggcta aagacgatca

9661 tgaga a atattcaaag tgttcgagct gaatatattta at gagt ttttgatagc  
 9721 tttatttttt aagtatttat atatttataa ctcatacataa aataaagtat atataagaatc  
 9781 taacagcaat ggcatttaat gtattggcta tgtttacttg acaaatgaaa ttatgggttg  
 9841 caacttttag ggaaatcaat ttagtttacc aagagactat aaatgctatg gagccaaaac

## (2) INFORMATION FOR SEQ ID NO:2543:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10442 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2543:

1 gatcgttagc ttctcctgat aaactaattg cctcacattg tcaactgcaa tcgacaccta  
 61 ttaatgggtc tcacctccca actgcttccc cctctgttct tctgtctagc atgtgcccgc  
 121 aactttgtcc acggacacaa gtgcgatatc accttacagg agatcatcaa aactttgaac  
 181 agcctcacag agcagaagac tctgtgcacc gagttgaccg taacagacat ctttgcctcc  
 241 tccaagaaca caactgagaa ggaaaccttc tgcagggtcg cgactgtgct ccggcagttc  
 301 tacagccacc atgagaagga cactcgctgc ctgggtgcga ctgcacagca gttccacagg  
 361 cacaagcagc tgatccgatt cctgaaacgg ctgcacagga acctctgggc cctggcgggc  
 421 ttgaattcct gtcctgtgaa ggaagccaac cagagtacgt tggaaaactt cttggaaagg  
 481 ctaaagacga tcatgagaga gaaatattca aagtgttoga gctgaatatt ttaatttatg  
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## (2) INFORMATION FOR SEQ ID NO:2544:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3541 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2544:

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3481 ccttgggttg agtaatgtc gtctgtgtgt tttagtttca tcacctgta tctgtgttg
3541 ctgaggagag tggaaacagaa ggggtggagt tttgtataaa taaagtttct ttgtctc

```

## (2) INFORMATION FOR SEQ ID NO:2545:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2545:

```

1 ggatcctaata caagacccca gtgaacagaa ctgaccctg ccaaggcttg gcagtttcca
61 tttcaatcac tgtcttccca ccagtatttt caatttcttt taagacagat taatctagcc
121 acagtcata tagaacatag ccgatctgaa aaaaacattc ccaatattta tgtattttag
181 cataaaattc tgtttagtgg tctaccttat actttgtttt gcacacatct ttttaaggga
241 agttaatttt ctgattttta gaaatgcaaa tgtggggcaa tgatgtatta acccaaagat
301 tcttcgtaat agaaaatgtt tttaaagggg ggaaacaggg atttttatta ttaaaagata
361 aaagtaaatt tattttttta gatataaggc attggaacaa tttagtttca cgatagcca
421 ttattaggca ttctctatct gattgttaga aattattcat ttctcaaa acagacaata
481 aattgactgg ggacgcagtc ttgtactatg cactttcttt gccaaaggca aacgcagaa
541 gtttcagagc catgaggatg cttctgcatt tgagtttgct agctcttggg gctgcctacg
601 tgtatgccat cccacagaa attcccacaa gtgcattggg gaaagagacc ttggcactgc

```

```

661 tttcttga tcgaactctg ctgatagcca atgaggtaat tttctatg attcctacag
721 tctgtaaaagt gcataggtaa tcatttgtga tgggtccttt actatatata gagatctgtt
781 ataaataata agattctgag cacattagta catgggtgat aactacatca ccagcaaac
841 ttctgttaaa agttatgaat gctgggtgctg tgtaaaaatg attgtatttc ctttcctctc
901 cagactctga ggattcctgt tcctgtacat aaaaatgtaa gttaaattat gattcagtaa
961 aatgatggca tgaataagta aatttcctgt ttttaagctgt aaatcattag ttatcattgg
1021 aactatttaa ttttctatat tttgttttca tatgggtggc tgtgaatgct tgtacttata
1081 aatatgagga atgacttttt atcaagtaga atccttttaa caagtggatt aggctctttg
1141 gtgatgttgt tagtttgctt cccaaagagc atcgtgtcag ggattctttc cagaaggatt
1201 ccacactgag tgagaggtgc gtgctagtct ccgtgcagtt ctgactcttt ctcactctaa
1261 cgtgtttctg aaagtattag caactcagaa ttatatTTTT agaaccatga tcagtagaca
1321 ttaaaatata taacaaatgc cctatatata taatttctgc atacttaaatt aattatgact
1381 atatgtatgt gttgtatgca tttgaatatg tcctgggtcat attaaaatgt aaaatatata
1441 gttttattag tctaaataga ataaaactac cagctagaac tgtagaaaac cattgatatg
1501 agtttaaatgt ataatgcatt acacttccaa aacattTTTT tccagttaca taattaagtt
1561 atatccttta taaaactcct cagtaatcat ataagcttca tctacttttt gaaaatttta
1621 tcttaatatg tgggtgtttg ttgcctagaa aacaaacaaa aaactctttg gagaagggaa
1681 ctcatgtaaa taccacaaaa caaagcctaa ctttgtggac caaattgttt ttaataatta
1741 ttttttaatt gatgaattaa aaagtatata tatttattgt gtacaatatg atgttttgaa
1801 gtatgtatac attgcagaat ggacaatgga ccaaattttt ataccttgtc ttgattattt
1861 gcatttttaa aattttcctc atttagcacc aactgtgcac tgaagaaatc tttcagggaa
1921 taggcacact ggagagtcaa actgtgcaag ggggtactgt ggaaagacta ttcaaaaact
1981 tgtccttaat aaagaaatc attgacggcc aaaaagtaag ttacacacat tcaatggaag
2041 ctatatttgt ctggctgtgc ctatttctat ggaattgaca gtttctctga atacctattg
2101 tcatttttct ttttccacag aaaaagtgtg gagaagaaag acggagagta aaccaattcc
2161 tagactacct gcaagagttt cttggtgtaa tgaacaccga gtggataata gaaagttagg
2221 actaaactgg tttgttgca ccaaagattt tggaggagaa ggacatttta ctgcagttag
2281 aatgagggcc aagaaagagt caggccttaa ttttcagtat aatttaactt cagagggaaa
2341 gtaaatattt caggcatact gacatttgc cagaaagcat aaaattctta aaatatattt
2401 cagatatcag aatcattgaa gtattttcct ccaggcaaaa ttgatatact ttttcttat
2461 ttaacttaac attctgtaaa atgtctgtta acttaatagt atttatgaaa tggttaagaa
2521 tttggtaaat tagtatttat ttaatgttat gttgtgttct aataaaacaa aaatagacaa
2581 ctgttcaatt tgctgtctgc ctctgtctta gcaattgaag ttagcacagt ccattgagta
2641 catgccagct ttggaggaag ggtctgagca catgtggctg agcatccca tttctctgga
2701 gaagtctcaa ggttgcaagg cacaccagag gtggaaagta tctagcagga cttagtgggg
2761 atgtggggag cagggacaca ggcaggaggt gaacctgggt ttctctctac agtatatcca
2821 gaactggga tgggtcaggg taaatggtag ggaataaattg aatgaatgtg ctttccaaga
2881 ctgattgtag aactaaaatg agttgttaag cgtccctgg aagaaggga cgtgtgggaa
2941 ctgtaactag gttcctgccc agcctgtgag aagaatttgg cagatcaatc tcattgccag
3001 tatagagagg aagccagaaa cctctctgca caaggcctgc aggggttctt accccacctg
3061 accctgcacc ataacaaaag gaacagagag aactgtgtag ggcagtccca ttagaaagac
3121 tgagttccgt attcccgggg gcagggcagc accaggccgc acaacactcc attctgctg
3181 cttatggcta tcagtagcat cactagagat tcttctgttt gagaaaactt ctcaaggatc
3241 c

```

## (2) INFORMATION FOR SEQ ID NO:2546:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 781 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2546:

```

1 atgcactttc ttgccaaag gcaaacgcag aacgtttcag agccatgagg atgcttctgc
61 atttgagttt gctagctctt ggagctgcct acgtgtatgc catccccaca gaaattccca
121 caagtgcatt ggtgaaagag accttggcac tgctttctac tcatcgaact ctgctgatag
181 ccaatgagac tctgaggatt cctgttctctg tacataaaaa tcaccaactg tgactgaag
241 aaatctttca gggaataggc aacttgagga gtcaaactgt gcaagggggt actgtggaaa
301 gactattcaa aaacttgtcc ttaataaaga aatacattga cggccaaaaa aaaaagtgtg
361 gagaagaaag acggagagta aaccaattcc tagactacct gcaagagttt cttggtgtaa
421 tgaacaccga gtggataata gaaagttag actaaactgg tttgttgca ccaaagattt
481 tggaggagaa ggacatttta ctgcagttag aatgagggcc aagaaagagt caggccttaa
541 ttttcaatat aatttaactt cagagggaaa gtaaatattt caggcatact gacactttgc
601 cagaaagcat aaaattctta aaatatattt cagatatcag aatcattgaa gtattttcct
661 ccaggcaaaa ttgatatact ttttcttat ttaacttaac attctgtaaa atgtctgtta
721 acttaatagt atttatgaaa tggttaagaa tttggttaat tagtatttat ttaatgttat
781 gttgtgttct aataaaacaa aaatagacaa ctgttc

```

## (2) INFORMATION FOR SEQ ID NO:2547:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4022 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2547:

```
1 ggatcctaata caagacccca gtgaacagaa ctgaccctg ccaaggcttg gcagtttcca
61 tttcaatcac tgtcttccca ccagtatatt caatttcttt taagacagat taatctagcc
121 acagtcatag tagaacatag ccgatctgaa aaaaacattc ccaatatatta tgtatttttag
181 cataaaattc tgttttagtg tctaccttat actttgtttt gcacacatct ttttaagagga
241 agttaatttt ctgattttta gaaatgcaaa tgtggggcaa tgatgtatta acccaaagat
301 tcttcgtaat agaaaatggt tttaaagggg ggaaacaggg atttttatta ttaaaagata
361 aaagtaaaatt tattttttta gatataaggc attggaacaa tttagtttca cgatatgccca
421 ttattaggca ttctctatct gattgttaga aattattcat ttctctaaag acagacaata
481 aattgactgg ggacgcagtc ttgtactatg cactttcttt gccaaaggga aacgcagaac
541 gtttcagagc catgaggatg cttctgcatt tgagtttgct agctcttgga gctgcctacg
601 tgtatgccat cccacagaa attcccacaa gtgcattggt gaaagagacc ttggcactgc
661 tttctactca tcgaactctg ctgatatgca atgaggtaat tttctttatg attcctacag
721 tctgtaaaagt gcataaggtaa tcatattgtg tggttctttt actatatata gagatctggt
781 ataaataata agattctgag cacattagta catgggtgat aactacatca ccagcaaaaca
841 ttctgttaaa agttatgaat gctgggtgtg tgtaaaaatg attgtatttc ctttctcttc
901 cagactctga ggattcctgt tctgtacat aaaaatgtaa gttaaattat gattcagtaa
961 aatgatggca tgaataagta aatttcctgt tttaaagctg aaatcattag ttatcattgg
1021 aactatttaa tttctatat tttgttttca tatgggtggc tgtgaatgct tgtacttata
1081 aatagagga atgacttttt atcaagtaga atccttttaa caagtggatt aggtctcttg
1141 gtgatgttgt tagtttgctt cccaaagagc atcgtgtcag ggattctttc cagaaggatt
1201 ccacactgag tgagaggtgc gtgctagtct ccgtgcagtt ctgactcttt ctcactctaa
1261 cgtgtttctg aaagtattag caactcagaa ttatattttt agaaccatga tcagtagaca
1321 ttaaaatata taacaaatgc cctatatata taatttctgc atacttaaat aattatgact
1381 atatgatggt gttgtatgca tttgaatatg tcctggctat attaaaatgt aaaatatata
1441 gttttattag tctaaataga ataaaactac cagctagaac tgtagaaaaca cattgatatg
1501 agtttaaatgt ataatgcatt acacttccaa aacatttttt tccagttaca taattaagtt
1561 atatccttta taaaactcct cagtaatcat ataaagcttca tctacttttt gaaaatttta
1621 tcttaatatg tgggtggttg ttgcctagaa aacaaacaaa aaactctttg gagaaggga
1681 ctcatgtaaa taccacaaaa caaagcctaa ctttgtggac caaaattggt ttaataatta
1741 ttttttaatt gatgaattaa aaagtatata ttttattgt gtacaatatg atgttttgaa
1801 gtatgtatac attgcagaat ggacaatgga ccaaattttt atacctgtgc ttgattattt
1861 gcattttaaa aattttcttc atttagcacc aactgtgcac tgaagaaatc tttcagggaa
1921 taggcacact ggagagtcaa actgtgcaag ggggtactgt ggaaagacta ttcaaaaact
1981 tgtccttaat aaagaaatca attgacggcc aaaaagtaag ttacacacat tcaatggag
2041 ctatatattgt ctggctgtgc ctatttctat ggaattgaca gtttctgtga atacctattg
2101 tcatttttct tttttcacag aaaaagtgtg gagaagaaag acggagagta aaccaattcc
2161 tagactacct gcaagagttt cttgtgtgta tgaacaccga gtggataata gaaagttgag
2221 actaaactgg ttgttgagc ccaaagattt tggaggagaa ggacatttta ctgcagttag
2281 aatgagggcc aagaaagagt caggccctaa ttttcagtat aatttaactt cagagggaaa
2341 gtaaatattt caggcatact gacactttgc cagaagcat aaaattctta aaatatattt
2401 cagatatcag aatcattgaa gtattttctt ccaggcaaaa ttgatatact tttttcttat
2461 ttaacttaac attctgtaaa atgtctgtta acttaatagt atttatgaa ttggttaagaa
2521 tttggtaaat tagtatttat ttaatgttat gttgtgttct aataaaacaa aaatagacaa
2581 ctgttcaatt tgctgtgtgc ctctgtctta gcaattgaag ttagcacagt ccattgagta
2641 catgcccagt ttggaggga ggtctgagca catgtggctg agcatcccca tttctctgga
2701 gaagtctcaa ggttgcaagg cacaccagag gtggaagtga tctagcagga cttagtgggg
2761 atgtggggag caggacaca ggcaggaggt gaacctggtt ttctctctac agtatatcca
2821 gaacctggga tgggtgcagg taaatggtag ggaataaatg aatgaatgtg ctttccaaga
2881 ctgattgtag aactaaaatg agttgtaagg cgtcccctgg aagaaggcca gtgtgggaac
2941 ctgtaactag gttcctgccc agcctgtgag aagaatttgg cagatcaatc tcattggcag
3001 tatagagagg aagccagaaa ccctctctgc caaggcctgc aggggttctt accccacctg
3061 accctgcacc ataacaaaag gaacagagag aactgtgtag ggcagtccca ttagaaagac
3121 tgagttccgt attcccggg gcagggcagc accaggccgc acaacactcc attctgcctg
3181 cttatggcta tcagtagcat cactagagat tcttctgttt gagaaaactt ctcaaggatc
3241 c
1 atgcactttc tttgccaaag gcaaacgcag aacgtttcag agccatgagg atgcttctgc
61 atttgagttt gctagctctt ggagctgcct acgtgtatgc catccccaca gaaattccca
121 caagtgcatt ggtgaaagag accttgccac tgctttctac tcatcgaaact ctgctgatag
181 ccaatgagac tctgaggatt cctgttctctg tacataaaaa tcaccaactg tgcactgaag
241 aaatctttca gggaataggc aactggaga gtcaaactgt gcaaggggtt actgtggaaa
301 gactattcaa aaacttgtcc ttaataaaga aatacattga cggccaaaaa aaaaagtgtg
361 gagaagaaa acggagagta aaccaattcc tagactacct gcaagagttt cttggtgtaa
421 tgaacaccga gtggataata gaaagttgag actaaactgg tttgttgag ccaaagattt
481 tggaggagaa ggacatttta ctgcagttag aatgagggcc aagaagagt caggccctaa
```



541 ttttcaat aatttaactt cagagggaaa gtaaataattt cagacttact gacactttgc  
 601 cagaaagcat aaaattctta aaatatattt cagatatcag aatcattgaa gtattttcct  
 661 ccaggcaaaa ttgatatact ttttcttat ttaacttaac attctgtaaa atgtctgtta  
 721 acttaaatgt atttatgaaa tggtaaagaa tttggtaaat tagtatttat ttaatgttat  
 781 gttgtgttct aataaaacaa aaatagacaa ctgttc

## (2) INFORMATION FOR SEQ ID NO:2548:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1981 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2548:

1 tagatgctgg ggttcagcc acgagcatag acacgacaga cacggtcctc gccatcttct  
 61 gttgagtact ggtcggaaaca agaggatcgt ctgtagacag gatatgatca tcgtggcgca  
 121 tgtattactc atccttttgg: gggccactga gatactgcaa gctgacttac ttcctgatga  
 181 aaagatttca cttctccac ctgtcaattt caccattaaa gttactgggt tggctcaagt  
 241 tcttttaca tggaaaccaa atcctgatca agagcaaaagg aatgttaatc tagaatatca  
 301 agtgaaaata aacgctccaa aagaagatga ctatgaaacc agaatacactg aaagcaaatg  
 361 tgtaaccatc ctccacaaag gcttttcagc aagtgtgagg accatcctgc agaacgacca  
 421 ctactactg gccagcagct gggcttctgc tgaacttcac gcccaccag ggtctcctgg  
 481 aacctcaatt gtgaatttaa cttgcaccac aaacactaca gaagacaatt attcacgttt  
 541 aaggtcatat caagtttccc ttcactgcac ctggcttggt ggcacagatg cccctgagga  
 601 cagcagatg tttctctact ataggatgg ctcttgact gaagaatgcc aagaatacag  
 661 caaagacaca ctggggagaa atatcgcatg ctggtttccc aggacttta tcctcagcaa  
 721 agggcgtgac tggcttgagg tgcttgtaa cggctccagc aagcactctg ctatcaggcc  
 781 ctttgatcag ctgtttgccc ttcacgccat tgatcaaata aatcctccac tgaatgtcac  
 841 agcagagatt gaaggaactc gtctctctat ccaatgggag aaaccagtgt ctgcttttcc  
 901 aatccattgc tttgattatg aagtaaaaat acacaataca aggaatggat atttgcatg  
 961 agaaaaattg atgaccaatg cattcatctc aataattgat gatctttcta agtacgatgt  
 1021 tcaagtgaga gcagcagtga gctccatgtg cagagaggga gggctctgga gtgagtggag  
 1081 ccaacctatt tatgtgggaa atgatgaaca caagcccttg agagagtgggt ttgtcattgt  
 1141 gattatggca accatctgct tcatcttggt aattctctcg cttatctgta aaatatgtca  
 1201 tttatggatc aagttgtttc caccaattcc agcaccaaaa agtaatatca aagatctctt  
 1261 tgtaaccact aactatgaga aagctggaat ttaaattcaa gcatgtttta acttttggtt  
 1321 taaggtactt ggggtgtacct ggcagtgtg taagctcttt acattaatta attactctc  
 1381 taggtactgt tatcttcatt ttataaaciaa ggcagctgaa gttgagagaa ataagtaacc  
 1441 tgtcctaggt cacacaatta ggaaatgaca gatctggcag tctatttcca ggcagtctat  
 1501 ttccacgagg tcatgagtgc gaaagaggga ctaggggaa aatgattaac tccagggagc  
 1561 tgacttttct agtgtgctta cctgttttgc atctctcaag gatgtgccat gaagctgtag  
 1621 ccagggtgaa ttgtaccaca gccctgacat gaacacctga tggcagctgc tgggttgag  
 1681 cctagacaaa aacatgaaga accatggctg ctgcctgagc ccatcgtgct gtaattatag  
 1741 aaaaccttct aagggaagaa tatgtgata tttttcagat aagtaccctt ttataaaaa  
 1801 tcctccaagt tagccctcga ttttccatgt aaggaaacag aggctttgag ataagtctg  
 1861 tctcctaagg gacaaagcca ggacttgatc ctgtcttaaa aatgcaaaat gtagtacttc  
 1921 ttccatcaaa ggtagacatg cactaaggga caggtttttg cttggtatca gaatacattt  
 1981 ttaaaagctg tgtaagaatt gaacgggctg tactaggggg tata

## (2) INFORMATION FOR SEQ ID NO:2549:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 901 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2549:

1 gatctttcta agtacgatgt tcaagtgaga gcagcagtga gctccatgtg cagagaggga  
 61 gggctctgga gtgagtggag ccaacctatt tatgtgggaa atgatgaaca caagcccttg  
 121 agagagtgggt ttgtcattgt gattatggca accatctgct tcatcttggt aattctctcg  
 181 cttatctgta aaatatgtca tttatggatc aagttgtttc caccaattcc agcaccaaaa  
 241 agtaatatca aagatctctt tgtaaccact aactatgagg tctctgcat tttcatatac  
 301 atcttagatt cggtgacaaa ttttctacaa aaaaagaaaag ctgggtccag tgagacggaa  
 361 attgaagtca tctgttatat agagaagcct ggagttgaga ccctggagga ttctgtgttt  
 421 tgactgtcac tttggcatcc tctgatgaac tcacacatgc ctcatgacct cagtgaagag  
 481 aacagggatg ctggctcttg gctaagaggt gttcagaatt taggcaacac tcaatttacc  
 541 tgcaagcaa tacaccaga cacaccagtc ttgtatctct taaaagtatg gatgcttcat  
 601 ccaaatcgcc tcacctacag cagggaagtt gactcatcca agcattttgc catgtttttt  
 661 ctccccatgc cgtacagggt agcacctcct cacctgcaa tctttgcaat ttgcttgact  
 721 cacctcagac ttttcattca caacagacag cttttaaggc taacgtccag ctgtatttac



781 ttctggtgt gcccgtttgg ctgtttaagc tgccaattgt agcactcagc taccatctga  
 841 ggaagaaagc attttgcatc agcctggagt gaaccatgaa cttggattca agactgtctt  
 901 ttctatagca agtgagagcc acaaattcct c

## (2) INFORMATION FOR SEQ ID NO:2550:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1321 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2550:

1 ccgctgcttc tcatcgcatg gccaccgcat ttctcaggcc aggcacattg agcattggtc  
 61 ctgtgcctga cgctatgcta gatgctgggg ttgcagccac gagcatagac acgacagaca  
 121 cggtcctcgc catcttctgt tgagtactgg tcggaacaag aggatcgtct gtagacaggc  
 181 tacagattgt tttagattga agtttctgt catgttact catctttaa tcctcatagt  
 241 aaaaaggata tgatcatcgt ggcgcagtga ttactcatcc ttttgggggc cactgagata  
 301 ctgcaagctg acttacttcc tgatgaaaag atttcacttc tcccactgt caatttcacc  
 361 attaaagtta ctggtttggc tcaagttcct ttacaatgga aaccaaattcc tgatcaagag  
 421 caaaggaaatg ttaattctaga atatcaagtg aaaataaacy ctccaaaaga agatgactat  
 481 gaaaccagaa tcaactgaaag caaatgtgta accatcctcc acaaaggctt ttcagcaagt  
 541 gtgcggacca tcctgcagaa cgaccactca ctactggcca gcagctgggc ttctgtgaa  
 601 cttcatgccc caccagggtc tcctggaacc tcaattgtga atttaacttg caccacaaac  
 661 actacagaag acaattattc acgtttaagg tcataccaag tttcccttca ctgcacctgg  
 721 ctgtttggca cagatgcccc tgaggacacg cagtattttc tctactatag gtatggctct  
 781 tggactgaag aatgccaaaga atacagcaaa gacacactgg ggagaaatat cgcattgtgg  
 841 tttcccagga cttttatcct cagcaaaggc cgtgactggc tttcggtgct tgttaacggc  
 901 tccagcaagc actctgctat caggcccttt gatcagctgt ttgcccttca cgccattgat  
 961 caataaatac ctccactgaa tgtcacagca gagattgaag gaactcgtct ctctatccaa  
 1021 tgggagaaac cagtgtctgc ttttccaatc cattgctttg attatgaagt aaaaatacac  
 1081 aatacaagga atggatattt gcagatagaa aaattgatga ccaatgcatt catctcaata  
 1141 attgatgac tttctaagta cgatgttcaa gtgagagcag cagtgagctc catgtgcaga  
 1201 gaggcagggc tctggagtga gtggagccaa cctatttatg tggggttctc aagataaagg  
 1261 agataacatc cagctttcct gccccacacc gtatctgaaa taaaaacaac agcagggata  
 1321 gcagatt

## (2) INFORMATION FOR SEQ ID NO:2551:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1621 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2551:

1 ccgctgcttc tcatcgcatg gccaccgcat ttctcaggcc aggcacattg agcattggtc  
 61 ctgtgcctga cgctatgcta gatgctgggg ttgcagccac gagcatagac acgacagaca  
 121 cggtcctcgc catcttctgt tgagtactgg tcggaacaag aggatcgtct gtagacaggc  
 181 tacagattgt tttagattga agtttctgt catgttact catctttaa tcctcatagt  
 241 aaaaaggata tgatcatcgt ggcgcagtga ttactcatcc ttttgggggc cactgagata  
 301 ctgcaagctg acttacttcc tgatgaaaag atttcacttc tcccactgt caatttcacc  
 361 attaaagtta ctggtttggc tcaagttcct ttacaatgga aaccaaattcc tgatcaagag  
 421 caaaggaaatg ttaattctaga atatcaagtg aaaataaacy ctccaaaaga agatgactat  
 481 gaaaccagaa tcaactgaaag caaatgtgta accatcctcc acaaaggctt ttcagcaagt  
 541 gtgcggacca tcctgcagaa cgaccactca ctactggcca gcagctgggc ttctgtgaa  
 601 cttcatgccc caccagggtc tcctggaacc tcaattgtga atttaacttg caccacaaac  
 661 actacagaag acaattattc acgtttaagg tcataccaag tttcccttca ctgcacctgg  
 721 ctgtttggca cagatgcccc tgaggacacg cagtattttc tctactatag gtatggctct  
 781 tggactgaag aatgccaaaga atacagcaaa gacacactgg ggagaaatat cgcattgtgg  
 841 tttcccagga cttttatcct cagcaaaggc cgtgactggc tttcggtgct tgttaacggc  
 901 tccagcaagc actctgctat caggcccttt gatcagctgt ttgcccttca cgccattgat  
 961 caataaatac ctccactgaa tgtcacagca gagattgaag gaactcgtct ctctatccaa  
 1021 tgggagaaac cagtgtctgc ttttccaatc cattgctttg attatgaagt aaaaatacac  
 1081 aatacaagga atggatattt gcagatagaa aaattgatga ccaatgcatt catctcaata  
 1141 attgatgac tttctaagta cgatgttcaa gtgagagcag cagtgagctc catgtgcaga  
 1201 gaggcagggc tctggagtga gtggagccaa cctatttatg tgggtaagta gcttatgttt  
 1261 attttacatt ggcagccttc cttgtgatca aaaaaggtaa tcccagaaac gtaccogttc  
 1321 actcgtgggt cttaaaatgg tttcatatct ctattgtgac taattttctc tcggtctact  
 1381 gccttttcaa tcaggaatag atttgccatg aagccagtga agtttttaag tgtctaggct  
 1441 tctcattagt gccaaactctc ctgacactgg tgccctgttt ttttccaaag tttgtttcta  
 1501 cttctatcca ttttttaaat taaacttttt attttgaaat aattatcaca ctcaaacgt  
 1561 gtgggaagaa ataatagaga tcctgtgtct ctttcatcca gttttcctca agggtaacat

1621 cttac      ratagtacaa tagtggaata gaattttgg tg

(2) INFORMATION FOR SEQ ID NO:2552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2552:

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1  ccgctgcttc tcatcgcatg gccaccgcat ttctcaggcc aggcacattg agcattggtc
61  ctgtgcctga cgctatgcta gatgctgggg ttgcagccac gagcatagac acgacagaca
121 cggctcctgc catcttctgt tgagtactgg tcggaacaag aggatcgctc gtagacaggc
181 tacagattgt ttagattgta agtttcctgt catgttcaact catctttaaa tctctatagt
241 aaaaaggata tgatcatcgt ggcgcatgta ttactcatcc ttttgggggc cactgagata
301 ctgcaagctg acttacttcc tgatgaaaag atttcaactc tcccacctgt caatttcacc
361 attaaagtta ctggtttggc tcaagttctt ttacaatgga aaccaaattc tgatcaagag
421 caaagggaatg ttaattctaga atatcaagtg aaaataaacg ctccaaaaga agatgactat
481 gaaaccagaa tcaactgaaag caaatgtgta accatcctcc acaaaggctt ttcagcaagt
541 gtgcggacca tcctgcagaa cgaccactca ctactggcca gcagctgggc ttctgctgaa
601 cttcatgccc caccagggtc tcctggaacc tcaattgtga atttaacttg caccacaaac
661 actacagaag acaattattc acgtttaagg tcataccaag ttcccttcca ctgcacctgg
721 cttgttggca cagatgcccc tgaggacacg cagtattttc tctactatag gtatggctct
781 tggactgaag aatgccaaaga atacagcaaa gacacactgg ggagaaatat cgcatgctgg
841 tttccagga cttttatcct cagcaaaggg cgtgactggc tttcggtgct tgtaacggc
901 ttcagcaagc actctgctat caggcccttt gatcagctgt ttgcccttca cgccattgat
961 caaataaatc ctccactgaa tgtcacagca gagattgaag gaactcgtct ctctatccaa
1021 tgggagaaac cagtgtctgc ttttccaatc cattgctttg attatgaagt aaaaatacac
1081 aatacaagga atggatattt gcagatagaa aaattgatga ccaatgcatt catctcaata
1141 attgatgata tttctaagta cgatgttcaa gtgagagcag cagtgaagtc catgtgcaga
1201 gaggcagggc tctggagtga gtggagccaa cctatttatg tgggaaatga tgaacacaag
1261 cctctgagag agtggtttgt cattgtgatt atggcaacca tctgcttcat cttgttaatt
1321 ctctcgctta tctgtaaaat atgtcattta tggatcaagt tgtttccacc aattccagca
1381 ccaaaaagta atatacaaga tctctttgta accactaact atgagaaaagc tgggtccagt
1441 gagacggaaa ttgaagtcac ctgttatata gagaagcctg gagttgagac cctggaggat
1501 tctgtgtttt gactgtcact ttggcattct ctgatgaact cacacatgcc tcaagtgcctc
1561 agtgaagaag acagggatgc tggctcttgg ctaagagggtg ttcagaattt aggcaacact
1621 caatttacct gcgaagcaat acaccagac acaccagtct tgtatctctt aaaagtatgg
1681 atgcttcac caaatcgctt cacctacagc agggaaagtg actcatccaa gcattttgcc
1741 atgtttttt tcccattgcc gtacagggtg gcacctctc accctgcaat ctttgcaatt
1801 tgcttgactc acctcagact ttcattcaca acagacagct ttaaggcta acgtccagct
1861 gtatttactt ctggctgtgc cgtttggtg ttttaagctgc caattgtagc actcagctac
1921 catctgagga agaaagcatt ttgcatcagc ctggagtga ccatgaactt ggattcaaga
1981 ctgtctttt tatagcaa

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(2) INFORMATION FOR SEQ ID NO:2553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2553:

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1  gtcttttgaa aggatctgcc gctgcttctc atcgcatggc caccgcattt ctcaggccag
61  gcacattgag cattggtcct gtgcctgacg ctatgctaga tgctggggtt gcagccacga
121 gcatagacac gacagacacg gtcctcgcca tcttctgttg agtactggtc ggaacaagag
181 gatcgctctg agacaggata tgatcatcgt ggcgcatgta ttactcatcc ttttgggggc
241 cactgagata ctgcaagctg acttacttcc tgatgaaaag atttcaactc tcccacctgt
301 caatttcacc attaaagtta ctggtttggc tcaagttctt ttacaatgga aaccaaattc
361 tgatcaagag caaagggaatg ttaattctaga atatcaagtg aaaataaacg ctccaaaaga
421 agatgactat gaaaccagaa tcaactgaaag caaatgtgta accatcctcc acaaaggctt
481 ttcagcaagt gtgcggacca tcctgcagaa cgaccactca ctactggcca gcagctgggc
541 ttctgctgaa cttcatgccc caccagggtc tcctggaacc tcaattgtga atttaacttg
601 caccacaaac actacagaag acaattattc acgtttaagg tcataccaag ttcccttcca
661 ctgcacctgg cttgttggca cagatgcccc tgaggacacg cagtattttc tctactatag
721 gtatggctct tggactgaag aatgccaaaga atacagcaaa gacacactgg ggagaaatat
781 cgcatgctgg tttcccagga cttttatcct cagcaaaggg cgtgactggc ttgctgtgct
841 tgtaacggc tccagcaagc actctgctat caggcccttt gatcagctgt ttgcccttca
901 cgccattgat caaataaatc ctccactgaa tgtcacagca gagattgaag gaactcgtct
961 ctctatccaa tgggagaaac cagtgtctgc ttttccaatc cattgctttg attatgaagt
1021 aaaaatacac aatacaagga atggatattt gcagatagaa aaattgatga ccaatgcatt

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1081 catctcaata attgatgac tttctaagta cgaatgttcaa gtgagagcag cagtgaagctc  
1141 catgtgcaga gaggcagggc tctggagtga gtggagccaa cctatttatg tgggtaagta  
1201 gcttatgttt attttacatt ggcagccttc ctgtgatca aaaaaggtaa tcccagaaac  
1261 gtacccgttc actcgtgggt cttaaaatgg tttcatatct ctattgtgac taattttctc  
1321 tcggtctact gccttttcaa tcaggaatag atttgccatg aagccagtga agtttttaag  
1381 tgtctaggct tctcattagc gccac

## (2) INFORMATION FOR SEQ ID NO:2554:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1981 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2554:

1 cggctcctgc catcttctgt tgagtactgg tcggaacaag aggatcgtct gtagacagga  
61 tatgatcatc gtggcgcagt tattactcat ccttttgggg gccactgaga tactgcaagc  
121 tgacttactt cctgatgaaa agatttcaact tctcccacct gtcaatttca ccattaaagt  
181 tactgttttg gctcaagttc ttttacaatg gaaaccaaact cctgatcaag agcaaaggaa  
241 tgttaatacta gaatatcaag tgaaaataaa cgctccaaaa gaagatgact atgaaaccag  
301 aatcactgaa agcaaagtgt taaccatcct ccacaaaggc ttttcagcaa gtgtgaggac  
361 catcctgcag aacgaccact cactactggc cagcagctgg gcttctgctg aacttcatgc  
421 cccaccaggg tctcctggaa cctcagttgt gaatttaact tgcaccacaa aactacaga  
481 agacaattat tcacgtttaa ggtcatacca agtttccctt cactgcacct ggcttgttg  
541 cacagatgcc cctgaggaca cgcagtattt tctctactat aggtatggct ctggaactga  
601 agaattgcaa gaatacagca aagacacact ggggagaaat atcgcatgct ggtttcccag  
661 gacttttata ctcagcaaaag ggcgtgactg gcttgccgtg cttgttaacg gctccagcaa  
721 gcactctgct atcaggccct ttgatcagct gtttgccctt cagccattg atcaataaaa  
781 tcttccactg aatgtcacag cagagattga aggaactcgt ctctctatcc aatgggagaa  
841 accagtgtct gcttttccaa tccattgctt tgattatgaa gtaaaaatac acaatacaag  
901 gaatggatat ttgcagatag aaaaattgat gaccaatgca ttcatctcaa taattgatga  
961 tctttctaag tacgatgttc aagtgaagc agcagtgaac tccatgtgca gagaggcagg  
1021 gctctggagt gactggagcc aacctattta tgtgggaaat gatgaacaca agccttgag  
1081 agagtgtgtt gtcatgttga ttatggcaac catctgcttc atcttgtaa tctctcgtc  
1141 tatctgtaaa atatgtcatt tatggatcaa gttgtttcca ccaattccag caccaaaaag  
1201 taatatcaaa gatctctttg taaccactaa ctatgagaaa gctgggtcca gtgagacgga  
1261 aattgaagtc atctgttata tagagaagcc tggagttagg accctggagg attctgtgtt  
1321 ttgactgtca ctttggcatc ctctgatgaa ctcacacatg cctcagtgcc tcagtgaaaa  
1381 gaacagggat gctggctctt ggctaagagg tgttcagaat ttaggcaaca ctcaatttac  
1441 ctgcgaagca atacaccag acacaccagt cttgtatctc ttaaaagtat ggatgcttca  
1501 tccaaatcgc ctcacctaca gcagggaagt tgactcatcc aagcattttg ccatgtttt  
1561 tctccccatg ccgtacaggg tagcacctcc tcacctgcca atctttgcaa tttgcttgac  
1621 tcacctcaga cttttcattc acaacagaca gcttttaagg ctaacgtcca gctgtattta  
1681 cttctggctg tgcccgtttg gctgtttaag ctgccaatg tagcactcag ctaccatctg  
1741 aggaagaaag cattttgcat cagcctggag tgaatcatga acttgattc aagactgtct  
1801 tttctatagc aagtgaagc cacaattcc tcacccccct acattctaga atgatctttt  
1861 tctaggtaga ttgtgtatgt gtgtgtatga gagagagaga gagagagaga gagagagaga  
1921 gagaaattat ctcaagctcc agaggcctga tccaggatag atcatttgaa accaactaat  
1981 ttaaaagcat aatagagcta atatat

## (2) INFORMATION FOR SEQ ID NO:2555:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11167 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2555:

1 tagatgctgg ggttgacgcc acgagcatag acacgacaga caggtcctc gccatcttct  
61 gttgagtact ggtcgaaca agaggatcgt ctgtagacag gatatgatca tctgtggcga  
121 tgtattactc atccttttgg gggccactga gatactgcaa gctgacttac ttcctgatga  
181 aaagatttca cttctccac ctgtcaattt caccattaaa gttactggtt tggctcaagt  
241 tcttttaca tggaaccaa atcctgatca agagcaaagg aatgttaatc tagaatatca  
301 agtgaataa aacgctccaa aagaagatga ctatgaaacc agaactcgtg aaagcaaatg  
361 tgtaaccatc ctccacaaag gcttttcagc aagtgtgcgg accatcctgc agaacgacca  
421 ctactactg gccagcagct gggcttctgc tgaacttcat gcccaccag ggtctcctgg  
481 aacctcaatt gtgaatttaa cttgcaccac aaacactaca gaagacaatt attcagttt  
541 aaggtcatag caagtctccc ttcactgcac ctggcttggt ggcacagatg cccctgagga  
601 cagcagtat tttctctact ataggtatgg ctcttgact gaagaatgcc aagaatcag  
661 caaagacaca ctggggagaa atatcgcatg ctgggttccc aggaatttta tctcagcaa  
721 agggcgtgac tggcttgagg tgcttgtaa cggctccagc aagcactctg ctatcaggcc

781 ctttgatgag ctgtttgccc ttcacgccat tgatcaaata aatctccac tgaatgtcac  
841 agcagagatt gaaggaactc gtctctctat ccaatgggag aaaccagtgt ctgcttttcc  
901 aatccattgc tttgattatg aagtaaaaaat acacaatata aggaatggat atttgagat  
961 agaaaaattg atgaccaatg cattcatctc aataattgat gatcttttcta agtacgatgt  
1021 tcaagtgaga gcagcagtga gctccatgtg cagagaggca gggctctgga gtgagtggag  
1081 ccaacctatt tatgtgggaa atgatgaaca caagcccttg agagagtgggt ttgtcattgt  
1141 gattatggca accatctgct tcatcttggt aattctctcg cttatctgta aaatatgtca  
1201 tttatggatc aagtgtgttc caccaattcc agcaccaaaa agtaatatca aagatctctt  
1261 tgtaaccact aactatgaga aagctggaat ttaaatcaaa gcatgtttta acttttggtt  
1321 taaggctactt ggggtgtacct ggcagtgttg taagctcttt acattaatta attaatctct  
1381 taggtactgt tatcttcatt ttataaaca ggcagctgaa gttgagagaa ataagtaacc  
1441 tgtcctaggt cacacaatta ggaaatgaca gatctggcag tctattttcca ggcagtctat  
1501 ttccacgagg tcatgagtgc gaaagaggga ctaggggaag aatgattaac tccaggggagc  
1561 tgacttttct agtgtgctta cctgttttgc atctctcaag gatgtgccat gaagctgtag  
1621 ccaggtggaa ttgtaccaca gccctgacat gaacacctga tggcagctgc tgggttgag  
1681 cctagacaaa aacatgaaga accatggctg ctgcctgagc ccatcgtgct gtaattatag  
1741 aaaaccttct aagggaagaa tatgtctgata ttttctcagat aagtaccctt ttataaaaa  
1801 tctccaagt tagccctcga ttttccatgt aaggaaacag aggccttgag ataagtctctg  
1861 tctcctaagg gacaaagcca ggacttgatc ctgtcttaaa aatgcaaaat gtagtacttc  
1921 ttccatcaaa ggtagacatg cactaaggga caggttttgg cttggtatca gaatacattt  
1981 ttaaaagctg tgtaagaatt gaacgggctg tactaggggg tata  
1 gatcttttcta agtacgatgt tcaagtgaga gcagcagtga gctccatgtg cagagaggca  
61 gggctctgga gtgagtggag ccaacctatt tatgtgggaa atgatgaaca caagcccttg  
121 agagagtgggt ttgtcattgt gattatggca accatctgct tcatcttggt aattctctcg  
181 cttatctgta aaatatgtca tttatggatc aagttgtttc caccaattcc agcaccaaaa  
241 agtaatatca aagatctctt tgtaaccact aactatgagg tctctgcat tttcatatac  
301 atcttagatt cggctgacaa ttttctacaa aaaaagaaag ctgggtccag tgagacggaa  
361 attgaagtca tctgttatat agagaagcct ggagtggaga ccctggagga ttctgtgttt  
421 tgactgtcac tttggcatcc tctgatgaac tcacacatgc ctgagtgcct cagtgaagag  
481 aacagggatg ctggctcttg gctaagaggt gttcagaatt taggcaacac tcaatttacc  
541 tgcgaagcaa tacaccaga cacaccagtc ttgtatctct taaaagtatg gatgcttcac  
601 ccaaatcgcc tcacctacag cagggaagtt gactcatcca agcatttttg catgtttttt  
661 ctccccatgc cgtacagggt agcacctcct cacctgccaa tctttgcaat ttgcttgact  
721 cacctcagac ttttcattca caacagacag cttttaaggc taacgtccag ctgtatttac  
781 ttctggctgt gccggtttgg ctgtttaagc tgccaattgt agcactcagc taccatctga  
841 ggaagaaagc attttgcatc agcctggagt gaaccatgaa cttggattca agactgtctt  
901 ttctatagca agtgagagcc acaaattcct c  
1 ccgctgcttc tcatcgcatg gccaccgat ttctcaggcc aggcacattg agcattggtc  
61 ctgtgcctga cgctatgcta gatgctgggg ttgcagccac gagcatagac acgacagaca  
121 cggctcctgc catcttctgt tgagtactgg tcggaacaag aggatcgtct gtagacaggc  
181 tacagattgt ttagattga agtttctctgt catgttccat catctttaaa tctcatagt  
241 aaaaaggata tgatcatcgt ggcgcatgta ttactcatcc ttttgggggc cactgagata  
301 ctgcaagctg acttacttcc tgatgaaaag atttcacttc tcccacctgt caatttcacc  
361 attaaagtta ctggtttggc tcaagttctt ttacaatgga aaccaaattc tgatcaagag  
421 caaaggaatg ttaatctaga atatcaagtg aaaataaacg ctccaaaaga agatgactat  
481 gaaaccagaa tcactgaaag caaatgtgta accatcctcc acaaagggt ttgagcaagt  
541 gtgcggacca tctgcagaa cgaccactca ctactggcca gcagctgggc ttctgtgaa  
601 cttcatgccc caccagggtc tcttggaaacc tcaattgtga atttaacttg caccacaaac  
661 actacagaag acaattattc acgtttaagg tcataccaag ttcccttca ctgcacctgg  
721 cttgttggca cagatgcccc tgaggacacg cagtattttc tctactatag gtatggctct  
781 tggactgaag aatgccaaaga atacagcaaa gacacactgg ggagaaatat cgcatgctgg  
841 tttccaggga cttttatcct cagcaaaggg cgtgactggc tttcggtgct tggttaacggc  
901 tccagcaagc actctgctat caggcccttt gatcagctgt ttgcccttca cgccattgat  
961 caaataaatc ctccactgaa tgtcacagca gagattgaag gaactcgtct ctctatccaa  
1021 tgggagaaac cagtgtctgc ttttccaatc cattgctttg attatgaagt aaaaatacac  
1081 aatacaagga atggatattt gcagatagaa aaattgatga ccaatgcatt catctcaata  
1141 attgatgatc tttctaagta cgatgttcaa gtgagagcag cagtgaagtc catgtgcaga  
1201 gaggcagggc tctggagtga gtggagccaa cctattttatg tgggggtctc aagataaagg  
1261 agataacatc cagcttttct gccccacacc gtatctgaaa taaaaacaac agcagggata  
1321 gcagatt  
1 ccgctgcttc tcatcgcatg gccaccgat ttctcaggcc aggcacattg agcattggtc  
61 ctgtgcctga cgctatgcta gatgctgggg ttgcagccac gagcatagac acgacagaca  
121 cggctcctgc catcttctgt tgagtactgg tcggaacaag aggatcgtct gtagacaggc  
181 tacagattgt ttagattga agtttctctgt catgttccat catctttaaa tctcatagt  
241 aaaaaggata tgatcatcgt ggcgcatgta ttactcatcc ttttgggggc cactgagata  
301 ctgcaagctg acttacttcc tgatgaaaag atttcacttc tcccacctgt caatttcacc  
361 attaaagtta ctggtttggc tcaagttctt ttacaatgga aaccaaattc tgatcaagag  
421 caaaggaatg ttaatctaga atatcaagtg aaaataaacg ctccaaaaga agatgactat

481 gaaaccagaa tcaactgaaag caaatgtgta accatcctcc acaaaggctt ttcagcaagt  
541 gtgaggacca tcctgcagaa cgaccactca ctactggcca gcagctgggc ttctgctgaa  
601 cttcatgccc caccagggtc tcctggaacc tcaattgtga atttaacttg caccacaaac  
661 actacagaag acaattattc acgtttaagg tcataccaag tttcccttca ctgcacctgg  
721 cttgttgcca cagatgcccc tgaggacacg cagtattttc tctactatag gtatggctct  
781 tggactgaag aatgccaaga atacagcaaa gacacactgg ggagaaatat cgcatgctgg  
841 tttcccagga cttttatcct cagcaagggt cgtgactggc tttcgggtgt tgtaaacggc  
901 tccagcaagc actctgctat caggcccttt gatcagctgt ttgcccttca cgccattgat  
961 caaataaatc ctccactgaa tgtcacagca gagattgaag gaactcgtct ctctatccaa  
1021 tgggagaaac cagtgtctgc ttttccaatc cattgctttg attatgaagt aaaaatacac  
1081 aatacaagga atggatattt gcagatagaa aaattgatga ccaatgcatt catctcaata  
1141 attgatgac tttctaagta cgatgttcaa gtgagagcag cagtgaagtc catgtgcaga  
1201 gaggcagggc tctggagtga gtggagccaa cctatttatg tgggaaatga tgaacacaag  
1261 attttacatt ggcagccttc cttgtgatca aaaaaggtaa tcccagaaac gtaccggctc  
1321 actcgtgggt cttaaaatgg tttcatatct ctattgtgac taattttctc tcgggtctact  
1381 gccttttcaa tcaggaatag atttgccatg aagccagtga agtttttaag tgtctaggct  
1441 tctcattagt gccaactctc ctgacactgg tgcctgtttt ttttccaagt ttgttttcta  
1501 cttctatcca ttttttaaat taaacttttt attttgaaat aattatcaca ctcacaagct  
1561 gtgggaagaa ataatagaga tcctgtgtct ctttcatcca gttttcctca agggtaacat  
1621 ctacaaaac tatagtacaa tagtgaata gaattttgg tgtt  
1 ccgctgcttc tcactgcatg gccaccgcat ttctcaggcc aggcacattg agcattggct  
61 ctgtgctga cgctatgcta gatgtgggg ttgcagccac gagcatagac acgacagaca  
121 cggctcctgc catcttctgt tgagtactgg tcggaacaag aggatcgtct gtagacaggc  
181 tacagattgt tttagattga agtttctgt catgttact catctttaa tcctcatagt  
241 aaaaaggata tgatcatcgt ggcgatgta ttactcatcc ttttgggggc cactgagata  
301 ctgcaagctg acttacttcc tgatgaaaag atttacttcc tcccacctgt caatttcacc  
361 attaaagtta ctggtttggc tcaagttctt ttacaatgga aaccaaattc tgatcaagag  
421 caaaggaatg ttaattctaga atatcaagtg aaaaataacg ctccaaaaga agatgactat  
481 gaaaccagaa tcaactgaaag caaatgtgta accatcctcc acaaaggctt ttcagcaagt  
541 gtgaggacca tcctgcagaa cgaccactca ctactggcca gcagctgggc ttctgctgaa  
601 cttcatgccc caccagggtc tcctggaacc tcaattgtga atttaacttg caccacaaac  
661 actacagaag acaattattc acgtttaagg tcataccaag tttcccttca ctgcacctgg  
721 cttgttgcca cagatgcccc tgaggacacg cagtattttc tctactatag gtatggctct  
781 tggactgaag aatgccaaga atacagcaaa gacacactgg ggagaaatat cgcatgctgg  
841 tttcccagga cttttatcct cagcaagggt cgtgactggc tttcgggtgt tgtaaacggc  
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1441 gagacggaat ttgaagtcatt ctgttatata gagaagcctg gagttgagac cctggaggat  
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1681 atgcttcac caaatcgctt cacctacagc aggaaggtg actcatccaa gcattttgac  
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1981 ctgtcttttc tatagcaa  
1 gtcttttgaa aggatctgcc gctgcttctc atcgcatggc caccgcattt ctcaggccag  
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241 cactgagata ctgcaagctg acttacttcc tgatgaaaag atttacttcc tcccacctgt  
301 caatttcacc attaaagtta ctggtttggc tcaagttctt ttacaatgga aaccaaattc  
361 tgatcaagag caaaggaatg ttaattctaga atatcaagtg aaaaataacg ctccaaaaga  
421 agatgactat gaaaccagaa tcaactgaaag caaatgtgta accatcctcc acaaaggctt  
481 ttcagcaagt gtgaggacca tcctgcagaa cgaccactca ctactggcca gcagctgggc  
541 tttcgtgaa cttcatgccc caccagggtc tcctggaacc tcaattgtga atttaacttg  
601 caccacaaac actacagaag acaattattc acgtttaagg tcataccaag tttcccttca  
661 ctgcacctgg cttgttgcca cagatgcccc tgaggacacg cagtattttc tctactatag  
721 gtatggctct tggactgaag aatgccaaga atacagcaaa gacacactgg ggagaaatat  
781 cgcagctgg tttcccagga cttttatcct cagcaagggt cgtgactggc ttgctgtgct

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841 tgttaacggc tccagcaagc actctgctat caggcccttt gatcctgt ttgcccttca
901 cgccattgat caaataaatc ctccactgaa tgtcacagca gagattgaag gaactcgtct
961 ctctatccaa tgggagaaac cagtgtctgc ttttccaatc cattgctttg attatgaagt
1021 aaaaatacac aatacaagga atggatattt gcagatagaa aaattgatga ccaatgcatt
1081 catctcaata attgatgatc tttctaagta cgatgttcaa gtgagagcag cagtgaagtc
1141 catgtgcaga gaggcagggc tctggagtga gtggagccaa cctatttatg tgggtaagta
1201 gcttatgttt attttacatt ggcagccttc cttgtgatca aaaaaggtaa tcccagaaac
1261 gtacccggtc actcgtgggt cttaaaatgg tttcatatct ctattgtgac taattttctc
1321 tcggtctact gccttttcaa tcaggaatag atttgccatg aagccagtga agtttttaag
1381 tgtctaggct tctcattagc gccac
1 cggtcctcgc catcttctgt tgagtactgg tcggaacaag aggatcgtct gtagacagga
61 tatgatcatc gtggcgcatg tattactcat ccttttgggg gccactgaga tactgcaagc
121 tgacttactt cctgatgaaa agatttcaact tctcccacct gtcaatttca ccattaaagt
181 tactggtttg gctcaagttc ttttacaatg gaaaccaaact cctgatcaag agcaaaaggaa
241 tgttaactca gaatatcaag tgaaaataaa cgctccaaaa gaagatgact atgaaccag
301 aatcactgaa agcaaatgtg taaccatcct ccacaaaggc ttttcagcaa gtgtgaggac
361 catcctgcag aacgaccact cactactggc cagcagctgg gcttctgctg aacttcattg
421 cccaccaggg tctcctggaa cctcagttgt gaatttcaact tgcaccacaa acactacaga
481 agacaattat tcacgtttaa ggtcatacca agtttccctt cactgcacct ggcttgttg
541 cacagatgcc cctgaggaca cgcagtattt tctctactat aggtatggct cttggactga
601 agaatgccaa gaatacagca aagacacact ggggagaaat atcgcatgct ggtttcccag
661 gacttttatc ctcagcaaaag ggcgtgactg gcttgccgtg cttgttaacg gctccagcaa
721 gcactctgct atcaggccct ttgatcagct gtttgcctt cagccattg atcaataaaa
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901 gaatggatat ttgcagatag aaaaattgat gaccaatgca ttcattctca taattgatga
961 tctttctaag tacgatgttc aagtgaagc agcagtgaag tccatgtgca gagaggcagg
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1261 aattgaagtc atctgttata tagagaagcc tggagttgag accctggagg attctgtgtt
1321 ttgactgtca ctttggcatc ctctgatgaa ctcacacatg cctcagtgcc tcagtgaaaa
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1441 ctgcgaagca atacacccag acacaccagt cttgtatctc ttaaaagtat ggatgcttca
1501 tccaaatcgc ctcacctaca gcagggaagt tgactcatcc aagcattttg ccatgtttt
1561 tctccccatg ccgtacaggg tagcacctcc tcacctgcca atctttgcaa tttgcttgac
1621 tcaactcaga cttttcattc acaacagaca gcttttaagg ctaacgtcca gctgtattta
1681 cttctggctg tgcccgtttg gctgtttaag ctgccaattg tagcactcag ctaccatctg
1741 aggaagaaag cattttgcat cagcctggag tgaatcatga acttggtatc aagactgtct
1801 tttctatagc aagtgaagc cacaattcc tcacccccct acattctaga atgatctttt
1861 tctaggtaga ttgtgtatgt gtgtgtatga gagagagaga gagagagaga gagagagaga
1921 gagaaattat ctcaagctcc agaggcctga tccaggatac atcatttgaa accaactaat
1981 ttaaaagcat aatagagcta atatat

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## (2) INFORMATION FOR SEQ ID NO:2556:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5161 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2556:

```

1 gaattcagta acccaggcat tattttatcc tcaagtctta ggttggttgg agaaagataa
61 caaaaagaaa catgatttg cagaaacaga caaacctttt tggaaagcat ttgaaaatgg
121 cattccccct ccacagtgtg ttcacagtgt gggcaaatc actgctctgt cgtactttct
181 gaaaatgaag aactgttaca ccaaggtgaa ttatttataa attatgtact tgcccagaag
241 cgaacagact tttactatca taagaaccct tcttgggtgt gctctttatc tacagaattc
301 aagacctttc aagaaaggtc ttggattctt ttcttcagga cactaggaca taaagccacc
361 tttttatgat ttgttgaaat ttctactcc atcccttttg ctgatgatca tgggtcctca
421 gaggtcagac ttggtgtcct tggataaaga gcatgaagca acagtggctg aaccagagtt
481 ggaacccaga tgctctttcc actaagcata caactttcca ttagataaca cctccctccc
541 accccaacca agcagctcca gtgcaccact ttctggagca taaacatacc ttaactttac
601 aacttgagtg gccttgaata ctgttcctat ctggaatgtg ctgttctctt tcatcttctt
661 ctattgaagc cctcctatc ctcaatgcct tgctccaact gcctttggaa gattctgctc
721 ttatgcctcc actggaatta atgtcttagt accactgtgc tattctgcta tatagtcagt
781 ccttacattg ctttcttctt ctgatagacc aaactcttta aggacaagta cctagtctta
841 tctatttcta gatccccac attactcaga aagttactcc ataaatgttt gtggaactga
901 tttctatgtg aagacatgtg ccccttcact ctgttaacta gcattagaaa aacaaatctt
961 ttgaaaagtt gtagtatgcc cctaagagca gtaacagttc ctagaactc tctaaaatgc

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1021 ttagaaaaag atttatttta aattacctcc ccaataaaat gattggctcg cttatcttca  
1081 ccatcatgat agcatctgta attaactgaa aaaaaataat tatgccatta aaagaaaatc  
1141 atccatgatc ttgttctaac acctgccact ctagtactat atctgtcaca tgggtctatga  
1201 taaagttatc tagaaaaaa aaagcataca attgataatt caccaaattg tggagcttca  
1261 gtatttttaa tgtatttaa aattaaataa ttttaaagat caaagaaaac tttcgtcata  
1321 ctccgtattt gataaggaac aaataggaag tgtgatgact caggtttgcc ctgaggggat  
1381 gggccatcag ttgcaaatcg tggaaatttcc tctgacataa tgaaaagatg aggggtgcata  
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1501 tcagagacag cagagcacac aagcttctag gacaagagcc aggaagaaac caccggaagg  
1561 aaccattctc actgtgtgta aacatgactt ccaagctggc cgtggctctc ttggcagcct  
1621 tcctgatttc tgcagctctg tgtgaaggta agcacatctt tctgacctac agcgttttcc  
1681 tatgtctaaa tgtgatcctt agatagcaaa gctattcttg atgcttttgt aacaaacatc  
1741 ctttttattc agaaaacagaa tataatctta gcagtcaatt aatgttaaat tgaagattta  
1801 gaaaaaacta tatataacac ttaggaaata taaaggtttg atcaatatag atattctgct  
1861 tttataattt ataccaggta gcatgcatat atttaacgta aataagtaat ttatagtatg  
1921 tcctattgag aaccacggtt acctatatta tgtattaata ttgagttgag caaggttaact  
1981 cagacaattc cactccttgt agtatttcat tgacaagcct cagattttgtc attaatctct  
2041 gtctggttta aagataccct gattatagac caggcatgta taacttattt atatatctct  
2101 gttattctt tctgaaggca atttctatgc tggagagtct tagcttgctc actataaata  
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2281 tgactgtttt ttaaaacaaa gaactaactg aggtcaaggg ctaggagata ttcaggaatg  
2341 agttcactag aaacatgatg ccttccatag tctccaaata atcatattgg aattagaagg  
2401 aagtagctgg cagagctgtg cctgttgata aaatcaatcc ttaatcactt tttcccccaa  
2461 cagggtgcagt tttgccagg agtgctaaag aacttagatg tcagtgcata aagacatact  
2521 ccaaaccctt ccaccccaaa tttatcaaag aactgagagt gattgagagt ggaccacact  
2581 ggcaccaac agaaattatg taagtacttt aaaaagatt agatattttg ttttagcaaa  
2641 cttaaaatta aggaagggtg aaatattttg gaaagttcca ggtgttaga ttacagttagt  
2701 aaatgaaaca aaacaaaata aaaatatttg tctacatgac atttaaatat ggtagcttcc  
2761 acaactacta taaatgttat tttggactta gactttatgc ctgacttaag gaatcatgat  
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3361 ttattttagg gctgagaatt cataaaaaaa ttcattctct gtggtatcca agaatacagt  
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3601 atttgaatct acaaaaaaca acaataaatt tttaaatata aggattttcc tagatattgc  
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3781 ggacaataaa ttttgccata aagtcaaatt tagctggaaa tcttggtatt ttttctgta  
3841 aatctggcaa cctagtctg ctaggcagga tccacaagtc cttgttccca tgtgccttgg  
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3961 gtgaggacat gtggaagcac ttttaagttt ttcatacata cataaattat tttcaagtgt  
4021 aacttattaa cctatttatt atttatgtat ttatttaagc atcaaatatt tgtgcaagaa  
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4201 taacaaaaca acaattggg taccaggtta aattttcatt tcagatatat aacaaaataat  
4261 ttttttagat aagtacatta ttgtttatct gaaattttta ttgaactaac aatcctagtt  
4321 tgatactccc agtctgtca ttgcccagtg tgttggtagt gctgtgtga attacggaat  
4381 aatgagttag aactattaaa acagccaaaa ctccacagtc aatattatga atttctgtct  
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4981 aggagtaaaa ctgataaatg tgaggcaaaag aagtttaaaa tatggttaaa gcctaagcat  
5041 atttgcaaac aaatcaaaaa atactctgag aagtaaaaac ataattattt aattaacaaa

5101 tttcag taaattttat aacaaattag acacagttga aaa att agaaaactag  
 5161 aaaatagaac aaaagaaact tctggaattc a

## (2) INFORMATION FOR SEQ ID NO:2557:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1981 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2557:

1 tattcatcaa gtgccctcta gctgttaagt cactctgac tctgactgca gctcctactg  
 61 ttggacacac ctggccggtg cttcagtttag atcaaaccat tgctgaaact gaagaggaca  
 121 tgtcaaatat tacagatcca cagatgtggg attttgatga tctaaatttc actggcatgc  
 181 cacctgcaga tgaagattac agcccctgta tgctagaaac tgagacactc aacaagtatg  
 241 ttgtgatcat cgcctatgcc ctagtgttcc tgctgagcct gctgggaaac tccctggtga  
 301 tgctggtcat cttatacagc agggctcggc gctcctcac tgatgtctac ctgctgaacc  
 361 tggccttggc cgacctactc ttggccctga ccttgcccat ctgggcccgc tccaagggtga  
 421 atggctggat ttttgccaca ttctgtgca aggtggtctc actcctgaag gaagtcaact  
 481 tctacagtgg catcctgctg ttggcctgca tcagtgtgga ccgttacctg gccattgtcc  
 541 atgccacacg cacactgacc cagaagcgtc acttggtcaa gttgtttgt cttggctgct  
 601 ggggactgtc tatgaatctg tccctgccct tcttcctttt ccgccaggct taccatccaa  
 661 acaattccag tccagtttgc tatgaggtcc tgggaaatga cacagcaaaa tggcggatgg  
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 901 tctgctggc agacaccctc atgaggacc aggtgatcca ggagagctgt gagcgccgca  
 961 acaacatcgg ccgggccctg gatgccactg agattctggg atttctccat agctgcctca  
 1021 accccatcat ctacgccttc atcgccaaa attttcgcca tggattctc aagatcctgg  
 1081 ctatgcatgg cctggtcagc aaggagtct tggcacgtca tctgtttacc tctacactt  
 1141 ctctgtctgt caatgtctct tccaacctct gaaaaccatc gatgaaggaa tatctcttct  
 1201 cagaaggaaa gaataaccaa caccctgagg ttgtgtgtgg aagtgatct ggctctggac  
 1261 aggcactatc tgggttttgg ggggacgcta taggatgtgg ggaagttagg aactggtgct  
 1321 ttcaggggcc acaccaacct tctgaggagc tgttgaggta cctccaagga ccggcctttg  
 1381 caccctccatg gaaacgaagc accatcattc ccgttgaacg tcacatcttt aaccactaa  
 1441 ctggctaatt agcatggcca catctgagcc ccgaatctga cattagatga gagaacaggg  
 1501 ctgaagctgt gtcctcatga gggctggatg ctctcgttga ccctcacagg agcatctcct  
 1561 caactctgag tgtaagcgt tgagccacca agctggtggc tctgtgtgct ctgatccgag  
 1621 ctgagggggg tggttttccc atctcagggtg tgttgcatgt tctgctggag acattgaggc  
 1681 aggcactgcc aaaacatcaa cctgccagct ggccttgta ggagctggaa acacatgttc  
 1741 cccttggggg tgggtgatga acaaagagaa agaggggttg gaagccagat ctatgccaca  
 1801 agaaccctct ttaccccat gaccaacatc gcagacacat gtgctggcca cctgtgagc  
 1861 cccaagtga acgagacaag cagcccttag cccttcccct ctgcagcttc caggctggcg  
 1921 tgcagcatca gcattcctag aaagccatgt gcagccacca gtccattggg caggcagatg  
 1981 ttctaataa agcttctgtt ccgtgct

## (2) INFORMATION FOR SEQ ID NO:2558:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1741 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2558:

1 cctacagggtg aaaagcccag cgaccagtc aggatttaag tttacctcaa aaatggaaga  
 61 ttttaacatg gagagtgaac gctttgaaga tttctggaaa ggtgaagatc ttagtaatta  
 121 cagttacagc tctaccctgc ccccttttct actagatgcc gcccatgtg aaccagaatc  
 181 cctggaaatc aacaagtatt ttgtggtcat tatctatgcc ctggtattcc tgctgagcct  
 241 gctgggaaac tccctcgtga tgctggtcat cttatacagc agggctcggc gctcctcac  
 301 tgatgtctac ctgctgaacc tagccttggc cgacctactc tttgccctga ccttgcccat  
 361 ctgggcccgc tccaagggtg atggctggat ttttgccaca ttctgtgca aggtggtctc  
 421 actcctgaag gaagtcaact tctatagtgg catcctgcta ctggcctgca ctagtgtgga  
 481 ccgttacctg gccattgtcc atgccacagc cacactgacc cagaagcgtc acttggtcaa  
 541 attcatatgt ctcagcatct ggggtctgtc cttgtctctg gccctgcctg tcttactttt  
 601 ccgaaggacc gtctactcat ccaatgttag cccagcctgc tatgaggaca tgggcaacaa  
 661 tacagcaaac tggcggatgc tgttacggat cctgccccag tcccttggct tcatcgtgcc  
 721 actgctgatc atgctgttct gctacggatt caccctgcgt acgctgttta agggccacat  
 781 ggggcagaag caccgggcca tgcgggtcat ctttgtgtc gtctcatct tctgtctttg  
 841 ctggtgcccc tacaacctgg tctgtgtggc agacaccctc atgaggaccc aggtgatcca  
 901 ggagacctgt gagcgccgca atcacatcga ccgggctctg gatgccaccg agattctggg  
 961 catccttcac agctgcctca accccctcat ctacgccttc attggccaga agtttcgcca



```

1021 tggactcctc aagattctag ctatacatgg cttgatcagc aaggactccc tgcccaaaga
1081 cagcaggcct tcctttgttg gctcttcttc agggcacact tccactactc tctaagacct
1141 cctgcctaag tgcagccccg tggggttctt cccttctctt cacagtcaca ttccaagcct
1201 catgtccact ggttcttctt ggtctcagtg tcaatgcagc ccccatgtg gtacacaggaa
1261 gcagaggagg ccacgttctt actagtctcc cttgcatggg ttagaaaagt tgccctgggtg
1321 cctaccccc tgcataatt actatgtcat ttgctggagc tctgcccctc tgcccctga
1381 gcccatggca ctctatgttc taagaagtga aaatctacac tccagtgaag cagctctgca
1441 tactcattag gatggctagt atcaaaagaa agaaaatcag gctggccaac gggatgaaac
1501 cctgtctcta ctaaaaatac aaaaaaaata aaaaaaatta gccggcgctg gtggtgagtg
1561 cctgtaatac cagctacttg ggaggctgag atgggagaa cacttgaaac cgggaggcag
1621 aggttgcatg gagccgagat tgtgcccttg cactccagcc tgagcgacag tgagactctg
1681 tctcagtcga tgaagatgta gaggagaaac tggaaacttc gagcgttgct gggggggatt
1741 gtaaaatggt

```

## (2) INFORMATION FOR SEQ ID NO:2559:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1801 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2559:

```

1 ggatccaagt aggtatgagt gtcctgtagt tattatccac agggaaacatt ctacaaagtt
61 ttgggagact gtaatgtcat gggaaatgca agaataatgtg tccagcatgg aagggaatca
121 gtatgggaagt cttttgataa atttggcat ttactactaa cattgcctca aaactttaga
181 ctacctgcca tatacaaat agaggtgaaa attacttcca tgtaataac aagccaacac
241 aaagaatcct atcccagttt cttggatgga taggcaagaa tctgggtaag gtttattgtg
301 caataatcct cttctctctt ctataggcca ggatttaagt ttacctcaa aatggaaaat
361 tttggctggg aaaattacat gtgggaagac atcttcagtg gagattttag taattacagt
421 ttcagctatg accctacccc ttttctacta gattctgccc catgttggcc agaattcccta
481 gaaatcaatt atgttttgat catcatctat gccctgatgt ttctactgaa cgtgatgtga
541 aactccctgc cgatgctggt catcttattc agctgagtca gccactgtca ccgatgtcta
601 cctgctgacc ctggccttgg ccgacctgtt ctttccctg acattgccc tcttggctgc
661 ctccaagatg aatggctgga tttttggcac aatctgtgcc aggtggtcta gtcctgaag
721 gaagtcaact tctacggtgg tattctacta ctggcctgcc gcagcatgga ctgtacctg
781 gccattgtcc atgccacacg cacactgacc cagcagcgcc acttggtcaa gttcatatgt
841 ctgggtttgt ggaacctgtt cctgttactg tcctacgca tcttgcttt ccgaaggacc
901 ttctacccat ccaatgttag ccagctctgc tatgaggaca tgggcaacaa tacagcaaac
961 tgggtgatgc tgttacggat cctgcccaga tcctttggct tcatcgtgcc gctgcatca
1021 tgctgttctg ctacagattc accctgcata cgctgtttaa ggcccatatg gggcagaagc
1081 actggaccat gtgggtcatc tttgctgttg tctcatttt cctgctctgc tggctgcctt
1141 acaacctggt cctgctggca gacacctca tgggaacca gatgaccaat gagacctgtg
1201 agcgcgcaa cgacatcaac caggccctgg atgccactga gattctggg atccttcaca
1261 gctacctcaa tcccctcatc tacgccttca ttggccagaa gttttgccat ggacttctca
1321 agattatagc catacacggc ttgatcagca aggactccct gcccaaagac agcaggcctt
1381 cctttgttgg ctcttcttca gggcacactt ccactactc ctaagacctc ttgcctaagt
1441 gcagtcctgt ggggttctc ccttcttctc acagtcacat tccaagctc atgtccacta
1501 gctcttcttg gtctcagtg cagtgcagcc cccactgttg tcgcaggaag cagaggaggc
1561 cacgttctta ctagtctccc ttgcatgatt tagaaagcct gccctgttac ctcacctctt
1621 gccataatta ctacatcact tgcctggagc ctgtccctcc tgcccttgag ctcatggcac
1681 tctatgttct aagaagtga aatctacact ccagtggagc agctctgcat actcattag
1741 atgggttaatg tcagaagaaa gaaaatcata aaatagaagg tgtccacaaa ggtgcagatg
1801 ataagtg

```

## (2) INFORMATION FOR SEQ ID NO:2560:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1501 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2560:

```

1 gtcaggattt aagtttacct caaaaatgga agattttaac atggagagtg acagctttga
61 agatttcttg aaaggtgaag atcttagtaa ttacagttac agctctaccc tgcccccttt
121 tctactagat gccgccccat gtgaaccaga atccctggaa atcaacaagt attttgggt
181 cattatctat gccctggat tctgctgag cctgctggga aactccctcg tgatgctgtg
241 catcttatac agcagggtcg cccgctccgt cactgatgtc tacctgctga acctagcctt
301 ggccgacctc ctctttgccc tgaccttgcc catctgggcc gcctccaagg tgaatggctg
361 gatttttggc acattcctgt gcaaggtggt ctactcctg aaggagtgca acttctatag
421 tggcatcctg ctactggcct gcatcagtg ggaccgttac ctggccattg tccatgccac
481 acgcacactg acccagaagc gctacttggt caaattcata tgtctcagca tctggggtct

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541 gtccttggc ctggccctgc ctgtcttact ttccgaagg accgcttact catccaatgt  
601 tagccagcc tgctatgagg acatgggcaa caatacagca aactggcgga tgctgttacg  
661 gatcctgcc cagtcctttg gcttcacgt gccactgctg atcatgctgt tctgtacgg  
721 attcaccctg cgtacgctgt ttaaggcca catggggcag aagcaccggg ccatgcgggt  
781 catctttgct gtcgtcctca tcttctgtct ttgctggctg ccctacaacc tggctctgct  
841 ggcagacacc ctcatgagga ccaggtgat ccaggagacc tgtgagcgc gcaatcacat  
901 cgaccgggct ctggatgcca ccgagattct gggcatcctt cacagctgcc tcaaccctt  
961 catctacgcc ttcatggcc agaagtttcg ccatggactc ctcaagattc tagctatata  
1021 tggcttgatc agcaaggact cctggcccaa agacagcagg ccttccttg ttggctcttc  
1081 ttcagggcac acttcacta ctctctaaga cctcctgcct aagtgcagcc cgtggggttc  
1141 ctcccttctc ttcacagtca cattccaagc ctcatgtcca ctggttcttc ttggtctcag  
1201 tgtcaatgca gccccattg tggtcacagg aagcagagga ggccacgttc ttactagttt  
1261 cccttgcatg gttagaaag ctgcccctgg tgcctcacc cttgccataa ttactatgtc  
1321 atttgctgga gctctgcca tctgcccct gagcccatgg cactctatgt tctaagaagt  
1381 gaaaatctac actccagtga gacagctctg catactcatt aggatggcta gtatcaaaag  
1441 aaagaaaatc aggtggcca acgggatgaa accctgtctc tactaaaaat acaaaaaaaa  
1501 aaaaaaaaaa

## (2) INFORMATION FOR SEQ ID NO:2561:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2221 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2561:

1 gggagaaaca tagggaatag aaaataagta agaaggggac acctgggaac aggtttgcct  
61 tcttgcatth tgcttaatgc tggcccttcc ctgaatgtct aagaccaacc tgggtccccac  
121 atccaaatgc acagacacag ctgaggatgg agaaggctaa agagggacag aggttagagac  
181 ataggctgag aggaggcagt tgtaggttga gctagggcta aggtgtttc cccatattcc  
241 atcttaccac aactcaggc caggccttag agttgtggaa ggtggagaac actgggaagc  
301 caacctccga agaagaccag gttggagtca aaggaggaag gagagctctc attgccaaac  
361 caacagggaa gccaaggata tcccagtaac tgctctcaca tcattgatga gaatgccttg  
421 aatccgagct actaaatcac atttcttcc ttctaaccctt ccagtttagat caaaccattg  
481 ctgaaactga agaggacatg tcaaataatta cagatccaca gatgtgggat ttgatgatc  
541 taaatttcac tggcatgcca cctgcagatg aagattacag cccctgtatg ctgaaactg  
601 agacactcaa caagtatggt gtgatcatcg cctatgccct agtgttctg ctagcctgc  
661 tgggaaactc cctgggtgatg ctggtcatct tatacagcag ggtcgccgc tccgtcactg  
721 atgtctacct gctgaacctg gccttgccg acctactctt tggcctgacc ttgccatct  
781 gggccgctc caaggtgaat ggctggattt ttggcacatt cctgtgcaag gtggtctcac  
841 tctgaagga agtcaacttc tacagtggca tctgtctgtt ggctgcatc agtgtggacc  
901 gttacctggc cattgtccat gccacacgca cactgaccca gaagcgtcac ttggtcaagt  
961 ttgtttgtct tggctgtggt ggactgtcta tgaatctgtc cctgcccttc ttcttttcc  
1021 gccaggctta ccattccaaac aattccagtc cagtttgcta tgaggtcctg ggaaatgaca  
1081 cagcaaaatg gcggatgggtg ttgcggatcc tgcctcacac ctttggcttc atcgtgccgc  
1141 tgtttgtcat gctgttctgc tatggattca cctgctgtac actgtttaag gccacatgg  
1201 ggcagaagca ccgagccatg aggtcatctt ttgctgtcgt cctcatcttc ctgctttgct  
1261 ggtgccccta caacctgggtc ctgctggcag acaccctcat gaggaccag gtgatccagg  
1321 agagctgtga gcgcccgaac aacatcgccc gggccctgga tgccactgag attctgggat  
1381 ttctccatag ctgcctcaac cccatcatct acgcttcat cggccaaaat ttctgccatg  
1441 gattccctca gatcctgggt atgcatggcc tggtcagcaa ggagttcttg gcacgtcatc  
1501 gtgttacctc ctacacttct tcgtctgtca atgtctcttc caacctctga aaaccatcga  
1561 tgaaggaata tctcttctca gaaggaaaga ataaccaaca ccttgaggtt gtgtgtggaa  
1621 ggtgatctgg ctctggacag gcactatctg ggttttgggg ggacgtata ggatgtgggg  
1681 aagttaggaa ctggtgtctt caggggccac accaaccttc tgaggagctg ttgaggtacc  
1741 tccaaggacc ggcctttgca cctccatgga aacgaagcac catcattccc gttgaacgtc  
1801 acatctttaa cccactaact ggctaattag catggccaca tctgagcccc gaatctgaca  
1861 ttgatgaga gaacagggtc gaagctgtgt cctcatgagg gctggatgct ctggttgacc  
1921 ctacacaggag catctcctca actctgagtg ttaagcgttg agccaccaag ctggtggctc  
1981 tgtgtgctct gatccgagct caggggggtg gttttcccat ctcaggtgtg ttgaggtgtc  
2041 tgcgtggagac attgaggcag gcaactgcaa aacatcaacc tgccagctgg cctgttgagg  
2101 agctggaaac acatgttccc cttgggggtg gtggatgaac aaagagaaag aggttttga  
2161 agccagatct atgccacaag aacccctttt acccccatga ccaacatcgc agacacatgt  
2221 gctggccacc tgcgtgagccc caagt

## (2) INFORMATION FOR SEQ ID NO:2562:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9245 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2562:

```
1  tattcatcaa gtgccctcta gctgttaagt cactctgata tctgactgca gctcctactg
61  ttggacacac ctggccggtg cttcagttag atcaaaacat tgctgaaact gaagaggaca
121 tgctaaatat tacagatcca cagatgtggg attttgatga tctaaatttc actggcactg
181 cactgcgaga tgaagattac agccctgtga tgctagaaac tgagacactc aacaagtatg
241 ttgtgatcat cgcctatgcc ctagtgttcc tgctgagcct gctgggaaac tccctggtga
301 tgctggtcat cttatacagc agggctcgcc gctccgtcac tgatgtctac ctgctgaacc
361 tggccttggc cgacctactc tttgccctga ccttgcccat ctgggcccgc tccaaggtga
421 atggctggat ttttggcaca ttctctgtga aggtggtctc actcctgaag gaagtcaact
481 tctacagtgg catcctgtcg ttggcctgca tcagtgtgga ccgttacctg gccattgtcc
541 atgccacacg cacactgacc cagaagcgct acttggtcaa gtttgtttgt cttggctgct
601 ggggactgtc tatgaatctg tccctggcct tcttctttt ccgccaggct taccatccaa
661 acaattccag tccagtgtgc tatgaggtcc tgggaaatga cacagcaaaa tggcggtagg
721 tgttgcggat cctgcctcac acctttggct tcacgtgtcc gctgtttgtc atgctgttct
781 gctatggatt caacctgcgt acaactgtta agggccacat ggggcagaag caccgagcca
841 tgagggatcat ctttgcctgc gtcctcatct tcctgctttg ctggtgccc tacaacctgg
901 tcctgctggc agacaccctc atgaggacc caggtgatcca ggagagctgt gagcgccgca
961 acaacatcgg ccgggcccctg gatgccactg agattctggg atttctccat agctgcctca
1021 accccatcat ctacgccttc atcgcccaaa attttcgcca tggattcctc aagatcctgg
1081 ctatgcatgg cctggtcagc aaggagtctt tggcacgtca tctgtttacc tctacactt
1141 cttcgtctgt caatgtctct tccaacctct gaaaaccatc gatgaaggaa tatctcttct
1201 cagaaggaaa gaataaccaa caccctgagg ttgtgtgtgg aaggtgatct ggctctggac
1261 aggcactatc tgggttttgg ggggacgcta taggatgtgg ggaagttagg aactggtgtc
1321 ttcaggggcc acaccaacct tctgaggagc tgttgaggtg cctccaagga ccggcctttg
1381 cactcccatg gaaacgaagc accatcattc ccgttgaacg tcacatcttt aaccactaa
1441 ctggctaatt agcatggcca catctgagcc ccgaatctga cattagatga gagaacaggg
1501 ctgaaactgt gtctcatgta gggctggatg ctctcgttga ccctcacagg agcatcctct
1561 caactctgag tgttaagcgt tgagccacca agctggtggc tctgtgtgct ctgatccgag
1621 ctcagggggg tggttttccc atctcagggt tgttgacgtg tctgctggag acattgaggc
1681 aggcactgcc aaaacatcaa cctgccagct ggccttgtga ggagctggaa acacatgttc
1741 cccttggggg tgggtgatga acaaaagaaa agagggtttg gaagccagat ctatgccaca
1801 agaaccctct ttaccccatc gaccaacatc gcagacacat gtgctggcca cctgctgagc
1861 ccaagtggga acgagacaag cagcccttag cccttcccct ctgcagcttc caggctggcg
1921 tgcagcatca gcatccctag aaagccatgt gcagccacca gtccattggg caggcagatg
1981 ttcctaataa agcttctgtt ccgtgct

1  cctacagggtg aaaagcccag cgaccagtc aggtatttaag tttacctcaa aaatggaaga
61  ttttaacatg gagagtgaac gctttgaaga tttctgaaa ggtgaagatc ttagtaatta
121 cagttacagc tctaccctgc ccccttttct actagatgcc gcccatgtg aaccagaatc
181 cctggaaatc aacaagtatt ttgtggtcat tatctatgcc ctggtattcc tgcctgacct
241 gctgggaaac tccctcgtga tgctggtcat cttatacagc agggctcgcc gctccgtcac
301 tgatgtctac ctgctgaacc tagccttggc cgacctactc tttgccctga ccttgcccat
361 ctgggcccgc tccaaggtga atggctggat ttttggcaca ttctctgtga aggtggtctc
421 actcctgaag gaagtcaact tctatagtgg catcctgcta ctggcctgca tcagtgtgga
481 ccgttacctg gccattgtcc atgccacaag cacactgacc cagaagcgct acttggtcaa
541 attcatatgt ctacgcatct ggggtctgtc cttgctcctg gccctgctg tcttactttt
601 ccgaaggacc gtctactcat ccaatgttag ccagccctgc tatgaggaca tgggcaacaa
661 tacagcaaac tggcggtatg tgttacggat cctgccccag tcccttggct tcacgtgtcc
721 actgctgac atgctgttct gctacggatt caccctgctg acgctgttta agggccacat
781 ggggcagaag caccgggcca tgcgggtcat ctttgcctgc gtcctcatct cctgctttg
841 ctggctgccc tacaacctgg tcctgctggc agacaccctc atgaggacc aggtgatcca
901 ggagacctgt gagcgccgca atcacatcga ccgggctctg gatgccacc agattctggg
961 catccttcac agctgcctca accccctcat ctacgccttc attggccaga agtttcgcca
1021 tggactcctc aagattctag ctatacatgg cttgatcagc aaggactccc tggccaaaga
1081 cagcaggcct tcccttgttg gctcttcttc agggcacact tccactactc tctaagacct
1141 cctgcctaag tgcagccccg tgggttctct ccttctctt cacagtcaaa ttccaagcct
1201 catgtccact ggttcttctt ggtctcagtg tcaatgcagc cccattgtg gtcacaggaa
1261 gcagaggagg ccacgttctt actagtcttc cttgcatggt ttagaaagct tgcctgtgtg
1321 cctcaccctc tgccataatt actatgtcat ttgctggagc tctgcccac ctgcccctga
1381 gccatggca ctctatgttc taagaagtga aaatctacac tccagtgaag cagctctgca
1441 tactcattag gatggctagt atcaaaaaga aaaaaatcag gctggccaac gggatgaaac
1501 cctgtctcta ctaaaaatac aaaaaaaaaa aaaaaatta gccgggctgt gtggtgagtg
1561 cctgtaatac cagctacttg ggaggctgag atgggagaat cacttgaacc cgggaggcag
1621 aggttgcatg gagccgagat tgtgccctg cactccagcc tgagcgacag tgagactctg
1681 tctcagttca tgaagatgta gaggagaaac tggaaactct gagcgttgct gggggggatt
1741 gtaaaatggt

1  ggatccaagt aggtattgag gtctcttagt tattatccac agggaaacat ctacaaagtt
61  ttgggagact gtaatgtcat gggaaatgca agaatatgtg tccagcatgg aagggaatca
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121 gtatggaggt cttttgataa attgtggcat ttatcactaa cattgctca aaactttaga  
181 ctacctgcca tatacaaatt agaggtgaaa attacttcca tgtaataatac aagccaacac  
241 aaagaatcct atcccagttt cttggatgga taggcaagaa tctgggtaag gtttattgtg  
301 caataatcct cttctctctt ctataggcca ggatttaagt ttacctcaaa aatggaaaat  
361 tttggctggg aaaattacat gtgggaagac atcttcagtg gagattttag taattacagt  
421 ttcagctatg accctacccc ttttctacta gattctgccc catgttgccc agaatcccta  
481 gaaatcaatt atgttttgat catcatctat gccctgatgt ttctactgaa cgtgatgtga  
541 aactccctgc cgatgctggc catcttatte agctgagtca gccactgtca ccgatgtcta  
601 cctgctgacc ctggccttgg ccgacctgtt cttttccctg acattgccc aattggctgc  
661 ctccaagatg aatggctgga tttttggcac aatctgtgcc aggtggctcta gctcctgaag  
721 gaagtcaact tctacgggtg tattctacta ctggcctgcc gcagcatgga ctgttacctg  
781 gccattgtcc atgccacacg cacactgacc cagcagcgcc acttggtcaa gttcatatgt  
841 ctgggtttgt ggaacctgtt cctgttactg tccctacgca tcttgctttt ccgaaggacc  
901 ttctacccat ccaatgttag cccagtctgc tatgaggaca tgggcaacaa tacagcaaac  
961 tgggtgatgc tgttacggat cctgccccag tcctttggct tcatcgtgcc gctgcgatca  
1021 tgcgtttctg ctacagattc accctgcata cgctgtttta ggcccatatg gggcagaagc  
1081 actgaccat gtgggtcatc ttgtctgttg tcttcatttt cctgctctgc tggctgcctt  
1141 acaacctggt cctgctggca gacacctca tgggaaccca gatgaccaat gagacctgtg  
1201 agcgccgcaa cgacatcaac caggccctgg atgccactga gattctgggc atccttcaca  
1261 gctacctcaa tcccctcatc tacgccttca ttggccagaa gttttgccat ggacttctca  
1321 agattatagc catacacggc ttgatcagca aggactccct gcccaaagac agcaggcctt  
1381 cctttgttgg ctcttcttca gggcacactt ccactactct ctaagacctc ttgcctaagt  
1441 gcagtcctgt ggggttcttc ccttctcttc acagtacat tccaagctc atgtccacta  
1501 gctctcttgg gtctcagttg cctgtcagcc ccactgtgg tcgcaggaag cagaggaggc  
1561 caggttctta ctagtctccc ttgcatgatt tagaaagcct gccctggtac ctcaccctt  
1621 gccataatta ctacatcact tgctggagct ctgtccctcc tgcccttgag ctcatggcac  
1681 tctatgttct aagaagtga aatctacact ccagtgaag agctctgcat actcattagg  
1741 atggttaatg tcagaagaaa gaaaatcata aaatagaagg tgtccacaaa ggtgcagatg  
1801 ataagtg  
1 gtcaggattt aagtttacct caaaaatgga agattttaac atggagagtg acagctttga  
61 agatttctgg aaaggtgaag atcttagtaa ttacagttac agctctaccc tgccccctt  
121 tctactagat gccgccccat ttggaaccaga atccctggaa atcaacaaga atttgtgtg  
181 cattatctat gccctggtat tcctgttgag cctgttgga aactccctcg tgatgctggt  
241 catcttatac agcagggtcg gccgtccgt cactgatgtc tacctgtgta acctagcctt  
301 ggccgacctt ctctttgccc tgaccttgcc catctgggcc gcctccaagg tgaatggctg  
361 gatttttggc acattcctgt gcaaggtggt ctactcctg aaggaagtca acttctatag  
421 tggcatcctg ctactggcct gcatcagttg ggaccgttac ctggccattg tccatgccac  
481 acgcacactg acccagaagc gctacttggt caaattcata tgtctcagca tctggggtct  
541 gtccttgctc ctggcctgct ctgtcttact ttccgaagg accgtctact catccaatgt  
601 tagccagacc tgctatgagg acatgggcaa caatacagca aactggcgga tgtgttacg  
661 gatcctgccc cagtcccttg gcttcacgtg gccactgctg atcatgctgt tctgtacgg  
721 attcaccctg cgtacgctgt ttaaggccca catggggcag aagcaccggg ccacgctggt  
781 catctttgct gtcgtcctca tcttctgct ttgctggctg ccctacaacc tggctctgct  
841 ggcagacacc ctcatgagga cccaggtgat ccaggagacc tgtgagcgcc gcaatcacat  
901 cgaccgggct ctggatgcca ccgagattct gggcatcctt cacagctgct tcaacccctt  
961 catctacgcc ttcattggcc agaagtttcc ccatggactc ctcaagattc tagctataca  
1021 tggcttgatc agcaaggact ccttgcccaa agacagcagg ccttcccttg ttggtcttc  
1081 ttcagggcac acttccacta ctctctaaga cctcctgcct aagtgcagcc cgtggggttc  
1141 ctcccttctc ttcacagtca cattccaagc ctcatgtcca ctggttcttc ttggtctcag  
1201 tgtcaatgca gccccattg tggctacagg aagcagagga ggccacgttc ttactagttt  
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1321 atttgctgga gctctgccc tctgcccct gagcccatg cactctatgt tctaagaagt  
1381 gaaaatctac actccagtga gacagctctg catactcatt aggatggcta gtatcaaaag  
1441 aaagaaaatc aggttgccca acgggatgaa accctgtctc tactaaaaat acaaaaaaaa  
1501 aaaaaaaaaa  
1 gggagaaaca tagggaatag aaaataagta agaaggggac acctgggaac aggtttgctt  
61 tcttgcatct tgcttaatgc tggcccttcc ctgaatgtct aagaccaacc tggctccac  
121 atccaaatgc acagacacag ctgaggatgg agaaggctaa agagggacag aggtagagac  
181 ataggctgag aggaggcagt tgtaggttga gctagggcta aggtgttttc cccatattcc  
241 atcttaccct aactcaggc caggccttag agttgtggaa ggtggagaac actgggaagc  
301 caacctccga agaagaccag gttggagtca aaggaggaag gagagctctc attgccaaac  
361 caacagggaa gccaaagata tcccagtaac tgctctcaca tcatgtatga gaatgccttg  
421 aatccgagct actaaatcac atttccctcc ttctaacctt ccagttagat caaacattg  
481 ctgaaactga agaggacatg tcaaataatta cagatccaca gatgtgggat tttgatgatc  
541 taaatttcac tggcatgcca cctgcagatg aagattacag cccctgtatg ctgaaactg  
601 agacactcaa caagtatgtt gtgatcatcg cctatgccct agtggtcctg ctgagcctgc  
661 tgggaaactc cctgggtgat ctgggtcatc tatacagcag ggtcggccgc tccgtcactg  
721 atgtctacct gctgaacctg gccttgcccg acctactctt tgccctgacc ttgcccactt

```

281  gggccgcctc caaggtgaat ggctggattt ttggcacatt cctgtgcaag gtggtctcac
841  tcctgaagga agtcaacttc tacagtggca tcctgctgtt ggctgcac agtgtggacc
901  gttacctggc cattgtccat gccacacgca cactgacca gaagcgtcac ttgtcaagt
961  ttgtttgtct tggtgtgttg ggactgtcta tgaatctgtc cctgcccttc ttcttttcc
1021 gccaggctta ccatccaaac aattccagtc cagtttgcta tgaggtcctg ggaatgaca
1081 cagcaaaatg gcggtgggtg ttgctggttc tgctcacac ctttggttc atcgtgccg
1141 tgattgtcat gctgttctgc tatggattca ccctgcgtac actgtttaag gccacatgg
1201 ggcagaagca ccgagccatg aggtgtcatc ttgtgtcgt cctcatcttc ctgctttgt
1261 ggctgcccta caacctggtc ctgctggcag acacctcat gaggaccag gtgatccagg
1321 agagctgtga gcgcgcaac aacatcgcc ggccctgga tgccactgag attctgggat
1381 ttctccatag ctgcctcaac cccatcatct acgccttcat cggccaaaat ttctgccatg
1441 gattcctcaa gatcctggct atgcatggcc tggtcagcaa ggagttcttg gcacgtcac
1501 gtgttacctc ctacacttct tegtctgtca atgtctctc caacctctga aaacctcga
1561 tgaaggaata tctcttctca gaaggaaga ataaccaaca ccctgaggtt gtgtgtgaa
1621 ggtgatctgg ctctggacag gcactatctg ggttttggg ggacgtata ggatgtggg
1681 aagttaggaa ctggtgtctt cagggggcac accaaccttc tgaggagctg ttgaggtacc
1741 tccaaggacc gccctttgca cctccatgga aacgaagcac catcattccc gttgaacgtc
1801 acatctttta cccactaact ggctaattag catggccaca tctgagcccc gaatctgaca
1861 ttagatgaga gaacagggtc gaagctgtgt cctcatgagg gctggatgct ctggtgacc
1921 ctacacaggag catctcttca actctgagtg ttaagcgttg agccaccaag ctggtggctc
1981 tgtgtgtctt gatccgagct caggggggtg tttttcccat ctcaggtgtg ttgcatgtc
2041 tgctggagac attgaggcag gcactgccaa aacatcaacc tgccagctgg cctgtgtagg
2101 agctggaaac acatgttccc cttgggggtg gtggatgaac aaagagaaag agggtttga
2161 agccagatct atgccacaag aaccccttt acccccatga ccaacatcgc agacacatgt
2221 gctggccacc tgctgagccc caagt

```

## (2) INFORMATION FOR SEQ ID NO:2563:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 541 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2563:

```

1  ccgctgtcaa gatgttctg gccatggtcc ttacctctgc cctgtctctg tgctccgtgg
61  caggccaggg gtgtccaacc ttggcgggga tcctggacat caacttctc atcaacaaga
121  tgcaggaaga tccagcttcc aagtgccact gcagtgttaa tgtgaccagt tgtctctgtt
181  tgggcattcc ctctgacaac tgcaccagac catgtttcag tgagagactg tctcagatga
241  ccaataccac catgcaaaac agataccac tgattttcag tcgggtgaaa aaatcagttg
301  aagtactaaa gaacaacaag tgtccatatt ttctctgtga acagccatgc aaccaacca
361  cggcaggcaa cgcgtgaca tttctgaaga gtcttctgga aattttccag aaagaaaaga
421  tgagagggat gagaggcaag atatgaagat gaaatattat ttatcctatt tattaattt
481  aaaaagcttt ctctttaagt tgctacaatt taaaaatcaa gtaagctact ctaaatcagt
541  atcagttgtg attatttgtt taacattgta tgtctttatt ttgaaataaa t

```

## (2) INFORMATION FOR SEQ ID NO:2564:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2761 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2564:

```

1  atatatatat gcataatagt ctctgtgtaa cagtaagtgg atgcagtaac tgggtgtgagg
61  gcaacttgga gagtgtgctt ggaggcacag agatgctcag ggctgcctgg actgcctcca
121  tgatggtggc ctgctctgta ttaggtgagt gttcaggaaa ggtgagggca gggcagccca
181  cagcttcaca gtggcccagg gaagcagggc aggcaggcta tgaggcctag taggcatctg
241  ggccagactt tgacactgag gccatggaat ggtggtgggt ctgagaacag acccaagtga
301  tcatgggctg aaggctatgt ccacagatcc aaggcgggat aggtgtact gggcagtgt
361  gtcagccagg ctccccagcg ggactggggg tgcaggggc agctctgtcc caggtggcag
421  acactggttt cccctcctgc tctcacaacc ggctgtttac caggtgttgt ctgagctgtg
481  gtgaggcttc cctggtgaca ttcaggagca gggagcctgc gagtaagggt gtatgcatct
541  gccctgactg cctggccctg tggtaagga tgggggaagg cagctctgcc tgcagctcca
601  cccatttat aaagcactgt ggtgccttct gctgggacat gtgctgagt gtgcctcgca
661  ggcaactgccc tcgggaagtt cacaggctta tgtggaagct ggtgggaatg ggccaagaag
721  agaggtgtca ggagccagg attgggcagg tcccaggctc ctgagcctca gtttcttcat
781  ctgtaggagg gtgtgacct tgccctgtc agcttaccag gtacagatgt aagttttcag
841  tgcagaggaa aagcagagaa ctccccctca gatggccata ccccttctg cctgtacca
901  actctccggt cctactttgt agctctcagg tgtacatgt ggatcctgcc ctaccatccc
961  ccttgccctg tctagaaacg aggcctgtg agcttggaac catccactc cctgctctca
1021 agccgtctgc tcctgggtta gcctgtggct gacctggcct gattctacat agatgtgggt

```

1081 gtttcttacc tgctggggca gcagttgtcc attctggggc ctggtcagc tctcagctgt  
1141 ggccgttgtg cctgtgcttc cccaggtcct ggtggtgact ccaaccctgc cctcacatat  
1201 cccaagagca ggctgactgc cttccccatt cccaccttcc cagtaactgc tgcaagaacg  
1261 gacagacact gctgcagaga acttgccacg gtgtttcatg ctgtggctgg tgggtccagg  
1321 ctgcacgctc cattctagga aaggggtgagg cttcctgac atcagcttta acaggggact  
1381 gtcttatggg tacctgtata cgctgccggg agtggggcag agtgggggta gactagtggc  
1441 tgctgcccac tgggggtgtg cgggttcctt aagggtctga gtctgtgtgc gtgtctggtt  
1501 ttttctcctc ctttatcagt aatcagtcct gtataaccag gctggccctg cttcctgctt  
1561 aggggctatc ggtgtaccat ctggagtgtc aaatgggggt atagggcgct agcggccttc  
1621 ccacacccaa gcacttctcg acaccagcc cctcatctct agccaacctc tggctccctt  
1681 agggatcctg gggctcaggc ctcacgctcc agcatccggg ggctttgccc ttctggtgtt  
1741 gctcttcttt gcagggtgct tggaaacagg gtgcaacaga gttcagaaag tgccatctgt  
1801 tgcatggata ccctgctgcc accctcgctc acctttctgg ggcagaacag ttggatgggt  
1861 ctttatttaa gaggacaaaa gggagagaga atgcatagag gctgggtctg gtggctcag  
1921 cctgtaatcc caacactttg ggaggccaag gcaggtggat cccttgaggt caggaggtca  
1981 agactagcct ggccaacatg gtgaaacccc gtctctacta aaaatacaaa aaaaaaaaaa  
2041 ttagctgggc atggcgggag atgcctgtaa tcccagctac tcgggagggt gaggcaggat  
2101 aatcacttga acccaggagg cggaggtgtc agtgagccaa gatcacacca ctgcactcta  
2161 gcctgggtga cagagggaga ctgtctcaaa aaaaaaaatt tgcttagaat ttgtctgtgt  
2221 gaccttgggc aagtcatctc cctccttgg gactcagttc cttgctgtg aacggggaca  
2281 gtgcttctcc cttacagagc tgttgtgaga attaaagtag aaaatgtacc tatggtggtt  
2341 gttggtagt accagttccc ccaaccctga cttccctgca ggtggggcgg tggggccggg  
2401 aatgggggat gggctggcag aggatgactg tcccagagag gactcttctc ggcaggtgtg  
2461 gagacctagc tgagtacagag gccaggatct aagtttgagg gtgttcttta caccctgcag  
2521 ccatgagtct ttggtgtagt caaatggcct ttctgagctc agttccttat cagtaaagcc  
2581 tggacagtgg tccaggacgc tggacactgt gtgagtgtta ggacacagga cactgtgtga  
2641 gtgcaggtgg ggacccatgg agcactctgc tggggagcaa ttcattggga gcaccctcc  
2701 agagagggat gatttgaca gggccctcag cccagtcctt tgcaggctgg accttggaga  
2761 gtgaggccct gaggcgagac atgggcacct ggctcctggc ctgcatctgc

## (2) INFORMATION FOR SEQ ID NO:2565:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17041 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2565:

1 ggatccatgc ccagaattat tcacgaaatt cacttaaaat agcatatatg cttgaaccca  
61 ggagtctgag gctgcagcga gctatgatca tgtcactgca ctccagccca gcctgggcca  
121 cagagcaaga ctctgtgtct aaagaaaatga aaataaaaaa aaataaaaaa gcatatacag  
181 gcaacaatcc aaatgttcat tgcagaaatt atgattatta ttgttttctc tttagaggca  
241 ggggtgtcact ctgttgccca gactaatctt gacctcctgt gatectcaag agatcctccg  
301 gtctctgctt cccaaagttc ttggattaca ggtgtgaggc actgggccta gacattgcag  
361 ggattattaa accatggtgc atactaccat taaaggtatg aggtaggttt tatatgctga  
421 cctagaaaga tgggtgaaca ccatagggga acaagaaggc tgcaaagtgg cagcacagca  
481 ggagtcttta agaaataggt atttgtttca gcttaagaag tgtctggctg ggcgtggtgg  
541 ctcacacctg taatcccagc acttagggag gcttaggtgg gcggatcact tgaggttagg  
601 agttcaagac cagcccagtc aacaccggtg aaaccccatc tctactaaa atacaaagaa  
661 attagctggg cttggtggca ggtggctgta atcccagcta ctcaggagct gaggcaggag  
721 aatcatctga acccgggagg ccgaggtgtc agtgagccta gatcgacca ctgcactcca  
781 gcctgggtga cagagtaaga ctcggtcaaa aaaaaaaaaa aaaaagaccg ggtgcgaggt  
841 ctctcgctg taatcccagc actttgggag gcctaggcag gaggatcaca aggtcaggag  
901 atcgagacca tcctggccaa catggtgaaa ccccatctct actaaaatac aaaaattagc  
961 cgggtgtgat ggcacacgcc tgtagtccca gctactcagg aggtgaggc aggggaatcg  
1021 cttgaaacca ggaggtggag gctgcagtga gccagatga cgccactgca ctccagcctg  
1081 ggcagagagc aagactccat ctcaaaaaag aaaaagaaaac aaacaaacaa acaaaatccc  
1141 caaaaagcaa aagtgtctgc atggacttgt gcctaactac tcacagtggc tacttcttgg  
1201 gggaggtgaa aggggaccct gttaaagaat ttttcttctg tattgttttt cttcaactga  
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1321 ctgggtgaag gagaacctgc acctctggtt ttggcaaagt gtagaagggg acaagggcac  
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1561 acttagaaga ttagtggtga cagacacttc tcagctctgc tcgggagagc agctctgtaa  
1621 tgcgcttgtg gtttcagatg tggcgccct gtgtgaacct gtcgtgcaaa gctcacgtca  
1681 ccaactgctg cagttatctc ctgaatcagg ctgagggctt ttgctgtgca ccagagata  
1741 gttgggtgac aaatcacctc caggttgggg atgcctcaga cttgtgatgg gactgggcag  
1801 atgcatctgg gaaggtgagt ctgtgctttg ggcttcccaa cctctcaagt cagcatgaaa  
1861 ttcagaaggc agagagggac atgtggccct ccaactcggg gccaggagg ccactgtggc

1921 atttgagagc gccaccctag ctttacctcc tctggtgtcc tggccttgtg tatctcttag  
1981 agatggcaaa atttgcagcc ctgacctcaa ggattacaaa ctaatttcca gtccctgtagg  
2041 ggtcatgggt tctgctgtgg ccagtgtggc actgagtttg tcaggcagaa ttcttaatta  
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2161 tgagaatggg catacttggg cctcagttgt gatggccatg ggggtggagct gaggtctagg  
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2281 gagccaggag gatgggtatg cccactgga gctgtgtgtg gggcagcagg tgaggggtggg  
2341 attccagagg gaggggtcaac ccagccaagc agaggaaggg gaggagaggg ttgttttgg  
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3001 caatatcctc actggagccc tgcccattgg cactgctcaa cccttggggc ctgtcagttc  
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3361 caggcattta cctcacggat gcagcactgc cctcatcct ctctctgaa agtgtgtggg  
3421 aaatgcttct tgggtccatc tctctccac cctgccttcc ctgcacctc tctatgaggt  
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3541 tgcccatccc taccctgtc agcaccttac atactctgtg cccaacagca ttggggattc  
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3781 acttcaatag taacttctga ggctgccagc ctctgaatg gtccagaaga accagacct  
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3901 ccagcacttt gggaggccaa agcaggtgaa tcacttgagg ccaggagtac gagaccagcc  
3961 tgacaaacat ggtgaaaccc tgtgtctact aaaaatacaa aaattagcca ggcgtgggtga  
4021 ctcatgcttg taaatgcttg taatccagc tacttggag gctgaagcag gaggatcact  
4081 tgaactcggg aggcagaggt tgcatgagc cgagatcacg ccactgtgtt ccagcctgag  
4141 cgacagagcg acactccgtc taaaaaaa aaatatatat atatatacac acatatatat  
4201 atgcataata gtctctgtgt aacagtaagt ggatgcagta actggtgtga gggcaacttg  
4261 gagagtgtgc ttggaggcac agagatgtc agggctgcct ggactgcctc catgatgggtg  
4321 gcctgtctctg tattaggtga gtgttcagga aaggtgaggg cagggcagcc cacagcttca  
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4561 ggctccccag cgggactggg ggtgtcaggg gcagctctgt cccagggtgc agacactggt  
4621 ttccccctct gctctcacia cgggctgtt accagggtgt gtctgagctg tggtagggct  
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4741 tgcctggccc tgtgttcaag gatgggggaa ggcagctctg cctgcagctc caccctattt  
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4981 ggggtgtgac cctgcctgc tcagcttacc aggtacagat gtaagtttct agtgcagagg  
5041 aaaagcagag aagttccctc cagatggcca taccctcttg tcgtgttacc caactctccg  
5101 gtctactttt gtagctctca ggtgtcacat gtggatcctg ccctaccatc ccccttccct  
5161 gtctagaac gaggcctgct gagcttggag ccatccact cctgtctctc aagcctctg  
5221 ctctgggtt agcctgtggc tggcctggcc tgattctaca tagatgtggg tgtttctcca  
5281 ctgctggggc agcagttgtc cattctgggg cctgggtcag ctctcagctg tggcgttgt  
5341 gcctgtgctt cccagggtcc tgggtgtgac tccaacctg ccctcacata tccaagagc  
5401 aggtgactg ccttcccat tcccacttt ccagtaactg ctgcaagaac ggacagacac  
5461 tgctgcagag aacttgccac ggtgtttcat gctgtggctg gtgggtccag gctgcagct  
5521 ccattctagg aaagggtgag gcttctctgat catcagctt aacaggggac tgtcctatgg  
5581 gtacctgtat acgctgccg gagtggggca gagtggggt agagtgtgc ctgctgccc  
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5701 tcttatcag taatcagct tgtataacca ggctggccct gcttctgct taggggtat  
5761 cggtgtacca tctggagttg caaatgggg gatagggcgt cagcggcctt cccacacca  
5821 agcacttctt gacaccagc cctcatctc tagccaacct ctggctcccc tagggatcct  
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## (2) INFORMATION FOR SEQ ID NO:2566:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2566:

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12061 ctggctctccc cggatcacat gatggcacca cagctgagga gtgggctctg cactcccccc  
12121 ccttccaccc atgttgggct cctacagccc aggcaccagt gagcaacttg ggggttgcat  
12181 cagccctctc cctcctgct gggctgttgg ttcattgccc ctgggtggga ggagggggag  
12241 agggagagct ccagttagtg gtctctggtt tttccctca gactcctcac tttgggcaaa  
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12361 gaatcttccc tccctgtccc cttcacactg tggctccagc ttactatga gaaaaatct  
12421 tttctctctc aatgaggagc gtatgttcca agattttgt ccaaaaatat aatttgaacc  
12481 atgaaccggg catctggctc ttggcagagt ctccctctt cccaagggtg gtatgtgtga  
12541 ctgtcaggag cctgggcagc tgacgacaag gctgagcagg tcagattgtg actgtccct  
12601 ggactgtcat cctgttgctg gcaccagctg ttccttagag aactaggaca cctgccacgg  
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12721 tgatggaggg tgtgtgtgt gtgatgcatt ggatggaggc tccctggctcc accaagggaa  
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12901 gtgtgtgtgt gtgtttatgt gtctgtgtgt gttcgtgtgt gtgtctgtgt gtgtgtttgt  
12961 gtgtgtatgt ctgtgtgtgt gtgtttatgt gtgtgtgtct gtatgtgttt aagtctgtgt  
13021 gtgtttgtgt gtgtgtgtct ctgtgtgtgt gtgtgtgtct gtgtgtgtgt ttatgtgtct  
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13501 tcggttcagg ctgcccgtgg caccaggccc tgtgctgggg gagtgctgag gagcctgaag  
13561 ggactcaggg tcccgtgatg aggctgggct ggcacatgga ggaaagacag aatgtccaag  
13621 acacaggcgc tgcttggcct ctgggtgtgt acctcaggag ggcttctctg agggaggagg  
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14101 ggcagcagc cagcaacaac aacaactact gtgccttggg ctgctatggg ggaaggcacc

14221 tctcagccct cccaggaaac acacagagct ctggggcccat cccagccctg gctgtggcc  
14281 tttcttgtga ccatcagggc ctggagaccc agcaaggagt tgcctgggtg ctggctgggc  
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14401 gcaaggctcg gtccctggaca ttctaggtcc ctgactcgcc agatgcatca tgtccatttt  
14461 gggaaaatgg actgaagttt ctggagccct tgtctgagac tgaacctcct gagaaggggc  
14521 ccctagcagc ggtcagaggt cctgtctgga tggaggctgg aggtcctccc ctcaacctct  
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14641 tccattgtcc cttttcttta tccctgacct ctctgagaag tggggtgtgg tctctcagct  
14701 gttctgacct cataccctta aagggccagc ctggggccag tggacacagg taaggacca  
14761 tgaccacctg gtgtgacctc tctgtgacct actgaggcac ctttctagag attaaaaggg  
14821 gcttgatggc tgttccaaa gtgttgatgg ctgggagaag gggccagagg aggagtggag  
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14941 tgacagttct ggggacagca agttggaggt tcaggggcag cttcaggaca gcaggatgga  
15001 ggctcagga caattcctgg gaggccagt cctctgttcc tcttctctc catcctcccc  
15061 cttgtccag gaaactgaga gctgagcctg gagcttccag acagtcatg ctgggggtga  
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15301 gatttgttgt ctcacaattc tgaagtccag aagttgaaa taaagatgtt ggcagtgttc  
15361 ccaaccacat gttcttgggc tcccatgaaa cagaagtga tattaggcca aggaagcttc  
15421 ccagacaaga ctttattaag tcttatgccc cgaaagtttg ggcagaagag agacgtgca  
15481 ggaggaagaa ttcttggtg actccccaag gggaatgcat tgtggtgtct taaggagggt  
15541 gacatacata atttatgagc tacatgagtg tcattgcaca tatggggtgg agcgaagggt  
15601 gctcagacgc atgctaacc atacgttgca tgatcagaaa atggcagata agccctccc  
15661 tgggtgagga ctttagtatt atcataagac cagggtcatt ctctggcct tgtgcacaag  
15721 caggtgatgg agtcaactcc cgtcagtaag acttatggcg ggatgtgct tatcttagtt  
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15841 aggtctagtg gtcagcgggc acgtatgga caatacgtta gtgggggtg gccagttccc  
15901 atttatactc tctcagcagg gccatgtctc ctctgaaggc actagggaag gattagtctt  
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16021 tttgttttgt tttgtgacg gatttttctt cttgttggc aggttgagt gcaatggcac  
16081 aatctcggct cactgcaacc tctctctccc aggtttaagc aattcttctg cctcagcctt  
16141 tggagtagct gtgattacaa ggcacctgct accacgcctg gctagttttt gtatttttag  
16201 tagagacggg gtttcgctat gttggccagg ctggtctcaa actcctgata tcaagtgatc  
16261 cgtctgtctc tgcctcccaa agtgttgga ttacaggcat gagccacctg gctggccaa  
16321 agttccagtc tttacaggga ttttctcttg tgtgcatctt tgtgtccaaa tttccctttt  
16381 ttaaaatcac aataatagtg aattaaggct ggccctaacc atttaattct aacttgatca  
16441 tctgcaaaga cactatttcc atataaggct acattcacag ctactgggtg taggacttca  
16501 acctagaggg cctgacttct ggccaacac atcatggccc atcccagcat gccccatccc  
16561 cttcctgggt gccccaggca gatcacagga gggcctgact gctgggcttt gggctgacat  
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16681 ctgaggcagg gcttgaactc tggaccagat tacagactag ctgaacagg caaaagcacc  
16741 cttccataag acacacccac tggtgccaag tgagtgtgcc gttctcatgt taacagctgg  
16801 aaattactgc ccttttccat ggcaatgacc tgaaagtac caccctttt ctagaaattt  
16861 ctaaataacc tctccttaa tttgtatata gttacaagtg ggtataaata tgtgtgcaga  
16921 actgcctctg agctgtact ctgggtgac tgcctatggg gcatccctgc tccataagga  
16981 gcagtacctc tgcgtccact gtgcacagct gcttaataaa aagttgctct ctaataccac  
17041 cgactcgccc ttgaattctt tctgggtga agc

## (2) INFORMATION FOR SEQ ID NO:2567:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2041 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2567:

1 aattcagaac tctcagccc cccaagaaaa aaatatcccc gtggaaattc ctttttaatg  
61 accgaggcgg gggaaatatg cgtctctgga tggccagtga ctgcagccc ccttccccga  
121 taggaaggcg ctgcgcgtcc ggggacctt cgttccctt tctgtcgcg gacctccctg  
181 gccctcggga gatctccatg gcgacgccgc gcgcgccca caacaggaaa gccttaggcg  
241 gcgcggcttg gtgctcgag acttaagagt acccagcccc tcgacgtggt ggatgtcgag  
301 ttttggggtc acacgcacag gcggtggcca agcaaacacc cgctcatatt tagtgcatga  
361 gcctgggttc gatttgccgg agcctcgcg gttagggcagg ggttcgagcg ccccttctcc  
421 ctgcctcgcc tctgcgctg ggggtgctg cctcagttt ccagcgacag gcagggattt  
481 cgagcgtccc cctcccctcc ctctcaaga tccaagctag ctgcctcagt tcccccgcg  
541 agcctgggac gccagcggag gggctcgcg cgtagggatc acgcagcttc cttccttttt  
601 ctgggagctg taaagacgcc tccgccaacg ccgaaagggg aagcgaggag gccgcggggg  
661 tgagtgcctc cgggtgtaga gagaggacgc cgatttcccc ggacgtgggt agaccgcgct  
721 tctcactccc caggttagc ggtcgccggg aggtgcctg ctctgctctg gccgttctc



781 gagaaa c cgtgtcagct aggtgtggac gtgacctagg ggg gggca tccctcagtg  
841 gagggagccc ggggaggatt cctgggcccc caccagggca gggggctcat ccaactcgatt  
901 aaagaggcct gcgtaagctg gagagggagg acttgagttc ggacccccctc gcagcctgga  
961 gtctcagttt accgctttgt gaaatggaca caataacagt ctccactctc cggggaagtt  
1021 ggcagtattt aaaagtactt aataaacgcc ttagcgcggt gtagaccgtg attcaagctt  
1081 agcctggccg ggaacggga ggcgtggagg ccgggagcag cccccgggt catcgccctg  
1141 ccaccgcccgc ccgattgctt tagcttggaa attccggagc tgaagcggcc agcgagggag  
1201 gatgaccctc tcggcccggg caccctgtca gtccggaaat aactgcagca tttgttccgg  
1261 aggggaaggc gcgaggtttc cgggaaagca gcaccgcccc ttggccccca ggtggctagc  
1321 gctataaagg atcacgcgcc ccagtcgacg ctgagctcct ctgctactca gaggttgcaac  
1381 ctacgcctcg ctatggctcc cagcagcccc cggcccgcg cgtccgcact cctgttctg  
1441 ctccgggctc tgttcccagg tgagtcgggg tggggattgc cgtccggcca gttctccgaa  
1501 gcccgggagg accggctccc gggtcaggct atgcatgctt aggtagctgt ttatgggaag  
1561 gaggggctag agacagcgat tgaaagcaac agccagtagg ttcgaatcca gacctgcat  
1621 accctccacgt gtggccttgg gctatagatt gcagctttaa aaaagggtag ggggttggag  
1681 atggagggga gggcggggcc tcgttttgtt gccaggccg gtcttgaact ccgggggtct  
1741 agccttacct cctgcctcag cctcccgagt agctgggatg aggtgtgaac cagccttgc  
1801 ttggctagat tgcgtctctt acagtttctc agctgtaaaa cgggaaacgt tatagcggcc  
1861 acctggcagg gtatcttggc ccagcgagc acctggcccc aggactcgat catgatggtt  
1921 tgggaacttg gctctgtgcc aacccaacaa ggcttaaggg acccccaccc ccctcaagat  
1981 gtatattctg ttcctcatcc tctctgcccc tggggaagtc cagggtcgct tctacttggg  
2041 gg

## (2) INFORMATION FOR SEQ ID NO:2568:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2941 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2568:

1 gcgccccagt cgacgtgag ctctctgct actcagagtt gcaacctcag cctcgctatg  
61 gctcccagca gccccggcc cgcgtgccc gcaactctgg tctgtctcgg ggctctgttc  
121 ccagacctg gcaatgccca gacatctgtg tccccctcaa aagtcacatct gcccggggga  
181 ggctccgtgc tgggtgacatg cagcacctcc tgtgaccagc ccaagttgtt gggcatagag  
241 accccgttgc ctaaaaagga gttgtcctg cctgggaaca accggaaggt gtatgaactg  
301 agcaatgtgc aagaagatag ccaaccaatg tgctattcaa actgccctga tgggcagtca  
361 acagctaaaa ccttctcac cgtgtactgg actccagaac ggggtgaaact ggcacccctc  
421 ccctcttggc agccagtggg caagaacctt accctacgct gccaggtgga ggggtgggca  
481 ccccgggcca acctcaccgt ggtgctgctc cgtggggaga aggagctgaa acgggagcca  
541 cgtgtggggg agcccgtga ggtcacgacc acggtgctgg tgaggagaga tcaccatgga  
601 gccaatctct cgtgccgac tgaactggac ctgcccggcc aagggtgtg gctgtttgag  
661 aacacctcgg cccctacca gctccagacc tttgtcctgc cagcgactcc cccacaactt  
721 gtcagcccc gggtcctaga ggtggacacg caggggaccg tgggtctgtt cctggacggg  
781 ctgttcccag tctcggaggc ccaggtcac ctggcactgg gggaccagag gttgaacccc  
841 acagtcacct atggcaacga ctcttctcgc gccaaaggct cagtcagtg gaccgcagag  
901 gacgagggca cccagcggt gacgtgtgca gtaatactgg ggaaccagag ccaggagaca  
961 ctgcagacag tgaccatcta cagctttccg gcgcccacg tgattctgac gaagccagag  
1021 gtctcagaag ggaccgaggt gacagtgaag tgtgaggccc accctagagc caaggtgacg  
1081 ctgaatgggg ttccagcgca gccactgggc ccgaggggcc agctcctgct gaaggccacc  
1141 ccagaggaca acgggcgag cttctcctgc tctgcaaccc tggagggtgc cggccagctt  
1201 atacacaaga accagaccgc ggagcttctg tctctgtatg gccccgact ggacgagagg  
1261 gattgtccgg gaaactggac gtggccagaa aattcccagc agactccaat gtgccaggct  
1321 tgggggaacc cattgccga gctcaagtgt ctaaaggatg gcactttccc actgcccatac  
1381 ggggaatcag tgactgtcac tcgagatctt gagggcacct acctctgtcg ggccaggagc  
1441 actcaagggg aggtcacccg cgaggtgacc gtgaatgtgc tctccccccg gtatgagatt  
1501 gtcacatca ctgtgttagc agccgagtc ataattgggc ctgcaggcct cagcagctac  
1561 ctctataacc gccagcggaa gatcaagaaa tacagactac aacaggccca aaaaggggacc  
1621 cccatgaaac cgaacacaca agccacgcct ccctgaacct atccccggac agggcctctt  
1681 cctcggcctt cccatattgg tggcagtggt gccacactga acagagtgga agacatatgc  
1741 catgcagcta cacctaccgc ccctgggacg ccggaggaca gggcattgtc ctcagtcaga  
1801 tacaacagca tttggggcca tggtaacctg acacctaaaa cactaggcca cgcattctgat  
1861 ctgtagtcac atgactaagc caagaggaag gagcaagact caagacatga ttgatggatg  
1921 ttaaagtcta gcctgatgag aggggaagtg gtgggggaga catagcccca ccatgaggac  
1981 atacaactgg gaaatactga aacttgctgc ctattgggta tgctgagccc cacagactta  
2041 cagaagaagt ggccctccat agacatgtgt agcatcaaaa cacaaaggcc cacacttctt  
2101 gacggatgcc agcttgggca ctgctgtcta ctgaccccaa cccttgatga tatgtattta  
2161 ttcatattgt attttaccag ctatttattg agtgtctttt atgtaggcta aatgaacata  
2221 ggtctctggc ctcacggagc tcccagtcga tgtcacattc aaggtcacca ggtacagttg  
2281 tacaggttgt aactgcagg agagtgcctg gcaaaaagat caaatggggc tgggacttct



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2341 cattggccaa cctgcctttc cccagaagga gtgatttttc tatcggcaca aaagcactat
2401 atggactggt aatggttcac aggttcagag attaccaggt gaggccttat tcttcccttc
2461 ccccaaaaac tgacaccttt gttagccacc tccccacca catacatttc tgccagtgtt
2521 cacaatgaca ctcagcgggtc atgtctggac atgagtggcc agggaaatag cccaagctat
2581 gccttgctct cttgtcctgt ttgcatttca ctgggagctt gcactatgac agctccagtt
2641 tcttgccagt atcaggggtc tgcaagcagt ggggaagggt gccaaaggtat tggaggactc
2701 cctcccagct ttggaagggt catccgctgt tgtgtgtgtg tgtatgtgta gacaagctct
2761 cgctctgtca cccagcctgg agtgacgtgg tgcaatcatg gttcactgca gtcttgacct
2821 tttgggctca agtgatcctc ccacctcagc ctctgagta gctgggacca taggctcaca
2881 acaccacacc tggcaaatgt gatttttttt ttttttttca gagacggggt ctgcacaatc
2941 tgcccagact tcctttgtgt tagttaataa agctttctca actgcc

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## (2) INFORMATION FOR SEQ ID NO:2569:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3001 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2569:

```

1 gctataagga tcacgcgccc cagtcgacgc tgagctcctc tgctactcag agttgcaacc
61 tcagcctcgc tatggctccc agcagccccc ggcccgcgct gccgcgactc ctggtcctgc
121 tcggggctct gttcccagga cctggcaatg cccagacatc tgtgtcccc tcaaaagtca
181 tcttgccccg gggaggtccc gtgctggtga catgcagcac ctctgtgac cagcccaagt
241 tgttgggcat agagaccccg ttgcctaaaa aggagttgct cctgcctggg aacaaccgga
301 aggtgtatga actgagcaat gtgcaagaag atagccaacc aatgtgctat tcaaactgcc
361 ctgtagggca gtcaacagct aaaaccttcc tcaccgtgta ctggactcca gaacgggtgg
421 aactggcacc cctcccctct tggcagccag tgggcaagaa ccttacctta cgctgccagg
481 tggaggggtg ggcaccccg gccaacctca ccgtggtgct gctccgtggg gagaaggagc
541 tgaaacggga gccagctgtg ggggagcccg ctgaggtcac gaccacggtg ctggtgagga
601 gagatcacca tggagccaat ttctcgtgcc gcaactgaact ggacctgagg ccccaagggc
661 tggagctgtt tgagaacacc tcggcccccct accagctcca gacctttgtc ctgccagcga
721 ctcccaccac acttgtcagc cccgggttcc tagaggtgga cacgcagggt accgtggtct
781 gttccctgga cgggctgttc ccagtctcgg agggccaggt ccacctggga ctgggggacc
841 agaggttgaa cccacagtc acctatggca acgactcctt ctcgccaag gcctcagtc
901 gtgtgaccgc agaggacgag ggcacccagc ggctgacgtg tgcagtaata ctggggaacc
961 agagccagga gacactcag acagtgaaca tctacagctt tccggcgccc aacgtgattc
1021 tgacgaagcc agaggtctca gaaggacgc aggtgacagt gaagtgtgag gccacccta
1081 gagccaaggt gacgtgaat ggggttccag cccagccact gggcccgagg gccagctcc
1141 tgctgaagc caccacagag gacaacgggc gcagcttctc ctgctctgca accctggagg
1201 tgcctggcca gcttatcac aagaaccaga cccgggagct tcgtgtcctg tatggcccc
1261 gactggacga gagggattgt ccgggaaact ggacgtggcc agaaaattcc cagcagactc
1321 caatgtgcca ggcttggggg aaccattgct ccgagctcaa gtgtctaaag gatggcactt
1381 tcccactgcc catcggggaa tcagtactgt tcaactcaga tcttgagggc acctacctct
1441 gtccggccag gagcactcaa ggggaggtca cccgcaaggt gacctggaat gtgctctccc
1501 cccggtatga gattgtcatc atcactgtgg tagcagccgc agtcataatg ggcaactgac
1561 gctcagcac gtacctctat aaccgccagc ggaagatcaa gaaatacaga ctacaacagg
1621 gccaaaaagg gaccccatg aaaccgaaca cacaagccac gcctccctga acctatccc
1681 ggacagggcc tcttctcgg ccttcccata ttggtggcag tgggtgccaca ctgaacagag
1741 tggaaagcat atgccatgca gctacacctt ccggccctgg gacgccggag gacagggcat
1801 tgcctcagc cagatacaac agcatttggg gccatggtac ctgcacacct aaaacactag
1861 gccacgcata tgatctgtag tcacatgact aagccaagag gaaggagcaa gactcaagac
1921 atgattgatg gatgttaaag tctagcctga tgagagggga agtgggtggg gagacatagc
1981 cccaccatga ggacatacaa ctgggaaata ctgaaacttg ctgcctattg ggtatgtga
2041 ggccccacag acttacagaa gaagtggccc tccatagaca tgtgtagcat caaaacacaa
2101 aggccacac ttctgacgg atgccagctt gggcactgct gtctactgac cccaacctt
2161 gatgatattg atttattcat ttgttatttt accagctatt tattgagtgt cttttatgta
2221 ggctaaatga acataggtct ctggcctcac ggagctccca gtccatgtca cattcaaggt
2281 caccaggtac agttgtacag gttgtacact gcaggagagt gcctggcaaa aagatcaaat
2341 ggggctggga cttctcattg gccaaactgc ctttcccagc aaggagtgat tttctatcg
2401 gcacaaaagc actatatgga ctggtaatgg ttcacaggtt cagagattac ccagtggagc
2461 cttattctct ctttcccccc aaaactgaca cttttgttag ccacctcccc acccacatgc
2521 atttctgcca gttttcacia tgacactcag cggtcattgt tggacatgag tgcccaggga
2581 atatgcccga gctatgcctt gtcctcttgt cctgtttgca tttcactggg agcttgcact
2641 attgcagctc cagtttctct cagtgtacag ggtcctgcaa gcagtgggga agggggccaa
2701 ggtattggag gactccctcc cagctttgga agcctcatcc gcgtgtgtgt gtgtgtgtgt
2761 atgtgtagac aagctctcgc tctgtcacc aggtggagt gcagtgggtc aatcatggtt
2821 cactgcagtc ttgacctttt gggctcaagt gatcctccca cctcagcctc ctgagttagt
2881 gggaccatag gctcacaaca ccacactgg caaatttgat ttttttttt tttttcagag
2941 acggggtctc gcaacattgc ccagacttcc tttgtgttag ttaataaagc tttctcaact

```

3001 gcc

## (2) INFORMATION FOR SEQ ID NO:2570:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1801 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2570:

```

1  ctcagcctcg ctatggctcc cagcagccccc cggccccgcgc tgccccgact cctggctcctg
61  ctccgggctc tgttcccagg acctggcaat gccagacat ctgtgtcccc ctcaaaagtc
121 atcctgcccc ggggaggtc cgtgctggtg acatgcagca cctcctgtga ccagcccaag
181 ttgttgggca tagagacccc gttgcctaaa aaggagttgc tcctgcctgg gaacaaccgg
241 aagggttatg aactgagcaa tgtgcaagaa gatagccaac caatgtgcta ttcaaaactgc
301 cctgatgggc agtcaacagc taaaaccttc ctcacctgtg actggactcc agaacgggtg
361 gaactggcac cctccccctc ttggcagcca gtgggcaaga accttacctt acgctgccag
421 gtggaggggtg gggcaccctc ggccaacctc accgtggtgc tgctccgtgg ggagaaggag
481 ctgaaacggg agccagctgt gggggagccc gctgaggtca cgaccacggt gctggtgagg
541 agagatcacc atggagccaa tttctcgtgc cgcactgaac tggacctgcg gccccaaggg
601 ctggagctgt ttgagaacac ctccggcccc taccagctcc agacctttgt cctgccagcg
661 actccccac aacttgtcag ccccgggtc cttagagtg acacgcaggg gacctgggtc
721 tgttccctgg acgggctgtt cccagtctcg gaggcccagg tccacctggc actgggggac
781 cagaggttga accccacagt cacctatggc aacgactcct tctcgcccaa ggcctcagtc
841 agtgtgaccg cagaggacga gggcaccctc cggctgacgt gtgcagtaat actggggaac
901 cagagccagg agacactgca gacagtgacc atctacagct ttccggcgcc caacgtgatt
961 ctgacgaagc cagaggtctc agaagggacc gaggtgacag tgaagtgtga ggcccacctt
1021 agagccaagg tgacgctgaa tggggttcca gccagccac tgggcccag ggcccagctc
1081 ctgctgaagg ccacccaga ggacaacggg cgcagcttct cctgctctgc aacctggag
1141 gtggccggcc agcttataca caagaaccag acccgggagc ttctgtctct gtatggcccc
1201 cgactggacg agagggattg tccgggaaac tggacgtggc cagaaaattc ccagcagact
1261 ccaatgtgcc aggcttgggg gaaccattg cccgagctca agtgtctaaa ggatggcact
1321 ttcccactgc ccatcgggga atcagtgaat gtcactcgag atcttgaggg cacctacctc
1381 tgtcgggcca ggagcactca aggggaggtc acccgcgagg tgaccgtgaa tgtgtctctc
1441 ccccggtatg agattgtcat catcactgtg gtagcagccg cagtcataat gggcactgca
1501 ggcctcagca cgtacctcta taaccgccag cggaagatca agaaatacag actacaacag
1561 gcccaaaaag ggaccccat gaaaccgaac acacaagcca cgctccctg aacctatccc
1621 gggacagggc ctcttcctcg gccttcccat attggtggca gtggtgccac actgaacaga
1681 gtggaagaca tatgccatgc agctacacct accggccctg ggacgcccga ggacagggca
1741 ttgtcctcag tcagatacaa cagcatttgg ggccatggta cctgcacacc taaaacacta
1801 ggccacgcat ctgatctgta gtcacatgac taagccaaga ggaagg

```

## (2) INFORMATION FOR SEQ ID NO:2571:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9784 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2571:

```

1  aattcagaac tcctcagccc cccaagaaaa aaatatcccc gtggaaattc ctttttaatg
61  accgaggcgg gggaaatatg cgtctctgga tggccagtga ctgcagccc ccttccccga
121 taggaagggc ctgcgcgtcc ggggaccctt cgttccctt tctgtgcgc gacctccctg
181 gcccctcgga gatctccatg gcgacgccgc gcgcgcccc caacaggaaa gccttagcgc
241 gcgcggcttg gtgctcgag acttaagagt acccagcccc tcgacgtggt ggatgtcgag
301 tcttggggtc acacgcacag gcggtggcca agcaaacacc cgctcatatt tagtgcata
361 gcctgggttc gagttgccg agctctcgcc gtagggcagg ggttcgagc ccccttctcc
421 ctgcctcgcc tctgcgcctg ggggtgctg cctcagtttc ccagcgacag gcagggattt
481 cgagcgtccc cctccccctc ctctcaaga tccaagctag ctgcctcagt ttcccccgcg
541 agcctgggac gccagcggag gggctcggcg cgtagggatc acgcagcttc cttccttttt
601 ctgggagctg taaagacgcc tccgccaacg ccgaaagggg aagcgaggag gccgccgggg
661 tgagtgcctt cgggtgtaga gagaggacgc cgatttcccc ggacgtggtg agaccgcgct
721 tcgtcactcc cacggttagc ggtcgccggg aggtgcctgg ctctgtctgt gccgtttctc
781 gagaaatgac cgtgtcagct aggtgtggac gtgacctagg gggaggggca tccctcagtg
841 gagggagccc ggggaggatt cctggcccc caccagga gggggtcat ccactcgatt
901 aaagaggcct gcgtaagctg gagagggagg acttgagttc ggaccccttc gcagcctgga
961 gtctcagttt accgctttgt gaaatggaca caataacagt ctccactctc cggggaagtt
1021 ggcagtattt aaaagtactt aataaacgcc ttagcgcggt gtagaccgtg attcaagctt
1081 agcctggccg ggaacgggga ggcgtggagg ccgggagcag cccccgggt catcgccctg
1141 ccaccgccgc ccgattgctt tagcttgga attccggagc tgaagcgccc agcgagggag
1201 gatgaccctc tcggcccggg caccctgtca gtcgggaaat aactgcagca tttgttccgg

```

1261 aggggaagggc ggcaggtttc cgggaaagca gcaccgcccc ttggccccca ggtggctagc  
1321 gctataaagg atcacgcgcc ccagtcgacg ctgagctcct ctgctactca gagggtgcaac  
1381 ctcagcctcg ctatggctcc cagcagcccc cggcccgccg tgccccgact cctggctctg  
1441 ctccggggctc tgttcccagg tgagtcgggg tggggattgc cgtcggggcca gttctccgaa  
1501 gcccgggagg accggctccc gggtcaggtc atgcatgctt aggttagctgt ttatgggaag  
1561 gaggggctag agacagcgat tgaaagcaac agccagtagg ttcgaatcca gaccctgcat  
1621 acctccacgt gtggccttgg gctatagatt gcagctttaa aaaagggtag ggggttggag  
1681 atggaggggga ggggcgggccc tctgtttgtt gccaggcccg gtcttgaaact ccgggggtct  
1741 agccttacct cctgcctcag cctcccgagt agctgggatg aggtgtgaac cacgccttgc  
1801 ttggctagat tgcgtctctt acagtttctc agctgtaaaa cgggaaacgt tatagcggcc  
1861 acctggcagg gtatcttggc ccagcgcagc acctggcccc aggactcgat catgatgggt  
1921 tgggaacttg gctctgtgccc aacccaacaa ggcttaaggg acccccaccc ccctcaagat  
1981 gtatattctg ttcctcatcc tctctgcccc tggggaagtc cagggtctgt tctacttggg  
2041 gg  
1 ggcceccagc cgacgtgag ctcctctgct actcagagtt gcaacctcag cctcgctatg  
61 gctcccagca gcccgcggcc cgcgctgccc gcaactcctg tctgtctcgg ggtctgttct  
121 ccaggacctg gcaatgccc gacatctgtg tccccctcaa aagtcacctt gcccggggga  
181 ggctccgtgc tgggtgacatg cagcacctcc tgtgaccagc ccaagttgtt gggcatagag  
241 acccgttgc ctaaaagga gttgctcctg cctgggaaca accggaagggt gtatgaactg  
301 agcaatgtgc aagaagatag ccaaccaatg tgctattcaa actgcctga tgggcagtca  
361 acagctaaaa ccttcctcac cgtgtactgg actccagaac ggggtggaact ggcacccctc  
421 ccctcttggc agccagtggg caagaacctt accctacgct gccaggtgga ggttggggca  
481 ccccggggcca acctcaccgt ggtgctgctc cgtggggaga aggagctgaa acgggagcca  
541 gctgtggggg agcccgtga ggtcacgacc acggtgctgg tgaggagaga tcaccatgga  
601 gccaatttct cgtgccgcac tgaactggac ctgcggcccc aagggtctga gctgtttgag  
661 aacacctcgg cccctacca gctccagacc tttgtcctgc cagcgactcc cccacaactt  
721 gtcagcccc gggctcctaga ggtggacacg caggggaccg tggctctgtt cctggacggg  
781 ctgttcccag tctcggaggc ccaggtccac ctggcactgg gggaccagag gttgaacccc  
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901 gacgagggca cccagcggct gacgtgtgca gtaatactgg ggaaccagag ccaggagaca  
961 ctgcagacag tgaccatcta cagctttccg gcgccaacg tgattctgac gaagccagag  
1021 gtctcagaag ggaccgaggt gacagtgaag tgtgaggccc accctagagc caaggtgacg  
1081 ctgaatgggg ttccagccca gccactgggc ccgaggggcc agctcctgct gaagggccacc  
1141 ccagaggaca acgggcgcag cttctcctgc tctgcaaccc tggaggtggc cggccagctt  
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1261 gattgtccgg gaaactggac gtggccagaa aattccagc agactccaat gtccaggct  
1321 tgggggaacc cattgcccga gctcaagtgt cttaaaggatg gcactttccc actgccatc  
1381 ggggaatcag tgactgtcac tcgagatctt gagggcacct acctctgtcg ggccaggagc  
1441 actcaagggg aggtcacccg cgaggtgacc gtgaatgtgc tctccccccg gtatgagatt  
1501 gtcacatca ctgtggtagc agccgcagtc ataattggga ctgcaggcct cagcacgtac  
1561 ctctataacc gccagcggaa gatcaagaaa tacagactac aacaggccca aaaagggacc  
1621 cccatgaaac cgaacacaca agccacgcct cctgaacct atccccggac agggcctctt  
1681 cctcggcctt cccatattgg tggcagtggt gccacactga acagagtga agacatagc  
1741 catgcagcta cacctaccgg cctgggagc cggaggaca gggcattgtc ctacgtcaga  
1801 tacaacagca tttggggcca tggtaacctg acacctaaaa cactaggcca cgcactgat  
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1981 atacaactgg gaaatactga aactgtctgc ctattgggta tgetgaggcc cacagactta  
2041 cagaagaagt ggcctccat agacatgtgt agcatcaaaa cacaaggcc cacacttctt  
2101 gacggatgcc agcttgggca ctgctgtcta ctgaccccaa cccttgatga tatgtttta  
2161 ttcatattgt attttaccag ctattttatt agtgtctttt atgtaggcta aatgaacata  
2221 ggtctctggc ctcacggagc tcccagttca tgtcacattc aaggtcacca ggtacagttg  
2281 tacaggttgt aactgcagg agagtgcctg gcaaaaagat caaatggggc tgggacttct  
2341 cattggccaa cctgcctttc ccagaaggga gtgatttttc tatcggcaca aaagcactat  
2401 atggactggt aatggttcac aggttcagag attaccagc gaggccttat tctcccttc  
2461 cccccaaaac tgacaccttt gttagccacc tccccacca catacatttc tgccagtgtt  
2521 cacaatgaca ctacgcggtc atgtctggac atgagtggcc agggaaatag cccaagctat  
2581 gcttgtctct cttgtcctgt ttgcatttca ctgggagcct gcactattgt agctccagtt  
2641 tcttcagtg atcagggtcc tgcaagcagt ggggaagggg gccaaaggtat tggaggactc  
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2821 tttgggctca agtgatcctc ccacctcagc ctcctgagta gctgggacca taggtccaca  
2881 acaccacacc tggcaaat tttttttttt ttttttttca gagacgggt ctcgcaacat  
2941 tgcccagact tcctttgtgt tagttaataa agctttctca actgcc  
1 gctataagga tcacgcgcc cagtcgacgc tgagctctc tgctactcag agttgcaacc  
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121 tcggggctct gttcccagga cctggcaatg cccagacatc tgtgtcccc tcaaaagtca  
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241 tgttgggcat agagaccccg ttgcctaaaa aggagtgtgt cctggcctggg aacaaccgga  
301 aggtgtatga actgagcaat gtgcaagaag atagccaacc aatgtgtat tcaaaactgcc  
361 ctgatgggca gtcaacagct aaaaccttcc tcaccgtgta ctggactcca gaacgggtgg  
421 aactggcacc cctccccctc tggcagccag tgggcaagaa ccttacccta cgctgccagg  
481 tggagggtgg ggcaccccg gccaacctca ccgtgtgtgt gctccgtggg gagaaggagc  
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601 gagatcacca tggagccaat ttctcgtgcc gcaactgaact ggacctggcg cccaagggc  
661 tggagctgtt tgagaacacc tcggccccct accagctcca gacctttgtc ctgccagcga  
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1141 tgctgaaggc caccacagag gacaacgggc gcagcttctc ctgctctgca acctgtgag  
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1321 caatgtgcca ggcttggggg aacccattgc ccgagctcaa gtgtctaaag gatggcactt  
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1621 cccaaaaagg gacccccatg aaaccgaaca cacaagccac gcctccctga acctatccc  
1681 ggacagggcc tcttccctcg ccttcccata ttggtggcag tgggtccaca ctgaacagag  
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2101 agggccacac ttcttgacgg atgccagctt gggcactgct gtctactgac cccaaccctt  
2161 gatgatattg atttattcat ttgttatttt accagctatt tattgagtgt cttttatgta  
2221 ggctaaatga acataggtct ctggcctcac ggagctccca gtccatgtca cattcaaggt  
2281 caccaggtac agttgtacag gttgtacact gcaggagagt gcctggcaaa aagatcaaat  
2341 ggggttgga cttctcattg gccaacctgc ctttcccag aaggagtgt ttttctatcg  
2401 gcacaaaagc actatatgga ctggtaatgg ttcacaggtt cacagattac ccagtagggc  
2461 cttattcttc ccttcccccc aaaactgaca cctttgttag ccacctcccc acccacatac  
2521 atttctgcca gtgttcacaa tgacactcag cggctcatgtc tggacatgag tgcccaggga  
2581 atatgcccac gctatgcctt gtctcttgt cctgtttgca tttcactggg agcttgactc  
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2761 atgtgtagac aagctctcgc tctgtcaccg aggctggagt gcagtgtgtc aatcatggtt  
2821 cactgcagtc ttgacctttt gggctcaagt gatcctccca cctcagcctc ctgagtactc  
2881 gggaccatag gctcacaaac ccacacctgg caaatttgat ttttttttt ttttccagag  
2941 acgggggtctc gcaacattgc ccagacttcc tttgtgttag ttaataaagg tttctcaact  
3001 gcc  
1 ctcagcctcg ctatggctcc cagcagcccc cggcccgcgc tgcccgcact cctggtcctg  
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301 cctgatgggc agtcaacagc taaaaccttc ctcaccgtgt actggactcc agaaccgggtg  
361 gaactggcac ccttccccctc ttggcagcca gtgggcaaga acctaccct acgctgccag  
421 gtggagggtg gggcaccocg ggccaacctc accgtgtgtc tgctccgtgg ggagaaggag  
481 ctgaaacggg agccagctgt gggggagccc gctgaggtca cgaccacggt gctggtgagg  
541 agagatcacc atggagccaa ttctcgtgc cgcactgaac tggacctgag gcccaggag  
601 ctggagctgt ttgagaacac ctcggccccc taccagctcc agacctttgt cctgccagcg  
661 actccccac aacttgcag ccccggtc ctagaggtgg acacgaggg gacctgggtc  
721 tgttccctgg acgggtgtt cccagctcgc gaggccagg tccacctggc actgggggac  
781 cagaggttga accccacagt cacctatggc aacgactcct tctcggccaa ggcctcagtc  
841 agtgtgaccg cagaggacga gggcaccag cggctgacgt gtgcagtaac actggggaac  
901 cagagccagg agacactgca gacagtgaac atctacagct ttccggcgcc caacgtgatt  
961 ctgacgaagc cagaggtctc agaagggacc gaggtgacag tgaagtgtga ggcccaccct  
1021 agagccaagg tgacgtgaa tggggttcca gccagccac tggggccgag ggcccagctc  
1081 ctgctgaagg ccaccccaga ggacaacggg cgcagcttct cctgctctgc aacctggag  
1141 gtggccggcc agcttataca caagaaccag acccgggagc ttcgtgtcct gtatggcccc  
1201 cgactggacg agagggttg tccgggaaac tggacgtggc cagaaaaattc ccagcagact

1261 ccaatgtgcc aggtttgggg gaacccattg cccgagctca agtgtctaaa ggatggcact  
1321 ttccactgc ccatcgggga atcagtact gtcactcgag atcttgaggg cacctacctc  
1381 tgtcgggcca ggagcactca aggggaggtc acccgcgagg tgaccgtgaa tgtgctctcc  
1441 ccccggtatg agattgtcat catcactgtg gttagcagccg cagtataat gggcactgca  
1501 ggcctcagca cgtacctcta taaccgccag cggaagatca agaaatacag actacaacag  
1561 gcccataaag ggaccccat gaaaccgaac acacaagcca cgcctcctc aacctatccc  
1621 gggacagggc ctcttcctcg gccttcccat attggtggca gtggtgcca actgaacaga  
1681 gtggaagaca tatgccatgc agctacacct accggccctg ggacgcccga ggacagggca  
1741 ttgtcctcag tcagatacaa cagcatttgg ggccatggta cctgcacacc taaaacacta  
1801 ggccacgcat ctgatctgta gtcacatgac taagccaaga ggaagg

## (2) INFORMATION FOR SEQ ID NO:2572:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4681 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2572:

1 gaattcctgc cactcttctt gcaacggccc aggagctcag agctccacat ctgaccttct  
61 agtcatgacc aggaccaggg cagcactcct cctgttcaca gccttagcaa cttctctagg  
121 tttcaacttg gacacagagg agctgacagc cttccgtgtg gacagcgctg ggtttggaga  
181 cagcgtgggc cagtatgcc aactcctgggt ggtggttggg gcccccaaaa agataacagc  
241 tgccaaccaa acgggtggcc tctaccagtg tggtacagc actggtgcct gtgagcccat  
301 cggcctgcag gtgcccccg aggccgtgaa catgtccctg ggcctgtccc tggcgtctac  
361 caccagccct tccagctcg tggcctgcgg cccacccgtg caccacagt gcgggaggaa  
421 catgtacctc accggaactt gcttctcctt gggccccacc cagctcacc agaggctccc  
481 ggtgtccagg caggagtgc caagacagga gcaggacatt gtgttctga tctgaggtc  
541 aggcagcatc tctcccgca actttgccc gatgatgaac ttcgtgagag ctgtgataag  
601 ccagttccag agaccagca cccagtttct cctgatgcag ttctccaaac aattccaaac  
661 acatttact ttcgaggaat tcaggcgac gtcaaaccct ctcagcctgt tggcttctgt  
721 tcaccagctg caagggttta catacagcg caccgcatc caaatgtcg tgcaccgatt  
781 gttccatgcc tcatatggg cccgtaggga tgccacaaa attctcatt tcatcactga  
841 tgggaagaaa gaaggcgaca gcctggatta taaggatgtc atccccatg ctgatgcagc  
901 aggcacatc cgtatgcaa ttgggttgg attagctttt caaacagaa attcttggaa  
961 agaattaaat gacattgcat cgaagccctc ccaggaacac atatttaaag tggaggactt  
1021 tgatgctctg aaagatattc aaaaccaact gaaggagaag atctttgcca ttgagggtac  
1081 ggagaccaca agcagtagct ccttcgaatt ggagatggca caggagggtc tcagcgctgt  
1141 gttcacacct gatggccccg ttctgggggc tgtggggagc ttcacctgtt ctggagggtc  
1201 cttcctgtac ccccaataa tgagccctac cttcatcaac atgtctcagg agaattggga  
1261 catgagggac tcttacctgg gttactccac cgaactggcc ctctggaag ggtgacag  
1321 cctggtcctg ggggcccccc gctaccagca caccgggaag gctgtcatc tcaccaggt  
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1501 ggccccccat tactacgagc agaccgagg gggccagggt tctgtgtgtc ccttggccag  
1561 ggggtggaga aggtggtggt gtgatgctgt tctctacggg gagcaggggc acccctggg  
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1861 ggtggacctg gctgtggggg cccggggcca ggtgtcctg ctcaggacca gacctgtgct  
1921 ctgggtgggg gtgagcatgc agttcatacc tgccgagatc cccaggctg cgtttgagt  
1981 tcgggagcag gtggtctctg agcagacctt ggtacagtcc aacatctgcc tttacattga  
2041 caaacgttct aagaacctgc ttgggagccg tgacctcaa agctctgtga ccttgacct  
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2281 gggcaagccc ctcttgcct tcagaaacct gcggcctatg ctggccgac tggctcagag  
2341 atacttcacg gcctccctac cctttgagaa gaactgtgga gccgaccata tctgccagga  
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2461 ggagctgaac gcagaagtga tgggtgtgaa tgacggggaa gactcctac gaaccacct  
2521 cactctctcc caccgcgca gactgtccta ccgctacgtg gcagagggcc agaaacaagg  
2581 gcagctgcgt tccctgcacc tgacatgtga cagcgcccca gttgggagc agggcacctg  
2641 gagcaccagc tgcagaatca accacctcat cttccgtggc ggcgcccaga tcaccttctt  
2701 ggctaccttt gacgtctccc ccaaggctgt cctgggagac cggctgcttc tgacagccaa  
2761 tgtgagcagt gagaacaaca ctcccaggac cagcaagacc accttccagc tggagctccc  
2821 ggtgaagtat gctgtctaca ctgtggttag cagccacgaa caattacca aatactcaa  
2881 cttctcagag tctgaggaga aggaaagcca tgtggccatg cacagatacc aggtcaataa  
2941 cctgggacag agggacctgc ctgtcagcat caacttctgg gtgctgtgg agctgaacca  
3001 ggaggctgtg tggatggatg tggaggtctc ccacccccag aacctatccc ttcggtgctc

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3061 ctcagagaaa atcgaccccc cagcatctga cttcctggcg cacattcaga agaatcccgt
3121 gctggactgc tccattgctg gctgcctgcg gttccgctgt gacgtccccc ccttcagcgt
3181 ccaggaggag ctggattcca cctgaaggcg caacctcagc tttggctggg tccgccagat
3241 attgcagaag aaggtgtcgg tcgtgagtgt ggctgaaatt acgttcgaca catcgtgta
3301 ctcccagctt ccaggacagg aggcatttat gagagctcag acgacaacgg tgctggagaa
3361 gtacaaggte cacaaccccc cccccctcat cgtaggcagc tccattgggg gtctgttget
3421 gctggcactc atcacagcgg tactgtacaa agttggcttc ttcaagcgte agtacaagga
3481 aatgatggag gaggcaaatg gacaaattgc cccagaaaac gggacacaga cccccagccc
3541 gcccagtgag aaatgatccc tctttgcctt ggacttcttc tcccgcgatt ttccccactt
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3721 tcaaggttcc aactggaaac cttaggaca gggctccctg tgtgttcccc aaaaggactt
3781 gacttgcaat ttctacctag aaatacatgg acaatacccc caggcctcag tctcccttct
3841 cccatgaggc acgaatgatc tttctttcct ttcctttttt ttttttttct tttctttttt
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3961 ggctcgctgc aacctccgcc tcccgggttc aagtaattct gctgtctcag cctcctgcgt
4021 agctgggact acaggcacac gccacctcgc ccggcccgat ctttctaaaa tacagtctctg
4081 aatatgctgc tcatcccccac ctgtcttcaa cagctcccca ttacctcag gacaatgtct
4141 gaactctcca gcttcgctg agaagtcccc ttccatccca gaggggtggc ttcaggcgcg
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4381 tggcctggaa gggaggagcg ccctctaggg agggacatgg ccccggtgcg gctgcagctc
4441 accagcccca ggggcagaag agaccacaac acttcttatt ttttgaggct atgaatatag
4501 tacctgaaaa aatgccaagc actagattat ttttttaaaa agcgtacttt aaatgtttgt
4561 gttaatacac attaaaacat cgcacaaaaa cgatgcattt accgctcctt gggaaataat
4621 ctgaaaggte taaaaataaa aaagccttct gtggaaaaaa aaaaaaaaaa aaaaaaaaaa
4681 aaaaaaaaaa aaaaaaaaaa aaaa
```

## (2) INFORMATION FOR SEQ ID NO:2573:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4621 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2573:

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1 gaattcctgc cactcttctt gcaacggccc aggagctcag agctccacat ctgaccttct
61 agtcatgacc aggaccaggg cagcactcct cctgttcaca gccttagcaa cttctctagg
121 tttcaacttg gacacagagg agctgacagc cttccgtgtg gacagcgctg ggtttggaga
181 cagcgtggtc cagtatgcca actcctgggt ggtggttggg gccccccaaa agataacagc
241 tgccaaccaa acgggtggcc tctaccagtg tggctacagc actggtgcct gtgagcccat
301 cggcctgcag gtgcccccg aggcctgaa catgtccctg ggcctgtccc tggcgtctac
361 caccagccct tcccagctgc tggcctgcgg cccaccgtg caccacgagt gcgggaggaa
421 catgtacctc accggactct gcttctcctt gggcccccac cagctcacc cagagctccc
481 ggtgtccagg caggagtgcc caagacagga gcaggacatt gtgttcctga tcgatggctc
541 aggcagcatc tctcccgca actttgccac gatgatgaac ttcgtgagag ctgtgataag
601 ccagttccag agaccagca cccagttttc cctgatgcag ttctccaaca aattccaaac
661 acatttact ttcgaggaat tcaggcgcac gtcaaacccc ctacagcctgt tggcttctgt
721 tcaccagctg caagggttta catacacggc caccgccatc caaatgtcg tgcaccgatt
781 gttccatgcc tcatatgggg ccgtaggga tgccacaaa attctcattg tcatcactga
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901 aggcacatc cgctatgcaa ttgggggttg attagctttt caaaacagaa attcttgaa
961 agaattaaat gacattgcat cgaagccctc ccaggaaac atatttaaag tggaggactt
1021 tgatgctctg aaagatatc aaaaccaact gaaggagaag atctttgcca ttgagggtac
1081 ggagaccaca agcagtagct cttcgaatt ggagatggca caggagggtc tcagcgctgt
1141 gttcacacct gatggccccg ttctgggggc tgtggggagc ttcacctggt ctggaggtgc
1201 cttcctgtac cccccaaata tgagccctac cttcatcaac atgtctcagg agaattgtga
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1321 cctggtcctg ggggcccccc gctaccagca caccgggaag gctgtcattc tcacctagg
1381 gtccaggcaa tggaggatga aggcgaagt cacggggact cagatcggt cctactcgg
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1561 ggggtggaga agtggtgtgt gtgatgctgt tctctacggg gagcagggcc acccctgggg
1621 tcgctttggg gcggtcttga cagtgtggg ggatgtgaat ggggacaagc tgacagacgt
1681 ggtcatcggg gcccaggag aggaggagaa ccggggtgct gtctacctgt ttcacggagt
1741 cttgggacc agcatcagcc cctcccacag ccagcgatc gcgggctccc agctctcctc
1801 caggctgcag tattttgggc aggcactgag cgggggtcaa gacctaccc aggatggact
1861 ggtggacctg gctgtggggg cccggggcca ggtgtcctg ctacaggaca gacctgtct
1921 ctgggtgggg gtgagcatgc agttcatacc tgccgagatc cccaggctct cgtttgagt
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1981 tcgggagcag gtggtctctg agcagaccct ggtacagtcc aacatctgcc ttacattga
2041 caaacgttct aagaacctgc ttgggagccg tgacctccaa agctctgtga ccttgaccct
2101 ggccctcgac cctggccgcc tgagtccccg tgccaccttc caggaaacaa agaaccggag
2161 tctgagccga gtccgagtcg tcgggctgaa ggcacactgt gaaaacttca acctgtgtct
2221 cccgagctgc gtggaggact ctgtgacccc cattaccttg cgtctgaact tcacgttgtt
2281 gggcaagccc ctccctgcct tcagaaacct gcggcctatg ctggccgcac tggctcagag
2341 atacttcacg gcctccctac cctttgagaa gaactgtgga gccgaccata tctgccagga
2401 caatctcggc atctccttca gcttcccagg cttgaagtcc ctgtgtgtgg ggagtacact
2461 ggagctgaac gcagaagtga tgggtgtgaa tgacggggaa gactcctacg gaaccaccat
2521 cacccttctcc caccgccgag gactgtccta ccgctacgtg gcagagggcc agaaacaagg
2581 gcagctgcgt tccctgcacc tgacatgtga cagcgcccca gttgggagcc agggcacctg
2641 gagcaccagc tgcagaatca accacctcat cttccgtggc ggcccccaga tcaccttctt
2701 ggctaccttt gacgtctccc ccaaggetgt cctgggagac cggctgtctc tgacagccaa
2761 tgtgagcagt gagaacaaca ctcccaggac cagcaagacc acctccagg tggagtctcc
2821 ggtgaagtat gctgtctaca ctgtgttag cagccacgaa caattcaca aatacctcaa
2881 cttctcagag tctgaggaga aggaaagcca tgtggccatg cacagatacc aggtcaataa
2941 cctgggacag agggacctgc ctgtcagcat caacttctgg gtgcctgtgg agctgaacca
3001 ggaggctgtg tggatggatg tggaggtctc ccaccccag aacccatccc ttcggtgtct
3061 ctcagagaaa atcgaccccc cagcatctga cttcctggcg cacattcaga agaatcccgt
3121 gctggactgc tccattgctg gctgcctgcg gttccgtgtg gacgtccctt ccttcagcgt
3181 ccaggaggag ctggatttca cctgaaggg caacctcagc tttggctggg tccgccagat
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3421 gctggcactc atcacagcgg tactgtacaa agttggcttc ttcaagcgtc agtacaagga
3481 aatgatggag gaggcaaatg gacaaattgc ccagaaaac gggacacaga cccccagccc
3541 gccagtgag aaatgatccc tctttgcctt ggacttcttc tcccgcgatt tccccactt
3601 acttaccttc acctgtcagg ctgacgggga ggaaccactg caccaccgag agaggctggg
3661 atgggcctgc ttctgtctt tgggagaaaa cgtcttgctt gggagggggc ctttgtctt
3721 tcaaggttcc aactgaaac cttaggaca gggccctgc tgtgttcccc aaaaggactt
3781 gacttgcaat ttctacctag aaatacatgg acaatacccc caggcctcag tctccctctt
3841 cccatgaggc acgaatgatc tttctttctt ttctttttt tttttttct tttcttttt
3901 tttttttt agacggagtc tcgctctgtc acccaggctg gagtgcagt gcgtgatctc
3961 ggctcgtgc aacctccgcc tcccgggttc aagtaattct gctgtctcag cctcctgcgt
4021 agctgggact acaggcacac gccacctcgc ccggcccgat ctttctaaaa tacagtctgt
4081 aatatgctgc tcatccccac ctgtcttcaa cagctccca ttacctcag gacaatgtct
4141 gaactctcca gcttcgcgtg agaagtcctc ttccatccca gagggtgggc ttcaggcgcc
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4261 gcatcagctc agggcttcat cgtggggctc tcagttccga tccccaggc tgaattggga
4321 gtgagatgcc tgcatgctgg gttctgcaca gctggcctcc cgcggttggg tcaacattgc
4381 tggcctggaa gggaggagcg ccctctaggg agggacatgg ccccggtgcg gctgcagctc
4441 accagcccca ggggcagaag agaccaacc acttctatt ttttgaggct atgaatatag
4501 tacctgaaaa aatgccaagc actagattat ttttttaaaa agcgtacttt aaatgttgt
4561 gtaatacac attaaaacat cgcacaaaaa cgtgcatct accgctcctt gggaaataat
4621 ctgaaaggtc taaaaataaa aaagccttct gtgg

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## (2) INFORMATION FOR SEQ ID NO:2574:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2574:

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1 ctcgccctgg tgggctgct ctccctcggg tgcgtcctct ctcaggagtg cacgaagttc
61 aaggtcagca gctgccggga atgcacgag tcggggcccg gctgcacctg gtgccagaag
121 ctgaacttca cagggccggg ggatcctgac tccattcgct gcgacaccgg gccacagctg
181 ctcatgaggg gctgtgcggc tgacgacatc atggacccca caagcctcgc tgaaacccag
241 gaagaccaca atgggggcca gaagcagctg tccccacaaa aagtgcagct ttacctgcga
301 ccaggccagg cagcagcgtt caacgtgacc ttccggcggg ccaagggtta ccccatcgac
361 ctgtactatc tgatggacct ctctactcc atgcttgatg acctcaggaa tgtcaagaag
421 ctagggtggc acctgctccg ggccctcaac gagatcaccg agtccggccg cattggcttc
481 gggctccttg tggacaagac cgtgctgccg ttcgtgaaca cgcacctga taagctgcga
541 aacccatgcc ccaacaagga gaaagagtgc ccgccccgt ttgccttcag gcacgtgctg
601 aagctgacca acaactccaa ccagtttcag accgaggtcg ggaagcagct gatttccgga
661 aacctggatg caccgcaggg tgggctggac gccatgatgc aggtcgccgc ctgccggag
721 gaaatcggtt ggcgcaacgt cagcggtgtg ctggtgtttg ccaactgatga cggcttccat
781 ttcgcggggc acggaaagct gggcgccatc ctgaccccca acgacggccg ctgtcacctg
841 gaggacaact tgtacaagag gagcaacgaa ttcgactacc catcggtggg ccagctggcg
901 cacaagctgg ctgaaaacaa catccagccc atcttcggg tgaccagtag gatggtgaag

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961 acctacgaga aactcaccga gatcatcccc aagtcagccg tgggggagct gtctgaggac  
1021 tccagcaatg tgggtccatct cattaagaat gcttacaata aactctcctc cagggtcttc  
1081 ctggatcaca acgcccctcc cgacaccctg aaagtcacct acgactcctt ctgcagcaat  
1141 ggagtgcgc acaggaacca gccagaggt gactgtgatg gcgtgcagat caatgtcccg  
1201 atcaccttcc aggtgaaggt cacggccaca gactgcatcc aggagcagtc gtttgtcatc  
1261 cgggcgctgg gcttcacgga catagtacc gtgcaggctc ttccccagtg tgagtgcggg  
1321 tgccgggacc agagcagaga ccgcagcctc tgccatggca agggctcctt ggagtgcggc  
1381 atctgcaggt gtgacactgg ctacattggg aaaaactgtg agtgccagac acagggccgg  
1441 agcagccagg agctggaagg aagctgccgg aaggacaaca actccatcat ctgctcaggg  
1501 ctgggggact gtgtctgcgg gcagtgcctg tgccacacca gcgacgtccc cggcaagctg  
1561 atatacgggc agtactgcga gtgtgacacc atcaactgtg agcgctacaa cggccaggtc  
1621 tgcggcggcc cggggagggg gctctgcttc tgcgggaagt gccgtgccca cccgggttt  
1681 gagggtcag cgtgccagtg cgagaggacc actgagggtt gcctgaaccc gcggcgtgtt  
1741 gagtgtagt gtctgtggcg gtgcccgtgc aacgtatgcg agtgccattc aggtaccag  
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1861 gccagtgcc tgaagtcca aaagggcccc tttgggaaga actgcagcgc ggcgtgtccg  
1921 ggccgtcagc tgtcgaacaa ccccgtaag ggcaggacct gcaaggagag ggactcagag  
1981 ggctgctggg tggcctacac gctggagcag caggacggga tggacgcta cctcatctat  
2041 gtggatgaga gccgagagtg tgtggcaggc cccaacatcg ccgccatcgt cgggggacc  
2101 gtggcaggca tctgtctgat cggcattctc ctgctggtca tctggaaggc tctgatccac  
2161 ctgagcgacc tccgggagta caggcgcttt gagaaggaga agctcaagtc ccagtggaa  
2221 aatgataatc cccttttcaa gagcgccacc acgacggtca tgaaccccaa gtttgcgtgag  
2281 agttaggagc a

## (2) INFORMATION FOR SEQ ID NO:2575:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11583 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2575:

1 gaattcctgc cactcttctt gcaacggccc aggagctcag agctccacat ctgaccttct  
61 agtcatgacc aggaccaggg cagcactcct cctgttcaca gccttagcaa cttctctagg  
121 tttcaacttg gacacagagg agctgacagc cttccgtgtg gacagcgtg ggtttggaga  
181 cagcgtgggt cagtatgcca actcctgggt ggtggttggg gcccccaaa agataacagc  
241 tggcaaccaa acgggtggcc tctaccagt tggctacagc actggtgcct gtgagcccat  
301 cggcctgcag gtgcccccg aggccgtgaa catgtccctg ggctgtccc tggcgtctac  
361 caccagccct tcccagctgc tggcctgcgg cccaccctg caccacaggt gcgggaggaa  
421 catgtacctc accggactct gcttctcctt gggccccacc cagctcacc agaggctccc  
481 ggtgtccagg caggagtggc caagacagga gcaggacatt gtgttcctga tcatggtc  
541 aggcagcatc tctcccgcga actttgcac gatgatgaac ttcgtgagag ctgtgataag  
601 ccagttccag agaccagca cccagtttct cctgatgcag ttctccaaca aattccaac  
661 acacttcaat ttcaggaat tcaggcgac gtcaaacccc ctgagcctgt tggcttctgt  
721 tcaccagctg caagggttta catacacggc caccgccatc caaaatgctg tgcaccgatt  
781 gttccatgcc tcatatggg cccgtaggga tgccacaaa attctcattg tcatcactga  
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961 agaattaaat gacattgcat cgaagccctc ccaggaacac atatttaaag tggaggactt  
1021 tgatgctctg aaagatattc aaaaccaact gaaggagaag atctttgcca ttgagggtac  
1081 ggagaccaca agcagtagct ccttcgaatt ggagatggca caggagggtt tcagcgtgt  
1141 gttcacacct gatggccccg tctgggggag tgtggggagc ttcacctggt ctggaggtgc  
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1261 catgagggac tcttacctgg gttactccac cgagctggcc ctctggaaag ggggtgcagag  
1321 cctggctcctg ggggcccccc gctaccagca caccgggaag gctgtcatct tcaccagggt  
1381 gtccaggcaa tgaggatga aggcgaagt cacggggact cagatcggct cctacttcgg  
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1561 ggggtggaga aggtggtggt gtgatgctgt tctctacggg gaggaggcc accctggggg  
1621 tgcctttggg gcggtcttga cagtgcctgg ggatgtgaat ggggacaagc tgacagacgt  
1681 ggtcatcggg gcccaggag aggaggagaa ccggggtgct gtctacctgt ttcacggagt  
1741 cttgggaccc agcatcagcc cctcccacag ccagcggatc gcgggctccc agctctcctc  
1801 caggctgcag tattttgggc aggcactgag cgggggtcaa gacctcacc aggatggact  
1861 ggtggacctg gctgtggggg cccggggcca ggtgctcctg ctgaggacca gacctgtgct  
1921 ctgggtgggg gtgagcatgc agttcatacc tgccgagatc cccaggctctg cgtttgagtg  
1981 tggggagcag gtgtctctg agcagacctt ggtacagtcc aacatctgcc tttacattga  
2041 aagaacttct aagaacctgc ttgggagccg tgacctcaa agctctgtga ccttgacct  
2101 ggcctctgac cctggccgccc tgagtcctcc tgccaccttc caggaaacaa agaaccgag  
2161 tctgagccga gtccgagtc tggggtgaa ggcacactgt gaaaacttca acctgtgct  
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## (2) INFORMATION FOR SEQ ID NO:2576:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 661 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2576:

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## (2) INFORMATION FOR SEQ ID NO:2577:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2577:

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3061 cgggagggcg cggggcgggg agcagccccc aggcgggtcc gggtcgcaag accatcccg
3121 cggcgcgct catcccaccc gccaccgca ggtgaactg cagcgagtac ttcccgctgt
3181 tctcggccac gctctgggtc gccggcatct tctttcatga aggtcgggt gtggggcagg
3241 ggcgcacgcg ctggaccccc gggaccgcgc cagggcgctc accaggcccg tgcgtacctc
3301 tcgcaggggc ggcggccctg tgcggcctgt tctacctgt cgcgcgcctc cgtacttcc
3361 agggctacgc gcgctccgcg cagctcaggt gagggccggg cggggagcgg ggcggggccg
3421 gggaaagatc gcgggcgggc ggggctcctg gggagcggga ccgaagctgg gggcgggca
3481 cgggccggag ccagcgcct ttggggattc ggtgggcgag ccctggcggc ggccagagga
3541 agtccccgtg gggccagggt tgcggcgggg aagaagcggg cctcctcgcg ccacctcccc
3601 gctgaccgcc gccgcaggc tggcaccgct gtacgcgagc gcgcgcgcc tctggtgct
3661 ggtggcgctg gctgcgctcg gcctgctcg ccacttctc ccggccgcgc tgcgcgcgc
3721 gctcctcgga cggctccgga cgtgctgcc gtgggcctga gaccaagcc cccgggccga
3781 cggagccggg aaagaagagc cggagcctcc agctgcccc gggagggcg ctcgcttccg
3841 catcctagtc tctatcatta aagttctagt gaccgagacc cgggctcgt tctctgggtc
3901 cgcgggggtg gcgcaccgcg ggctacggag cctggagggg ccagcccga gtcgggcag
3961 cccggggcg gcttcttagt ggcggcgtga gagtggctgc gaaggaacga gccctcccc
4021 tggggcgggg ctggatccg tcttcacct ctacccact ccctactcag cctcggggtc
4081 acaaggccgc ccagtcctgc cgggggtcac cctcctagc ctcagcgtc tctcaccgg
4141 tccccctcct caggggcctt ccctcgactc tcagccgcgc cagtccctc tcccctggcc
4201 ttcacagctg aactagata gagcctgtg ctctctccc aggtgaggc aggggtttt
4261 cttttggtca gcaactggat cccctcgta actgtagggt ttcagggcag cctccgagg
4321 tccgagagc tgcgggcacc atgggaacga agtgagtcag tgacaggcg tctcaaggaa
4381 atgtccagaa gccttgggga tccaggggag gccacagaa acaaagaagt gacttttagc
4441 caagtatgca ggagaaacgg aggag

```

## (2) INFORMATION FOR SEQ ID NO:2578:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2578:

```

1 tcttctctc ctgggcccgc ctctgagcag cagacggggc taagcgttcc ccagctcgcc
61 ttcacacaca gcccggtgcca ccacaccgac ggtaccatga aggacgaggt agctctactg
121 gctgctgtca cctcctggg agtccctgct caagcctact tctccctgca ggtgatctcg
181 gcgcgcaggc ccttccgcgt gtcgcgcgcg ctcaccaccg gccacccga gttcgagcgc
241 gtctaccgag ccaggtgaa ctgcagcgag tacttcccgc tgttctcgc cagcgtctgg

```

301 gtcgcccga tcttctttca tgaaggggag gcggccctgt gcggccctgt ctacctgttc  
361 gcgcgcctcc gctacttcca gggctacgcg cgctccgcgc agctcaggct ggcaccgctg  
421 tacgcgagcg cgcgcgcct ctggctgctg gtggcgctgg ctgcgctcgg cctgctcgcc  
481 cacttctctc cggccgcgct gcgcgcgcgc ctccctcgac ggctccggac gctgctgccc  
541 tgggcctgag accaaggccc ccgggcccgc ggagccggga aagaagagcc ggagcctcca  
601 gctgccccgg ggagggggcg tcgcttccgc atcctagtct ctatcattaa agttctagt  
661 accga  
1 gagctcacag agccccagc tggggcatat ctggtttccg ggggcagggg cgatacccag  
61 aggaggaaga agggattctg agagagccca acaggctccg agcctcaggc tggagctgag  
121 cttggggcag caaggaagga ccaggtgcga gggcagaacc atgcggcccg acccctgcag  
181 cagggcctgt ggctcccccc agctcctgcc cgtgcttctg ggtcagtctg gactttgcca  
241 cttctgacca aaagccaccg caaacccact caagccaaaa gaggaagtga ccgttaggcc  
301 caactgggaa ggctggcggc caggggacat ccaggcaggg cgaggggggc ggccgggggc  
361 gctccaggcg gggcgaggga gacaccaga actccaggca ggagtcctcg ggtgccacct  
421 ttctcttcca cctggccctg cgtgggctct gtcctcaggg tggcccgccg tagtccccct  
481 cccactctg agtttctgt cccaaagtcc taaggaagtt tccagaacta catctacca  
541 tcttgagtca gccttgctc agtgtccatc tcacaggcct ggaaggggca ggaagtcagca  
601 ctgtccagac cacaggccct gagtgtgggg agggcagccg tctaggaagg tgggtggagg  
661 ttgttacctt gaggcaagag ggctgcgggg cagaaagaca cagcaggtag ctgtgtgtgg  
721 agggccaaga gaggcctggg agaggatgg ccacaaagg ctgaccctcc cgccaccag  
781 ggggccttgg acaggtttcc tctggcagg gtggcccttg tgcaggaac ccctacaacg  
841 actaaggctg gcaggcatga ggtttctga aggagaaaga gcttgtggg ccagtggtg  
901 ctgggggggc gctgggactc cattctgaag ccaaaggcac tgggaagggc tccgcagag  
961 gaggttttgg caggggttgc caggaacagc ctggatgggg acaggggaca gataaggtg  
1021 gtggaggagt tagccgggag cctggggctg gctccagcat gatgtgggg tctgcaaggc  
1081 cctggagaaa gtgggtggg gcagcagggg gcacaccac agctggagct gaccagatg  
1141 gacagcttgg gctctgccac gcgggactag gcaaggaagg ggcacgaaca agcaggaagt  
1201 ggtgagcgcg tctccagcta gctgcttcc cctgcccaga ctttggtttc ctccctgctg  
1261 gcttggcctg gctccctggc tctgtgtggt atggtcacac ccccgtcac cccctccact  
1321 gagatggggc ggggagagca ccaggctgc tcttctctc ctgggcccgc ctctgagcag  
1381 cagacggggc taagcgttcc ccagctcgc ttcacacaca gcccgtgcca ccacaccgac  
1441 ggtaccatga aggacgaggt agctctactg gctgctgtca ccctcctggg agtccgtctg  
1501 caaggtgggc tggttcctat ctaggaagag ggtgggcctt agatccctac agcttgcctt  
1561 ctgcccccta ggcccagggt gagggcagag gtggggactc cagcccaggc ccaagctgga  
1621 agagggtggg gactttcagg gaactggggg gcacctggct gtgagagctg taggacttgg  
1681 ggggtggcaag ggtgccagga caaatggtag gatagccatg ggcttgggga agctgatctc  
1741 tgctcttccc agctgtcccc tctctgggag tcccagcaag cggcccccac tccctggctc  
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1861 ctccagcccc ctaaaagag cctgcttaat gcctttctca gactggccct aaaggacaca  
1921 ttccttggcc agatatcctt gccacctaa agacaccact actccacagt gtgtgggcta  
1981 ggataaggca cagcctgggg agggggctct gaaggggctg aacagacagg ccagcctgac  
2041 ctccagctgc tctgactg agctggatgg ccacctgtg acacctctc cgagggggcc  
2101 cagaaccaaa ggtgccaggc ctgcaggact cagggggaga tggctccagc ggaggtctgg  
2161 ggaggagcgc cacagccagc actggtctgt gtgtggtctg gcctggcctc acctgaccac  
2221 gagaagggtc cctgcccaca gagaaacttt agggccagcc caccctctgc aactacccca  
2281 gccctggggg cctgggggta ggctaggaga gtcccagctg caacctcctg ggagcaggag  
2341 agaaggtgtc tgtcagattt aggcctggga ccggaatgca ggaacagaga aactgaggtt  
2401 tggaggcaca gggacgcagg ctttagtgat cccggcctga ggcagggtca gaggccctg  
2461 ctgggtggcg ctggtaggtg ggtgaccagg gactgttagc tacagggagt gtgcttctt  
2521 gcacctggga ggatgcagcc agctctgccc tcagactccc gaggcacttc ctggccaggg  
2581 acctgaaagc tgcatttgc tgtgttttga gagtgaatg attcagaaac aaggactcaa  
2641 gtggtctctc tcgaggagca ggtgtccctg tgcctgaatc actcaccctc cccatacac  
2701 tcacaggttg ggacagggcc tctctgcgcc ccaggcttca gccctgccc cctcgctgaa  
2761 tgtcagggac acagggcagg ccagggatgg gtgagacgag aggtctcctc gggcggggag  
2821 gggggcgggt tccgccttag ggaggagagg acacggccaa gtgaagggcc agattgcagg  
2881 atccctccca ctcccctctc tggggcttcc ggtgtccaga cctgactccc gctcccctc  
2941 ctccccagc ctacttctcc ctgcaggtga tctcgcgcg cagggccttc cgcgtgtcgc  
3001 cgcgcgtcac caccggccca ccgcagttcg agcgcgtcta ccgagccag tgaggcgcg  
3061 cgggaggggc cggggcgggg agcagagccc agggcggtcc gggctcgcag accatcccgg  
3121 ccggcgcgct catccacccc gccaccgca ggggtgaactg cagcgagtag tcccgcgtgt  
3181 tctcgcacc gctctgggtc gccggcatct tctttcatga aggtcggggt gtggggcagg  
3241 ggcgcacgcg ctggaccccc gggaccgcg cagggcgctc accaggcccg tgcgtacctc  
3301 tcgcaggggc ggcggccctg tgcggcctgg tctacctgtt cgcgcgctc cgtacttcc  
3361 agggctacgc gcgctccgcg cagctcaggg gagggccggg cggggagcgg ggcggggcgg  
3421 gggaaagatc gcgggcgggc ggggctcctg gggagcggga ccgaagctgg gggcggcgga  
3481 cgggcccggg cccagcgcct ttggggattc ggtgggcgag ccctggcggc ggccagagga  
3541 agtccccgtg gggccagggt tgcggcgggg aagaagcggg cctcctcgcg ccacctcccc  
3601 gctgaccgcc gcccgaggc tggcaccgct gtacgcgagc gcgcgcgccc tctggctgct

3661 ggtggcgctg gctgcgctcg gctgctcgcc ccacttcctc ccggcgcgcg tgcgcgccc  
3721 gctcctcgga cggctccgga cgctgctgcc gtgggcctga gaccaaggcc cccgggcccga  
3781 cggagccggg aaagaagagc cggagcctcc agctgccccg gggagggcg ctcgcttccg  
3841 catcctagtc tctatcatta aagtcttagt gaccgagacc cgggctgctg tctctgggtc  
3901 cgcgggggtg gcgcaccgcg ggctacggag cctggagggg ccagcccga gtccgggcag  
3961 cccggggcg gcttcctagt ggcggcgtga gagtggctgc gaaggaacga gccctcccc  
4021 tggggcggga ctggatccgg tcttcacctc ctacccact ccctactcag cctcggggtc  
4081 acaaggccgc ccagtcctgc cgggggtcac cctcctagcg ctacgcggtc tctcaccgg  
4141 tccccctcct caggggcctt ccctcgactc tcagccgccc cagtcctcgt tccccctggc  
4201 ttcacagctg acactagata gagcctgtgg ctctctcccc aggtgaggcg aggggtttt  
4261 cttttggtca gcactggatc cccctcgta actgtagggt ttcagggcag ccctccagg  
4321 tccgcagagc tgcgggcacc atgggaacga agtgagtcag tgacaggcgg tctcaaggaa  
4381 atgtccagaa gccttgggga tccaggggag gccacagaa acaaagaagt gacttttagc  
4441 caagtatgca ggagaaacgg aggag

## (2) INFORMATION FOR SEQ ID NO:2579:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3001 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2579:

1 gccattctct cacatcccgt gcggtcagga agcccttctt gaactctgac ttcagttctt  
61 gctgcggttt ctgcccattt ttttcatatc ctctgacagc tgcgaggtca tctctgctct  
121 ggcttttctc caagcagaac aagtgggggc tctggaaggg ttaagggacc tcagtggcca  
181 ccattatact ttgcatcttt cctgagaagt gagagttgaa agggaagcag gaagggccat  
241 ggtcagattg aaggaaggac tttttagttt cttttttttt tttttgaaat ggagtcctgc  
301 tctgtcattc aggtctgagt gcagtggctg gatctcagct cactgcagcc tccacttctc  
361 ggggttcacat gattctcctg cctcagcctc ccaagtagct gagactacag gcacatgcca  
421 ctacacccag ctaacttttg tatttttagt agagacgggg tttcaccatg ttggccaggc  
481 tgggtctcaa ctgtaacat caagtgatct gctccctca gctcccaaa gtgctgggat  
541 taccggtatg aaccaccaca acctgccagg aatttttagt ttttagcttt tgcaggagac  
601 ttcaagggaa ggagacattc ctctgtccag gaaacgggta aggggaccat ttctgcattg  
661 ctggtttccc ctcttggcag ggtgggcag aggcatact gtctctgct cctcactcct  
721 gctcctcatg ctacgcctgc cagctcgccc tcaactttgt gtgtctaaag tggaaactgaa  
781 tagtagctgt gagaagatag gaaagaggtg gtgccaatct ccttgcccag atcataaatc  
841 cagactcagc agggtaacca catgggcaag cacaaggtag gtgcttgggg aaaggggaag  
901 taattggcat tctgtgtgat accaaggaga ccatttggat tttggcttct accaaagaga  
961 atggagaatt ggttgacctt aatggaacca gtccctttaa gtaaggggag gaaagggggt  
1021 gctggaagat ggccctcttc ccaccaccta gatcatagct tgaactgaag ccaaggacag  
1081 agtgcctgcc ccttcggcat ttactgatgt gccctcttta aatcatgatg ttatctaacc  
1141 caaaccaga cccaggacct agtcacagct ccaacctaca ctctctatta atcttaaac  
1201 aaagcgaaac aaacacaaaa agatatacgc attgtagcct ccaatctgag cccatttccc  
1261 ttctctggct accatacctc cttctcctat atgataccat tcaactactt gttcaattat  
1321 ccagtctaga cctgcattct gagggcacac ccagccttct cactccccac acccctcttt  
1381 cctctctcac tgctccttcc tgggtctctc tcatctggcc ccacctctaa ggagtcctcc  
1441 tgcttctctg gttgcctctg aaaacagact atccccctc ctagtgaagg gagtgggtag  
1501 gggtttcagc cccaccctca ggaagatgct tcttccctgt cctctgctct gtggtacttc  
1561 ctctctggct gatttagcaa acagcaccta gacctggggc caggcctttg gcagtgggac  
1621 agatccaggg ataggctaca ccacctgcc ctgacctggg gattggcatc agcttccaac  
1681 cagttcctgc caaagcttgt aagtcctccc gacggccatg aacactacat cttctgcagc  
1741 accccctca ctaggtgtag agttcatctc tctgctggct atcatcctgc tgtcagtggc  
1801 gctggctgtg gggcttccc gcaacagctt tgtggtgtgg agtatcctga aaaggatgca  
1861 gaagcgctct gtcactgccc tgatgggtgt gaacctggcc ctggccgacc tggccgtatt  
1921 gctcactgct ccctttttcc ttcacttctt ggcccaaggc acctggaggt ttggactggc  
1981 tggttgccgc ctgtgtcact atgtctgcgg agtcagcatg tacgccagcg tctgtcttat  
2041 cacggccatg agtctagacc gctcactggc ggtggccgcg ccctttgtgt cccagaagct  
2101 acgcaccaag cggatggccc ggcgggtgct ggcaggcatc tgggtgtgtg cctttctgct  
2161 ggccacaccc gtcctcgctg accgcacagt agtgccctgg aaaacgaaca tgagcctgtg  
2221 cttcccgcgg taccacagcg aagggcaccg ggcccttccat ctaatcttcg aggtgtcac  
2281 gggcttctct ctgccccttc tggctgtggt ggccagctac tcggacatag ggcgtcggct  
2341 acaggcccg cgcttcgccc gcagccgccc caccggccgc ctggtgggtg tcatcatcct  
2401 gaccttcgcc gccttctggc tgccctacca cgtggtgaac ctggtgagg cgggccgcgc  
2461 gctggccggc caggcccgcg ggttagggct cgtggggaag cggctgagcc tggccgcaa  
2521 cgtgtctcgc gcactcgctc tctgagcag cagcgtgaac cccgtgctgt acgcgtgcgc  
2581 cggcgccgcg ctgctgcgct cggcgggcgt gggcttcgtc gccaaagctg tggagggcac  
2641 gggttccgag gcgtccagca cgcgcccgcg ggccagcctg ggccagaccg ctaggagcgg  
2701 ccccgccgct ctggagcccg gcccttccga gagcctcact gcctccagcc ctctcaagtt  
2761 aaacgaactg aactaggcct ggtggaagga ggcgcacttt cctcctggca gaatgctagc

2821 tctgagccag ttcagtacct ggaggaggag caggggctgt gagggcgtgg agggcgtggg  
 2881 agcgtgggag gcgggagtg agtggagaa gagggagaga tggagcaaag tgagggccga  
 2941 gtgagagcgt gctccagcct ggctcccaca ggcagcttta accattaaaa ctgaagtctg  
 3001 aa

## (2) INFORMATION FOR SEQ ID NO:2580:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 841 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2580:

1 aaaagaagga cctgggcttt gggaagatct aaagaccag gaaggtctct ggggtgggata  
 61 aagccaagat gaaactcccc ctacttctgt ctcttctatt tggggcagtt tctgctcttc  
 121 atctaaggtc tgagacttcc acctttgaga cccctttggg tgctaagacg ctgcctgagg  
 181 atgaggagac accagagcag gagatggagg agacccttg cagggagctg gaggaagagg  
 241 aggagtgggg ctctggaagt gaagatgcct ccaagaaaga tggggctgtt gagtctatct  
 301 cagtgccaga tatggtgcac aaaaacctta cgtgtcctga ggaagaggac acagtaaaag  
 361 tgggtgggcat ccctgggtgc cagacctgcc gctacctcct ggtgagaagt ctccagacgt  
 421 ttagtcaagc ttggtttact tgccggaggt gctacagggg caacctgggt tccatccaca  
 481 acttcaatat taattatcga atccagtgtt ctgtcagcgc gctcaaccag ggtcaagtct  
 541 ggattggagg caggatcaca ggctcgggtc gctgcagacg ctttcagtgg gttgacggca  
 601 gccgctggaa ctttgcgtag tgggtgctc accagccctg gtcccgcggt ggtcactgcg  
 661 tggccctgtg taccagagga ggctactggc gtcgagccca ctgcctcaga agacttcctt  
 721 tcatctgttc ctactgagct ggtcccagcc agcagttcag agctgccctc tcttgggcag  
 781 ctgcctcccc tctctgctt gccatccctc cctccacctc cctgcaataa aatgggtttt  
 841 actgaaaa

## (2) INFORMATION FOR SEQ ID NO:2581:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 841 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO 2581:

1 aaaagaagga cctgggcttt gggaagatct aaagaccag gaaggtctct ggggtgggata  
 61 aagccaagat gaaactcccc ctacttctgt ctcttctatt tggggcagtt tctgctcttc  
 121 atctaaggtc tgagacttcc acctttgaga cccctttggg tgctaagacg ctgcctgagg  
 181 atgaggagac accagagcag gagatggagg agacccttg cagggagctg gaggaagagg  
 241 aggagtgggg ctctggaagt gaagatgcct ccaagaaaga tggggctgtt gagtctatct  
 301 cagtgccaga tatggtggac aaaaacctta cgtgtcctga ggaagaggac acagtaaaag  
 361 tgggtgggcat ccctgggtgc cagacctgcc gctacctcct ggtgagaagt ctccagacgt  
 421 ttagtcaagc ttggtttact tgccggaggt gctacagggg caacctgggt tccatccaca  
 481 acttcaatat taattatcga atccagtgtt ctgtcagcgc gctcaaccag ggtcaagtct  
 541 ggattggagg caggatcaca ggctcgggtc gctgcagacg ctttcagtgg gttgacggca  
 601 gccgctggaa ctttgcgtag tgggtgctc accagccctg gtcccgcggt ggtcactgcg  
 661 tggccctgtg taccagagga ggctactggc gtcgagccca ctgcctcaga agacttcctt  
 721 tcatctgttc ctactgagct ggtcccagcc agcagttcag agctgccctc tcttgggcag  
 781 ctgcctcccc tctctgctt gccatccctc cctccacctc cctgcaataa aatgggtttt  
 841 actgaaaa

## (2) INFORMATION FOR SEQ ID NO:2582:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1682 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2582

1 aaaagaagga cctgggcttt gggaagatct aaagaccag gaaggtctct ggggtgggata  
 61 aagccaagat gaaactcccc ctacttctgt ctcttctatt tggggcagtt tctgctcttc  
 121 atctaaggtc tgagacttcc acctttgaga cccctttggg tgctaagacg ctgcctgagg  
 181 atgaggagac accagagcag gagatggagg agacccttg cagggagctg gaggaagagg  
 241 aggagtgggg ctctggaagt gaagatgcct ccaagaaaga tggggctgtt gagtctatct  
 301 cagtgccaga tatggtgcac aaaaacctta cgtgtcctga ggaagaggac acagtaaaag  
 361 tgggtgggcat ccctgggtgc cagacctgcc gctacctcct ggtgagaagt ctccagacgt  
 421 ttagtcaagc ttggtttact tgccggaggt gctacagggg caacctgggt tccatccaca  
 481 acttcaatat taattatcga atccagtgtt ctgtcagcgc gctcaaccag ggtcaagtct  
 541 ggattggagg caggatcaca ggctcgggtc gctgcagacg ctttcagtgg gttgacggca  
 601 gccgctggaa ctttgcgtag tgggtgctc accagccctg gtcccgcggt ggtcactgcg  
 661 tggccctgtg taccagagga ggctactggc gtcgagccca ctgcctcaga agacttcctt

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721 tcactctgttc ctactgagct ggtcccagcc agcagttcag agctgcccctc tcctgggcag
781 ctgccctccc tectctgctt gccatccctc cctccacctc cctgcaataa aatgggtttt
841 actgaaaa
1 aaaagaagga cctgggcttt gggaagatct aaagaccag gaaggctctc ggggtgggata
61 aagccaagat gaaactcccc ctacttctgg ctcttctatt tggggcagtt tctgctcttc
121 atctaaggtc tgagacttcc acctttgaga cccctttggg tgctaagacg ctgctgaggg
181 atgaggagac accagagcag gagatggagg agaccccttg cagggagctg gaggaagagg
241 aggagtgggg ctctggaagt gaagatgcct ccaagaaaga tggggcgtt gagtctatct
301 cagtgccaga tatggtggac aaaaacctta cgtgtcctga ggaagaggac acagtaaaag
361 tgggtggcat ccctgggtgc cagacctgcc gctacctcct ggtgagaagt ctccagacgt
421 ttagtcaagc ttggtttact tgccggaggt gctacagggg caacctgggt tccatccaca
481 acttcaatat taattatcga atccagtgtt ctgtcagcgc gctcaaccag ggtcaagtct
541 ggattggagg caggatcaca ggctcgggtc gctgcagacg ctttcagtgg gttgacggca
601 gccgctggaa ctttgcgtac tgggtctgtc accagccctg gtcccgcggt ggtcactgcy
661 tggccctgtg taccgagga ggctactggc gtcgagccca ctgcccctaga agacttcctt
721 tcactctgttc ctactgagct ggtcccagcc agcagttcag agctgcccctc tcctgggcag
781 ctgccctccc tectctgctt gccatccctc cctccacctc cctgcaataa aatgggtttt
841 actgaaaa

```

## (2) INFORMATION FOR SEQ ID NO:2583:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 781 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2583

```

1 agcagagggg ctgagaccaa accagaaacc tccaattctc atgtggaagc ccatgccctc
61 accctccaac atgaaagcct ctgcagcact tctgtgtctg ctgtccacag cagctgcttt
121 cagcccccag gggcttgctc agccagttgg gattaatact tcaactacct gctgctacag
181 atttatcaat aagaaaatcc ctaagcagag gctggagagc tacagaagga ccaccagtag
241 ccactgtccc cggaagctg taatcttcaa gaccaaactg gacaaggaga tctgtgtgta
301 cccacacag aagtgggtcc aggactttat gaagcacctg gacaagaaaa cccaaactcc
361 aaagctttga acattcatga ctgaactaaa aacaagccat gacttgagaa acaataattt
421 tgtataccct gtcttttctc agagtgggtc tgagattatt ttaattctat tctaaggaat
481 atgagcttta tgaataatg tgaatcatgg tttttcttag tagattttaa aagttattaa
541 tatttttaatt taatcttcca tggattttgg tgggttttga acataaagcc ttggtatgat
601 atgtcatctc agtctgttaa aaactgtggg atgctcctcc cttctctacc tcatgggggt
661 attgtataag tccttgcaag aatcagtgcg aagatttgct ttaattgtta agatatgatg
721 tccctatgga agcatattgt tattatataa ttacatattt gcatatgtat gactcccaaa
781 ttttcacata aaatagattt ttgtaaaaaa

```

## (2) INFORMATION FOR SEQ ID NO:2584:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1081 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2584

```

1 ggtttctatt gacttgggtt aatcgtgtga ccgcggtggc tggcacgaaa ttgaccaacc
61 ctgggggttag tatagcttag ttaaactttc gtttattgct aaaggttaat cactgctggt
121 tcccgtgggg gtgtggctag gctaagcgtt ttgagctgca ttgctgcgtg cttgatgctt
181 gtcccttttg atcgtggtga tttagagggt gaactcactg gaatggggat gcttgcatgt
241 gtaattctac taagagctaa tagaaaggct aggaccaaac cagaaacctc caattctcat
301 gtggaagccc atgccctcac cctccaacat gaaagcctct gcagcacttc tgtgtctgct
361 gctcacagca gctgctttca gccccagggt gcttgtctcag ccagttggga ttaatacttc
421 aactacctgc tgctacagat ttatcaataa gaaaatccct aagcagagggc tggagagcta
481 cagaaggacc accagtagcc actgtccccg ggaagctgta atcttcaaga ccaaactgga
541 caaggagatc tgtgctgacc ccacacagaa gtgggtccag gactttatga agcacctgga
601 caagaaaacc caaactccaa agctttgaac attcatgact gaactgaaaa caagccatga
661 cttgagaaac aaataatttg tataccctgt cctttctcag agtgggtctg agattatttt
721 aatctaattc taaggaatat gagctttatg taataatgtg aatcaggtt tttcttagta
781 gattttaaaa gttattaata ttttaattta atcttccatg gattttgggt ggttttgaa
841 ataaagcctt ggatgtatat gtcactctcag tgctgtaaaa actgtggggt gctcctccct
901 tctctacctc atgggggtat tgtataagtc cttgcaagaa tcagtgcata gatttgcttt
961 aattgttaag atatgatgtc cctatggaag catattgtta ttataaattt acatatttgc
1021 atatgtatga ccccaattt ttcacataaa atagattttt gtataacaaa aaaaaaaaaa
1081 aaaaaa

```

## (2) INFORMATION FOR SEQ ID NO:2585:

## (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 1081 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2585

```
1 ggtttctatt gacttgggtt aatcgtgtga ccgcggtggc tggcacgaaa ttgaccaacc
61 ctgggggttag tatagcttag ttaaactttc gtttattgct aaagggttaat cactgctgtt
121 tcccgtgggg gtgtggctag gctaagcgtt ttgagctgca ttgctgctg cttgatgctt
181 gtcctttttg atcgtgggtga tttagagggt gaactcactg gaatggggat gcttgcattg
241 gtaatcttac taagagctaa tagaaaggct aggaccaaac cagaaacctc caattctcat
301 gtggaagccc atgccctcac cctccaacat gaaagcctct gcagcacttc tgtgtctgct
361 gctcacagca gctgctttca gccccagggt gcttgcctag ccagttggga ttaatacttc
421 aactacctgc tgctacagat ttatcaataa gaaaatccct aagcagaggc tggagagcta
481 cagaaggacc accagtagcc actgtccccg ggaagctgta atcttcaaga ccaaaactgga
541 caaggagatc tgtgtgacc ccacacagaa gtgggtccag gactttatga agcacctgga
601 caagaaaacc caaactccaa agctttgaac attcatgact gaactgaaaa caagccatga
661 cttgagaaac aaataatttg tataccctgt cctttctcag agtggttctg agattatttt
721 aatctaattc taaggaatat gagctttatg taataatgtg aatcatggtt tttcttagta
781 gattttaaaa gttattaata ttttaattta atcttccatg gattttgggt ggttttgaa
841 ataaagcctt ggatgtatat gtcattctag tgctgtaaaa actgtgggat gctctccct
901 tctctacctc atgggggtat tgtataagtc cttgcaagaa tcagtgcgaa gatttgcttt
961 aattgttaag atatgatgtc cctatggaag catattgtta ttatataatt acatatttgc
1021 atatgtatga ctcccaaatt ttcacataaa atagattttt gtataacaaa aaaaaaaaaa
1081 aaaaa
```

## (2) INFORMATION FOR SEQ ID NO:2586:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2881 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2586

```
1 ggatccttaa gccatcatgc aaaatatcta gccatgtgga gggaccactg gaaagatcac
61 acacacacac acacacacac acacacacac atacagagag agagagagac acctgagaaa
121 ttccatctgg tccaactgct ggctgttgaa gtcctcccag cccagacccc agacactgaa
181 tgaaggcctt gtgatatagt caagagcaaa aaaaccaga agattgttat tgttttaagt
241 cactgttttc agatagattg ctatgcagca atagattatt gaaatagaca ctacaatttt
301 aggtactatt attctaagaa tattgaattt tattttctg ctaattgtct attattttac
361 ttttctctgg gttttagaaa gccaccagga tttaagacag tgaagaattc ttgagtcctt
421 tgtagagttg aaccaaagtt tgaatgtctc tttgtggact cgtgtcctag ggataccact
481 ccaaaggga aagggaata tcccttacct atctttgact ttggtatccc tgattccttc
541 ctttttctat agaattgtgc tcatttcaga gaaactggtc tcttgataat agccatagat
601 tacatactgt ggtcttcctc tacatagacc ctacctcacc taccactcct ggtcttagct
661 gaaaaacagg ctagcctcga ctcatactgt catttccat cctcccactg aagtgcactg
721 gctcagcaga tttattactc catagattta ttactccatt ctatgattca tctctctgc
781 ttctataaaa aggagagac agagcttcca gagagcaga ggggctgaga ccaaaccaga
841 aacctccaat tctcatgttg aagcccatgc cctcaccctc caacatgaaa gcctctgcag
901 cacttctgtg tctgtgtctc acagcagctg ctttcagccc ccaggggctt gctcagccag
961 gtaaggctcc tctctccttc tccttgaagc acattgccc ctctctgggt tatcctggac
1021 caatcaagaa gacctgatac ccacagtctc actttaacag ctacttttcc aagataaggt
1081 aacttagaaa aaggataagg ggtgagccca accacacagc tgctgttggg tagagcctga
1141 actgaattc cagctgtgaa ccccaaatcc agctccttct aggattccag ctctgggaac
1201 accctcagtg cagttaccac tccagctgct tccagcagaa tttgggatca ggggtgatcaa
1261 agacaggagg cttctgggga tgggtgtgct ggctgtttcc agataccggg agaccagaaa
1321 tctggtctgt ggaagcccag cttccagaaa cagcagctct gcagaggttg tacgtatcag
1381 ggaaactcat gaccaagcat tgaatgtcga gagcctaaaa ggggatccat agttggggta
1441 cccttgctct aaggaattgg attattatat tagccctccc tagcaatgcc cagagtagcc
1501 atcaattcct cttccgtctt tcaactggtg atggtgcac cctatttcac agtccataaa
1561 agtgaaagg agtttatgaa atgcctcaaa gggcagagac attgggtttg ggatgggcag
1621 ctttccctc cacctcttcc tttcttctg attccttctt cttaccatc cctgttttac
1681 aacacagaa agccaggaca caccctcaat ggacttttct tcttgttgtt tcatgacagt
1741 tgggattaat acttcaacta cctgctgcta cagatttatc aataagaaaa tccctaagca
1801 gaggctggag agctacagaa ggaccaccag tagccactgt ccccggaag ctgtaatgta
1861 tgtggacgat gaccaccac cctcacacc tcagtcctag gttcttccct gggcaggga
1921 taggactagt atcagaatga gttggagtca aatactgtga tgcatacagc atctctaacc
1981 ttatcccaga catttgccag tgagaaacaa tacaagtaaa gaaagtggct tctcactctc
2041 agctccctt ccagctatca ttttacatct cagttcgttc cttcatctg gaaccaagag
2101 agattcactt gggctaccaa aaagagctgc ttctctgagt ccccttctt tgtttatct
2161 tcttcttca tccctgaggc atcccatca gctaggctga tgggctagac agatttccca
```

2221 tagacttggg cactactccca ggctgaaccc tcaaggtgtt ccatctgact gtctcctttc  
2281 tgctccacag cttcaagacc aaactggaca aggagatctg tgctgacccc acacagaagt  
2341 ggggtccagga ctttatgaag cacctggaca agaaaaccca aactccaaag ctttgaacat  
2401 tcatgactga actgaaaaca agccatgact tgagaaaaca ataatttgta taccctgtcc  
2461 tttctcagag tgggtctgag attattttta tctaattcta aggaatatga gctttatgta  
2521 ataattgtga tcatggtrtt tcttagtaga ttttaaaagt tattaatatt ttaatttaatt  
2581 cttccatgga ttttgggtgg ttttgaacat aaagccttgg atgtatatgt catctcagtg  
2641 ctgtaaaaac tgtgggatgc tcctcccttc tctacctcat gggggtattg tataagtcct  
2701 tgcaagaatc agtgcaaaga tttgctttta ttgttaagat atgatgtccc tatggaagca  
2761 tattgttatt atataattac atatttgc atgtatgact cccaaatttt cacataaaat  
2821 agatttttgt ataacagctg ccattcatgg ttttttaaag gataagtaat aaagctggtg  
2881 ggga

## (2) INFORMATION FOR SEQ ID NO:2587:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5824 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2587

1 agcagagggg ctgagaccaa accagaaacc tccaattctc atgtggaagc ccatgccctc  
61 accctccaac atgaaagcct ctgcagcact tctgtgtctg ctgctcacag cagctgcttt  
121 cagccccag gggcttgctc agccagttgg gattaatact tcaactacct gctgctacag  
181 atttatcaat aagaaaatcc ctaagcagag gctggagagc tacagaagga ccaccagtag  
241 ccactgtccc cggaagctg taatcttcaa gaccaaactg gacaaggaga tctgtgctga  
301 cccacacag aagtgggtcc aggactttat gaagcacctg gacaagaaaa cccaaactcc  
361 aaagctttga acattcatga ctgaactaaa aacaagccat gacttgagaa acaataaatt  
421 tgtataccct gtctttctc agagtgggtc tgagattatt ttaattctaa tctaaggaaat  
481 atgagcttta tgtaataatg tgaatcatgg tttttcttag tagattttaa aagttattaa  
541 ttttttaatt taatcttcca tggattttgg tgggttttga acataaagcc ttggatgtat  
601 atgtcatctc agtctgtaa aaactgtggg atgctcctcc cttctctacc tcatgggggt  
661 attgtataag tccttgcaag aatcagtgca aagatttgc ttaattgtta agatatgatg  
721 tccctatgga agcatattgt tattatataa ttacatattt gcatatgtat gactcccaaa  
781 ttttcacata aaatagattt ttgtaaaaaa  
1 ggtttctatt gacttgggtt aatcgtgtga ccgcggtggc tggcacgaaa ttgaccaacc  
61 ctggggttag tatagcttag ttaaactttc gtttattgct aaaggttaat cactgctggt  
121 tcccggtggg gtgtggctag gctaagcgtt ttgagctgca ttgctgctg cttgatgctt  
181 gtcccttttg atcgtggtga tttagagggt gaactcactg gaatggggat gcttgcatgt  
241 gtaatcttac taagagctaa tagaaaggct aggaccaaac cagaaacctc caattctcat  
301 gtggaagccc atgcccctac cctccaacat gaaagcctct gcagcacttc tgtgtctgct  
361 gctcacagca gctgctttca gccccaggg gcttgctcag ccagttggga ttaatacttc  
421 aactacctgc tgctacagat ttatcaataa gaaaatccct aagcagaggc tggagagcta  
481 cagaaggacc accagtagcc actgtccccg ggaagctgta atcttcaaga ccaaactgga  
541 caaggagatc tgtgctgacc ccacacagaa gtgggtccag gactttatga agcacctgga  
601 caagaaaacc caaactccaa agctttgaac attcatgact gaactgaaaa caagccatga  
661 cttgagaaac aaataatttg tataccctgt cctttctcag agtgggtctg agattatttt  
721 aatctaattc taaggaatat gagctttatg taataatgtg aatcatggtt tttcttagta  
781 gattttaaaa gttattaata ttttaattta atcttccatg gattttggtg ggttttgaac  
841 ataaagcctt ggatgtatat gtcactcag tgctgtaaaa actgtgggat gctcctccct  
901 tctctacctc atgggggtat tgtataagtc cttgcaagaa tcagtgcata gatttgcttt  
961 aattgttaag atatgatgtc cctatggaag catattgtta ttatataatt acatatttgc  
1021 atatgtatga ctcccaatt ttcacataaa atagattttt gtataacaaa aaaaaaaaaa  
1081 aaaaa  
1 ggtttctatt gacttgggtt aatcgtgtga ccgcggtggc tggcacgaaa ttgaccaacc  
61 ctggggttag tatagcttag ttaaactttc gtttattgct aaaggttaat cactgctggt  
121 tcccggtggg gtgtggctag gctaagcgtt ttgagctgca ttgctgctg cttgatgctt  
181 gtcccttttg atcgtggtga tttagagggt gaactcactg gaatggggat gcttgcatgt  
241 gtaatcttac taagagctaa tagaaaggct aggaccaaac cagaaacctc caattctcat  
301 gtggaagccc atgcccctac cctccaacat gaaagcctct gcagcacttc tgtgtctgct  
361 gctcacagca gctgctttca gccccaggg gcttgctcag ccagttggga ttaatacttc  
421 aactacctgc tgctacagat ttatcaataa gaaaatccct aagcagaggc tggagagcta  
481 cagaaggacc accagtagcc actgtccccg ggaagctgta atcttcaaga ccaaactgga  
541 caaggagatc tgtgctgacc ccacacagaa gtgggtccag gactttatga agcacctgga  
601 caagaaaacc caaactccaa agctttgaac attcatgact gaactgaaaa caagccatga  
661 cttgagaaac aaataatttg tataccctgt cctttctcag agtgggtctg agattatttt  
721 aatctaattc taaggaatat gagctttatg taataatgtg aatcatggtt tttcttagta  
781 gattttaaaa gttattaata ttttaattta atcttccatg gattttggtg ggttttgaac  
841 ataaagcctt ggatgtatat gtcactcag tgctgtaaaa actgtgggat gctcctccct  
901 tctctacctc atgggggtat tgtataagtc cttgcaagaa tcagtgcata gatttgcttt

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961 aattgttaag atatgatgtc cctatggaag catattgtta ttataaatt acatatttgc
1021 atatgtatga ctcccaaatt ttacataaaa atagattttt gtataacaaa aaaaaaaaaa
1081 aaaaa
1 ggatccttaa gccatcatgc aaaatatcta gccatgtgga gggaccactg gaaagatcac
61 acacacacac acacacacac acacacacac atacagagag agagagagac acctgagaaa
121 ttccatctgg tccaactgct ggctgttgaa gtcctcccag cccagacccc agacactgaa
181 tgaaggcctt gtgatatagt caagagcaaa aaaaccaga agattgttat tgttttaagt
241 cactgttttc agatagattg ctatgcagca atagattatt gaaatagaca ctacaatttt
301 aggtactatt attctaagaa tattgaattt ttttttctg ctaatgttct attattttac
361 ttttctctgg gttttaaaaa gccaccagga tttaaagacag tgaagaatct ttgagtcctt
421 tgtagagttg aaccaaagt tgaatgtctc tttgtggact cgtgtcctag ggataccact
481 ccaaagggaa aaggggaata tcccttacat atctttgact ttggatcccc tgattccttc
541 ctttttctat agaattgtgc tcatttcaga gaaactgggc tcttgataat agccatagat
601 tacatactgt ggtcttcctc tacatagacc ctacctcacc taccactcct ggtcttagct
661 gaaaaacagg ctagcctcga ctcatactgt catttcctat cctcccactg aagtgcactg
721 gctcagcaga tttattactc catagattta ttactccatt ctatgattca tctctctgct
781 ttccataaaa aggcagagac agagcttcca gagagcaga ggggctgaga ccaaaccaga
841 aacctccaat tctcatgtgg aagcccagtc cctcaccctc caacatgaaa gcctctgcag
901 cacttctgtg tctgtgtctc acagcagctg ctttcagccc ccaggggctt gctcagccag
961 gtaagggtccc tctctccttc tcttgaaag acattgcccc ctctctgggt tatcctggac
1021 caatcaagaa gacctgatac ccacagtctc actttaacag ctacttttcc aagataaggt
1081 aacttagaaa aaggataagg ggtgagccca accacacagc tgctgttggg tagagcctga
1141 actagaattc cagctgtgaa ccccaaattc agctccttct aggattccag ctctgggaac
1201 accctcagtg cagttaccac tccagctgct tccagcagaa ttggggatca ggggtatcaa
1261 agacaggagg cttctgggga tgggtgtgct ggctgtttcc agataccggg agaccagaaa
1321 tctggtctgt ggaagcccag cttccagaaa cagcagctct gcagaggttg tacgtatcag
1381 ggaaactcat gaccaagcat tgaatgtcga gagcctaaaa ggggatccat agttggggta
1441 cccttgctct aaggaattgg attattatat tagccctccc tagcaatgcc cagatagacc
1501 atcaattcct cttccgtctt tcaactgggt atggtgcac cctattttac agtccataaa
1561 agtgaaaggg agtttatgaa atgcctcaaa gggcagagac attggggttg ggatgggcag
1621 cttttccctc cactctctcc ttttttctg attccttctt ctaccattc cctgttttac
1681 aaacagaaag acccaggaca caccctcaat ggacttttct tcttgttgtt tcattgcagt
1741 tgggattaat acttcaacta cctgtgtcta cagatttatc aataagaaaa tccctaagca
1801 gaggctggag agctacagaa ggaccaccag tagccactgt ccccggaag ctgtaatgta
1861 tgtggacgat gaccaccac cctcacacc tcagtccctag gttcttccct gggcaggaaa
1921 taggactagt atcagaatga gttggagtca aatactgtga tgcatacagc atctctaacc
1981 ttatcccaga catttgccag tgagaaacaa tacaagtaaa gaaagtggct tctcactctc
2041 agctcccttt ccagctatca tttacatct cagttcgttc cttcatcctg gaaccaagag
2101 agattcactt gggctaccaaa aaagagctgc ttctctgagt ccccttcctt tgttttatct
2161 tcttccttca tccctgaggc atccccatca gctaggctga tgggctagac agatttccca
2221 tagacttggg cactcctcca ggctgaaccc tcaaggtgtt ccatctgact gctcctttc
2281 tgctccacag cttcaagacc aaactggaca aggagatctg tgctgacccc acacagaagt
2341 gggctccagga ctttatgaag cacttggaag agaaaaccca aactccaaag ctttgaacat
2401 tcatgactga actgaaaaca agccatgact tgagaaacaa ataatttcta taccctgtcc
2461 tttctcagag tggttctgag attattttta tctaattcta aggaatatga gctttatgta
2521 ataattgtga tcatggtttt tcttagtaga ttttaaaagt tattaatatt ttaatttaat
2581 cttccatgga ttttgggtgg ttttgaacat aaagccttgg atgtatatgt catctcagtg
2641 ctgtaaaaac tgtgggatgc tcctcccttc tctacctcat gggggtattg tataagtcct
2701 tgcaagaatc agtgcaaaga tttgctttaa ttgttaagat atgatgtccc ttggaagca
2761 tattgttatt atataattac atatttgcat atgtatgact cccaaatttt cacataaaat
2821 agatttttgt ataacagctg ccattcatgg ttttttaag gataagtaat aaagctggtg
2881 gggtg

```

## (2) INFORMATION FOR SEQ ID NO:2588:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2588

```

1 aaccgagagg ctgagactaa ccagaaaaga tccaattctc aaactgaagc tcgcactctc
61 gcctccagca tgaaagtctc tgccgccctt ctgtgcctgc tgctcatagc agccaccttc
121 attccccaag ggctcgctca gccagatgca atcaatgccc cagtcacctg ctgtttataac
181 ttcaccaata ggaagatctc agtcagagag ctgcgagct atagaagaat caccagcagc
241 aagtgtccca aagaagctgt gatcttcaag accattgtgg ccaaggagat ctgtgctgac
301 cccaagcaga agtgggttca ggattccatg gaccacctgg acaagcaaac ccaaactccg
361 aagacttgaa cactcactcc acaacccaag aatctgcagc taacttattt tcccctagct
421 ttcccagac accctgtttt attttattat aatgaatttt gttgttgat gtgaaacatt
481 atgccttaag taatgttaat tcttatttaa gttattgatg ttttaagttt atctttcatg

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541 gtactagtgt ttttagata cagagacttg gggaaattgc ttttcttt gaaccacagt  
 601 tctacccttg ggtgttttg aggtctttg caagaatcat taatacaag aattttttt  
 661 aacattccaa tgcattgcta aatattatt gtggaaatga atatttgta actattacac  
 721 caaataaata ttttttgta c

## (2) INFORMATION FOR SEQ ID NO:2589:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1501 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2589

1 agcccatgtc ctctcttttc aggtgatgac tttccctga ggaagccctg tagcgtgcct  
 61 ggaggaaggg gctctccaac cccagcccca cctagccacc atgaacactt cagccccacc  
 121 tgctgtcagc cccaacatca cgtctctggc accaggaag ggtccctggc aagtggcctt  
 181 cattgggatc accacgggccc tctgtcgcct agccacagt acaggcaacc tgctggtact  
 241 catctctttc aaggtcaaca cggagctcaa gacagtcaat aactacttcc tgctgagcct  
 301 ggctgtgct gacctcatca tcggtacctt ctccatgaac ctctatacca cgtacctgct  
 361 catgggccac tgggctctgg gcacgctggc ttgtgacctc tggctggccc tggactatgt  
 421 ggccagcaat gccctccgta tgaatctgct gctcatcagc tttgaccgct acttctccgt  
 481 gactcggccc ctgagctacc gtgccaagcg cacaccccg cgggcaagctc tgatgatcgg  
 541 cctggcctgg ctggttttct ttgtgctctg ggccccagcc atctctctct ggcagtacct  
 601 ggtaggggag cggacgatgc tagctgggca gtgctacatc cagttcctct cccagcccat  
 661 catcaccttt ggcacagcca tggctgcctt ctacctccct gtcacagtca tgtgcacgct  
 721 ctactggcgc atctaccggg agacagagaa ccgagcacgg gagctggcag cccttcaggg  
 781 ctccgagacg ccaggcaaa ggggtggcag cagcagcagc tcagagaggt ctacgccagg  
 841 ggctgagggc tcaccagaga ctctccagg ccgctgctgt cgtgctgccc gggccccagc  
 901 gctgctgcag gcctacagct ggaaggaaga agaggaagag gacgaaggct ccatggagtc  
 961 cctcacatcc tcagagggag aggagcctgg ctccgaagtg gtgatcaaga tgccaatggt  
 1021 ggaccccgag gcacaggccc ccaccaagca gccccacgg agctcccaa atacagtcaa  
 1081 gagggcgact aagaaagggc gtgatcgagc tggcaagggc cagaagcccc gtggaaagga  
 1141 gcagctggcc aagcggaaga cttctcgcct ggtcaaggag aagaaggcgg ctcgaccct  
 1201 gactgccatc ctctggcct tcactctcac ctggacaccg tacaacatca tgggtgctgg  
 1261 gtccaccttc tgcaaggact gtgtcccgga gacctgtgg gagctgggct actggctgtg  
 1321 ctacgtcaac agcacatca acccatgtg ctacgcactc tgcaacaaag ccttcgggga  
 1381 cacctttcgc ctgctgctgc tttgcccgtg ggacaagaga cgctggcgca agatcccaa  
 1441 gcgcctggc tccgtgcacc gcactccctc ccgccaatgc tgatagctcc ctctcctgca  
 1501 tccctccacc ccagtcctgg gg

## (2) INFORMATION FOR SEQ ID NO:2590:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1561 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2590

1 attttaaac aatgtttata ttatgtttgt taattttatt ctatttcctt gcaggtttaa  
 61 atgtttattt gctacttggc tactgattag agaacgcaaa atgaataact caacaaactc  
 121 ctctaacaat agcctggctc ttacaagtcc ttataagaca ttgaagtg tgtttattgt  
 181 cctgggtggt ggatccctca gtttggtgac cattatcggg aacatcctag tcatggtttc  
 241 cattaaagtc aaccgccacc tccagaccgt caacaattac tttttattca gcttggcctg  
 301 tgctgacctt atcataggtg ttttctccat gaacttgtag accctctaca ctgtgattgg  
 361 ttactggcct ttgggacctg tgggtgtgta ctttggcta gccctggact atgtggtcag  
 421 caatgcctca gttatgaatc tgctcatcat cagctttgac aggtacttct gtgtcacaaa  
 481 acctctgacc taccagtcac agcggaccac aaaaatggca ggtatgatga ttgcagctgc  
 541 ctgggtcttc tctttcatcc tctgggtccc agccattctc ttctggcagt tcattgtagg  
 601 ggtgagaact gtggaggatg gggagtgtca cattcagttt ttttccaatg ctgctgtcac  
 661 ctttggtacg gctattgag cttctattt gccagtgatc atcatgactg tgctatattg  
 721 gcacatatcc cgagccagca agagcaggat aaagaaggac aagaaggagc ctgttgccaa  
 781 ccaagacccc gtttctccaa gtctggtaga aggaaggata gtgaagccaa acaataacaa  
 841 catgccagc agtgacgatg ccctggagca caacaaaatc cagaatggca aagccccag  
 901 ggatcctgtg actgaaaact gtgttcaggg agaggagaag gagagctcca atgactccac  
 961 ctcagtcagt gctgttgctt ctaatatgag agatgatgaa ataaccagg atgaaaacac  
 1021 agtttccact tccctgggcc attccaaaga tgagaactct aagcaaacat gcatcagaat  
 1081 tggcaccaag accccaaaaa gtgactcatg taccaccaact aataccaccg tggaggtagt  
 1141 ggggtcttca ggtcagaatg gagatgaaaa gcagaatatt gtgcccgcga agattgtgaa  
 1201 gatgactaag cagcctgcaa aaaagaagcc tctctcttcc cgggaaaaga aagtcaccag  
 1261 gacaatcttg gctattctgt tggctttcat catcacttgg gcccataca atgtcatggt  
 1321 gctcattaac accttttgtg caccttgcat cccaacact gtgtggacaa ttggttactg

1381 gctttgttac atcaacagca ctatcaaccc tgccctgctat gcactttgca atgccacctt  
 1441 caagaagacc tttaaacacc ttctcatgtg tcattataag aacataggcg ctacaaggta  
 1501 aaatatcttt gaaaaagata gaaggtgggc aaggggagct tgagaagaat aaaagggata  
 1561 aacgagctc

## (2) INFORMATION FOR SEQ ID NO:2591:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1681 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2591

1 tccagtgtac ctccagatga ctccccatt ccctcctgta gttcatgctt ttctctcccc  
 61 ttctctccca gacacggcct acccaccctt ggcaaccaac atggccaact tcacacctgt  
 121 caatggcagc tgggcaatc agtccgtgag cctgggtcag tcatcatccc acaatcgcta  
 181 tgagacgggt gaaatggtct tcattgccac agtgacaggc tccctgagcc tgggtactgt  
 241 cgtgggcaac atcctgggtg tgctgtccat caaggtcaac aggcagctgc agacagtcaa  
 301 caactacttc ctcttcagcc tggcgtgtgc tgatctcatc ataggcgctt tctccatgaa  
 361 cctctacacc gtgtacatca tcaagggtca ctggcccttg ggcgcctgtg tctgcgacct  
 421 gtggctggcc ctggactacg tggtagcaa cgcctccgtc atgaaccttc tcatcatcag  
 481 ctttgaccgc tacttctgag tcaccaagcc tctcacctac cctgcccgcc gcaccaccaa  
 541 gatggcagc ctcatgattg ctgctgcctg ggtactgtcc ttcgtgctct gggcgctgct  
 601 catcttgctt tggcagtttg tggtagtaa ggcgacgggt cccgacaacc agtgcttcat  
 661 ccagttcctg tccaaccag cagtgcctt tggcacagcc attgctgcct tctacgtgcc  
 721 tctgtgtcat atgacgggtg tgtacatcca catctccctg gccagtcgca gccgagtcca  
 781 caagcaccgg cccgagggcc cgaaggagaa gaaagccaag acgctggcct tctcaagag  
 841 cccactaatg aagcagagcg tcaagaagcc cccgcccggt gaggcgcgcc gggaggagct  
 901 gcgcaatggc aagctggagg aggcctccct gccagcgctg ccaccgccac cgcgcccgt  
 961 ggctgataag gacacttcca atgagtccag ctacggcagt gccaccaga acaccaagga  
 1021 acgcccagcc acagagctgt ccaccacaga ggccaccag cccgccatgc ccgccctcc  
 1081 cctgcagccg cgggccctca acccagctc cagatggctc aagatccaga ttgtgacgaa  
 1141 cgagacagc aatgagtgtg tgacagccat tgagattgtg cctgccagc cggctggcat  
 1201 gcgccctgag gccaacgtgg cccgcaagtt cgcagcctc gctcgcaacc aggtgcgcaa  
 1261 gaagcggcag atggcgcccc gggagcgcaa agtgacacga acgatctttg ccattctgct  
 1321 agccttcctc ctacactgga cgcctacaa cgtcatgggt ctggtgaaca ccttctgcca  
 1381 gagctgcatc cctgacagcg tgtggtccat tggctactgg ctctgctacg tcaacagcac  
 1441 catcaaccct gcctgctatg ctctgtgcaa cgccaccttt aaaaagacct tccggcacct  
 1501 gctgctgtgc cagtatcgga acatcgccac tgccaggtag gcaggcagga gtgccctagg  
 1561 aggtgctggt gttgcgtgag tgtgctgggg ggaccacacg gctcacttgc tgtggggaag  
 1621 agttgcagc accattctgc gttcacgttt gctgaggagg aagttcagaa gaggctctgt  
 1681 ggctgcattc agagaccaga tct

## (2) INFORMATION FOR SEQ ID NO:2592:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1861 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2592

1 tcttttaacg tatgtaatgc aaagaacaaa caaataaagg cagaaatttt tctaactctg  
 61 ttctctctct ctttccccca gactatgtca gagagtcaaca atgaccttgc acaataacag  
 121 tacaacctcg cctttgtttc caaacatcag ctctcctggt atacacagcc cctccgatgc  
 181 agggctgccc cggggaaccg tcactcattt cggcagctac aatgtttctc gagcagctgg  
 241 caattttctc tctccagacg gtaccaccca tgaccctctg ggaggtcata ccgtctggca  
 301 agtggctctt atcgctttct taacgggcat cctggccttg gtgacctca tcggcaacat  
 361 cctggtaatt gtgtcattta aggtcaacaa gcagctgaag acggtcaaca actacttctt  
 421 cttaaagcct gcctgtgccg atctgattat cggggtcatt tcaatgaatc tgtttacgac  
 481 ctacatcatc atgaatcgat gggccttagg gaacttgccc tgtgacctct ggcttgcgat  
 541 tgactacgta gccagcaatg cctctgttat gaatcttctg gtcatcagct ttgacagata  
 601 cttttccatc acgagggccc tcacgtaccg agccaaacga acaacaaaga gagccggtgt  
 661 gatgatcggt ctggcttggg tcactctcct tgcctcttgg gctcctgcca tcttgttctg  
 721 gcaatacttt gttggaagaa gaactgtgcc tccgggagag tgcttcattc agttcctcag  
 781 tgagcccacc attacttttg gcacagccat cgctgctttt tatatgctg tcaccattat  
 841 gactatttta tactggagga tctataagga aactgaaaag cgtaccaaag aggttgcctg  
 901 cctgcaagcc tctgggacag aggcagagac agaaaacttt gtccacccca cgggcagttc  
 961 tcgaagctgc agcagttacg aacttcaaca gcaaagcatg aaacgctcca acaggaggaa  
 1021 gtatggccgc tgccacttct ggttcacaac caagagctgg aaaccagct ccgagcagat  
 1081 ggaccaagac cacagcagca gtgacagttg gaacaacaat gatgctgctg cctccttgga  
 1141 gaactccgcc tctccgacg aggaggacat tggctccgag acgagagcca tctactccat

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1201 cgtgctcaag cttccgggtc acagcaccat cctcaactcc accaagttac cctcatcgga
1261 caacctgcag gtgcctgagg aggagctggg gatgggtggac ttggagagga aagccgacaa
1321 gctgcaggcc cagaagagcg tggacgatgg aggcagtttt ccaaaaagct tctccaagct
1381 tcccatccag cttaggtcag ccgtggacac agctaagact tctgacgtca actcctcagt
1441 gggtaagagc acggccactc tacctctgtc cttcaaggaa gccactctgg ccaagaggtt
1501 tgctctgaag accagaagtc agatcactaa gcggaaaagg atgtccctgg tcaaggagaa
1561 gaaagcggcc cagaccctca gtgcgatctt gcttgccttc atcatcactt ggaccacctata
1621 caacatcatg gttctgtgtg acaccttttg tgacagctgc ataccctaaa ccttttggaa
1681 tctgggttac tggctgtgct acatcaacag caccgtgaac cccgtgtgct atgtctgtg
1741 caacaaaaca ttcagaacca ctttcaagat gctgctgctg tgccagtggt acaaaaaaaa
1801 gaggcgcaag cagcagttacc agcagagaca gtcggtcatt tttcacaagc gcgcaccgca
1861 gcaggccttg tagaatgagg ttgtatcaat agcagtgaca aaacgacaca tca

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## (2) INFORMATION FOR SEQ ID NO:2593:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6604 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2593

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1 agcccatgtc ctctcttttc aggtgatgac tttccctga ggaagccctg tagcgtgcct
61 ggaggaaggg gctctccaac ccagcccca cctagccacc atgaacactt cagcccccacc
121 tgctgtcagc cccaacatca ccgtcctggc accaggaag ggtccctggc aagtggcctt
181 cattgggatac accacgggcc tcctgtcgtc agccacagt acaggcaacc tgctggctact
241 catctctttc aaggtcaaca cggagctcaa gacagtcaat aactacttcc tgctgagcct
301 ggctgtgtct gacctcatca tcggtacctt ctccatgaac ctctatacca cgtacctgct
361 catggggcac tgggtctgtg gcacgtggc ttgtgacctc tggtggccc tggactatgt
421 ggccagcaat gcctccgtca tgaatctgct gctcatcagc tttgaccgct acttctccgt
481 gactcggccc ctgagctacc gtgccaagcg cacaccgccg cgggcagctc tgatgatcgg
541 cctggcctgg ctgggttctt ttgtgtctg ggccccagcc atcctcttct ggcagtacct
601 ggtaggggag cggacgatgc tagctgggca gtgctacatc cagtctctct cccagcccat
661 catcaccttt ggcacagcca tggctgcctt ctacctcctt gtcacagtca tgtgcacgct
721 ctactggcgc atctaccggg agacagagaa ccgagcacgg gagctggcag cccttcaggg
781 ctccgagacg ccaggcaaa ggggtggcag cagcagcagc tcagagaggt ctcagccagg
841 ggctgagggc tcaccagaga ctctccagg ccgctgtgtg cgctgtgccc gggccccag
901 gctgtgcag gcctacagct ggaaggaaga agaggaagag gacgaaggag ccatgatgct
961 cctcacatcc tcagagggag aggagcctgg ctccgaagtg gtgatcaaga tggcaatggt
1021 ggacccccag gcacaggccc ccaccaagca gccccacgg agctcccaa atacagtcaa
1081 gagggcgact aagaaaggc gtgatcgagc tggcaaggcc cagaagcccc gtggaaagga
1141 gcagctggcc aagcggaaga cttctcgtc ggtcaaggag aagaaggcgg ctccgacctt
1201 gagtgccatc ctctggcct tcacctcac ctggacaccg tacaacatca tgggtgtggt
1261 gtccaccttc tgcaaggact gtgttccga gacctgtgg gagctggggt actggctgtg
1321 ctacgtcaac agcaccatca acccctatgt ctacgcactc tgcaacaaag ccttccggga
1381 cacttttgcg ctgctgtgct tttgcccgtg ggacaagaga cgctggcgca agatcccaa
1441 gcgccctggc tccgtgcacc gcactccctc ccgccaatgc tgatagtccc ctctctgca
1501 tccctccacc ccagtccccg gg
1 attttaaac aatgtttata ttatgtttgt taattttatt ctatttcctt gcaggtttaa
61 atgtttattt gctacttggc tactgattag agaacgcaaa atgaataact caacaaactc
121 ctctaacaat agcctggtc ttacaagtcc ttataagaca tttgaagtgg tgttttattgt
181 cctgggtggt ggatccctca gtttgggtgac cattatcggg aacatccctg tcatggtttc
241 cattaaagt caccgcccac tccagaccgt caacaattac tttttattca gcttggcctg
301 tgctgacctt atcatagggt ttttctccat gaactgttac accctctaca ctgtgattgg
361 ttactggcct ttgggacctg tgggtgtgtg cctttggcta gccctggact atgtggctag
421 caatgcctca gttatgaatc tgctcatcat cagctttgac aggtacttct gtgtcacaaa
481 acctctgacc taccagtcac agcggaccac aaaaatggca ggtatgatga ttgcagctgc
541 ctgggtcctc tctttcatcc tctgggtccc agccattctc tcttggcagt tcattgtagg
601 ggtgagaact gtggaggatg gggagtgtca cattcagttt ttttccaatg ctgctgtcac
661 ctttgggtac gctattgcag ccttctattt gccagtgatc atcatgactg tgctatattg
721 gcacatatcc cgagccagca agagcaggat aaagaaggac aagaaggagc ctgttgcaa
781 ccaagacccc gtttctccaa gtctggtaca aggaaggata gtgaagccaa acaataacaa
841 catgcccagc agtgacgatg gcctggagca caacaaatc cagaatggca aagccccag
901 ggatcctgtg actgaaaact gtgttcaggg agaggagaag gagagctcca atgactccac
961 ctacgtcagt gctgttgctt ctaatatgag agatgatgaa ataaccagg atgaaaacac
1021 agtttccact tccctgggcc attccaaaga tgagaactct aagcaaacat gcatcagaat
1081 tggcaccag accccaaaaa gtgactcatg taccctaac aataaccacc tggaggtagt
1141 ggggtcttca ggtcagaatg gagatgaaa gcagaatatt gtgcccgcga agattgtgaa
1201 gatgactaag cagcctgcaa aaaagaagcc tctccttcc cgggaaaaga aagtcaccag
1261 gacaatcttg gctattctgt tggcttcat catcacttgg gcccataca atgtcatggt
1321 gctcattaac accttttgtg cacttgcac cccaacact gtgtggacaa ttggttactg

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1381 gctttgttac atcaacagca ctatcaaccc tgctgctat gcaacttgca atgccacctt  
1441 caagaagacc tttaaacacc ttctcatgtg tcattataag aacataggcg ctacaaggta  
1501 aaatatcttt gaaaaagata gaaggtgggc aaggggagct tgagaagaat aaaaggata  
1561 aacgagctc  
1 tccagtgtac ctccagatga cccccatt cctcctgta gttcatgctt ttctctccc  
61 ttctctccca gacacggcct acccaccctt ggcaaccaac atggccaact tcacacctgt  
121 caatggcagc tcgggcaatc agtccgtgcg cctggtcacg tcatcatccc acaatcgta  
181 tgagacggtg gaaatggtct tcattgccac agtgacaggc tccctgagcc tggtgactgt  
241 cgtgggcaac atcctggtga tgctgtccat caaggtcaac aggcagctgc agacagtcaa  
301 caactacttc ctcttcagcc tggcgtgtgc tgatctcatc ataggcgctt tctccatgaa  
361 cctctacacc gtgtacatca tcaagggcta ctggcccctg ggcgccgttg tctgcgacct  
421 gtggctggcc ctggactacg tggtagcaa cgcctccgtc atgaaccttc tcatcatcag  
481 ctttgaccgc tactttctgcg tcaccaagcc tctcacctac cctgcccggc gcaccaccaa  
541 gatggcaggc ctcatgattg ctgctgctg ggtactgtcc tctgtgctt gggcgctgc  
601 catcttgttc tggcagtttg tggtaggtg gcggacggtg cccgacaacc agtgcttcat  
661 ccagttcctg tccaaccag cagtgcctt tggcacaggc attgctgctt tctacctgcc  
721 tgtggtcatc atgacggtgc gtacatcca catctccctg gccagtcgca gccgagtcca  
781 caagcaccgg cccgagggcc cgaaggagaa gaaagccaag acgctggcct tctcaagag  
841 cccactaatg aagcagagcg tcaagaagcc cccgcccggg gaggccgccc gggaggagct  
901 gcgcaatggc aagctggagg agccccccc gccagcgtg ccaccgccac gcgccccgt  
961 ggctgataag gacacttcca atgagtcag ctgaggcagt gccaccaga acaccaagga  
1021 acgcccagcc acagagctgt ccaccacaga ggccaccacg cccgccatgc cggccctcc  
1081 cctgcagccg cgggcccctca acccagcctc cagatggctc aagatccaga ttgtgacgaa  
1141 gcagacagc aatgagtgtg tgacagccat tgagattgtg cctgccacgc cggctggcat  
1201 gcgcccctgc gccaacgtgg cccgcaagtt cgcacgcatc gctcgcaacc aggtgcgcaa  
1261 gaagcggcag atggcggccc gggagcgcaa agtgacacga acgatctttg ccattctgct  
1321 agccttcatc ctacacctga cgcctacaa cgtcatggtc ctggtgaaca ccttctgcca  
1381 gagctgcatc cctgacacgg tgtggtccat tggctactgg ctctgtacg tcaacagcac  
1441 catcaacctt gctgtctatg ctctgtgcaa cgccacctt aaaaagacct tccggcactt  
1501 gctgctgtgc cagtatcgga acatcggcac tgccaggtag gcaggcagga gtgccctagg  
1561 aggtgctggt gttgcgtgcg tgtgctggg ggaccacacg gctcacttgc tgtggggaag  
1621 agttgcaggc accattctgc gttcacgtt gctgaggagg aagttcagaa gaggctctgt  
1681 ggctgcattc agagaccaga tct  
1 tcttttaacg tatgtaatgc aaagaacaaa caataaagg cagaaatttt tctaactctg  
61 tctcttctct ctttccccca gactatgtca gagatcaca atgacctgc acaataacag  
121 tacaacctcg ctttgtttc caaacatcag ctctctctgg atacacagcc cctccgatgc  
181 agggctgccc cggggaaccg tcaactcatt cggcagctac aatgtttctc gagcagctgg  
241 caattttctc tctccagacg gtaccacga tgacctctg ggaggcata ccgtctggca  
301 agtggctctc atcgctttct taacgggcat cctggccttg gtgaccatca tcggcaacat  
361 cctggtaatt gtgtcattta aggtcaacaa gcagctgaag acggtcaaca actacttctt  
421 ctttaagcctg gcctgtgccc atctgattat cggggtcatt tcaatgaatc tgtttacgac  
481 ctacatcatc atgaatcgtt gggccttagg gaacttggcc tgtgacctct ggcttgccat  
541 tgactacgta gccagcaatg cctctgttat gaacttcttg gtcacagct ttgacagata  
601 cttttccatc acgagccgc tcacgtaccg agccaaacga acaacaaaga gagccggtgt  
661 gatgatcggt ctggcttggg tcatctcctt tgcctttgg gctcctgcca tcttgttctg  
721 gcaatacttt gttggaaga gaactgtgcc tccgggagag tgcttcattc agttcctcag  
781 tgagcccacc attacttttg gcacagccat cgtgctttt tatatgcctg tcaccattat  
841 gactatttta tactggagga tctataagga aactgaaaag cgtaccaaaag agcttgctgg  
901 cctgcaagcc tctgggacag aggcagagac agaaaacttt gtccacccca cgggcagttc  
961 tcgaagctgc agcagttacg aacttcaaca gcaaagcatg aaacgctcca acaggaggaa  
1021 gtatggccgc tgccacttct ggttcacaac caagagctgg aaacccagct ccgagcagat  
1081 ggaccaagac cacagcagca gtgacagttg gaacaacaat gatgctgctg cctccctgga  
1141 gaactccgcc tctccgacg agggagcat tggctccgag acgagagcca tctactccat  
1201 cgtgctcaag cttccgggtc acagcaccat cctcaactcc accaagtac cctcatcgga  
1261 caacctgcag gtgctgagg aggagctgg gatgggtggac ttggagagga aagccgacaa  
1321 gctgcaggcc cagaagagcg tggacgatgg aggcagtttt ccaaaaagct tctccaagct  
1381 tcccattccag ctagagtcag ccgtggacac agctaagact tctgacgtca actcctcagt  
1441 gggtaagagc acggccactc tacctctgtc cttcaaggaa gccactctgg ccaagaggtt  
1501 tgctctgaag accagaagtc agatcactaa gcggaaaagg atgtccctgg tcaaggagaa  
1561 gaaagcggcc cagaccctca gtgcgatctt gcttgcttc atcatcactt ggaccccata  
1621 caacatcatg gttctgtgta acaccttttg tgacagctgc atacccaaaa cttttggaa  
1681 tctgggtac tggctgtgct acatcaacag caccgtgaac cccgtgtgct atgctctgtg  
1741 caacaaaaca ttcagaacca ctttcaagat gctgctgctg tgccagtgtg acaaaaaaaa  
1801 gaggcgcaag cagcagtagc agcagagaca gtcggtcatt tttcacaagc gcgacccga  
1861 gcaggccttg tagaatgagg ttgtatcaat agcagtgaca aaacgacaca tca

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1201 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2594

```

1 atggataacg tcctcccggg ggactcagac ctctcccaa acatctccac taacacctcg
61 gaaccaatc agttcgtgca accagcctgg caaattgtcc tttgggcagc tgcttacacg
121 gtcattgtgg tgacctctgt ggtgggcaac gtggtagtga tgtggatcat cttagccac
181 aaaagaatga ggacagtga gaactatatt ctggtgaacc tggccttcgc ggaggcctcc
241 atggctgcat tcaatacagt ggtgaacttc acctatgctg tccacaacga atggtactac
301 ggctgtttct actgcaagtt ccacaacttc tccccatcg ccgttgctt cgccagtate
361 tactccatga cggctgtggc ctttgatagg tacatggcca tcatacatcc cctccagccc
421 cggctgtcag ccacagccac caaagtggtc atctgtgtca tctgggtcct ggctctcctg
481 ctggccttcc ccagggcta ctactcaacc acagagacca tgcccagcag agtcgtgtgc
541 atgatcgaat ggccagagca tccgaacaag atttatgaga aagtgtacca catctgtgtg
601 actgtgtgta tctacttctt cccctgtctg gtgattggct atgcatacac catagtggga
661 atcacactat gggccagtga gatccccggg gactcctctg accgctacca cgagcaagtc
721 tctgccaaag gcaaggtggt caaatgatg attgtcgtgg tgtgcacctt cgccatctgc
781 tggctgccct tccacatctt cttcctcctg ccctacatca accagatctt ctacctgaag
841 aagtttatcc agcaggtcta cctggccatc atgtggctgg ccatgagctc caccatgtac
901 aaccccatca tctactgtg cctcaatgac aggttccgtc tgggcttcaa gcatgccttc
961 cgggtgtgcc ctttcatcag cgcggcgac tatgaggggc tggaaatgaa atccaccggg
1021 tatctccaga ccagggcag tgtgtacaaa gtcagccgcc tggagaccac catctccaca
1081 gtgggtgggg ccacagagga ggagccagag gacggcccca aggccacacc ctcgctcctg
1141 gacctgacct ccaactgtct ttcacgaagt gactccaaga ccatgacaga gagcttcagc
1201 ttctctcca atgtgtctc ctagggatcc

```

## (2) INFORMATION FOR SEQ ID NO:2595:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1741 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2595

```

1 ctattgcagt atctttcagc ttccagtctt atctgaagac cccggcacca aagtgaccag
61 gaggcagaga agaacttcag aggagtctcg tcttgggctg cccgtgggtg agtgggaggg
121 tccgggactg cagaccggtg gcgatggcca ctctccagc agcagaaacc tggatagacg
181 ggggtggagg cgtgggtgca gacgcgtga acctgaccgc ctgctagct gccggggcgg
241 ccacgggggc agttgagact ggggtgctgc aactgctgga ccaagctggc aacctctctt
301 cctccccttc cgcgctggga ctgcctgtgg cttccccgc gccctccag ccctgggcca
361 acctaccaa ccagttcgtg cagccgtcct ggcgcatcgc gctctggtcc ctggcgtatg
421 gtgtggtggt ggcagtggca gttttgggaa atctcatcgt catctggatc atcctggccc
481 acaagcgcag gaggactgtc accaactact tccttgtgaa cctggcttcc tccgacgcct
541 ccattggcgc cttcaacacg ttggtcaatt tcattacgc gtttcatagc gagtgggtact
601 ttggcgccaa ctactgccgc ttccagaact tctttcctat cacagctgtg ttgcgcagca
661 tctactccat gacggccatt gcggtggaca ggtatatggc tattattgat cccttgaaac
721 ccagactgtc tgctacagca accaagattg tcattggaag tatttggtat ctagcatttc
781 tacttgctt ccctcagtg ctttattcca aaaccaaagt catgccagc cgtactctct
841 gctttgtgca atggccagaa ggtcccaaac aacatttcaac ttaccatatt atcgctatta
901 tactggtgta ctgtttccca ttgctcatca tgggtattac atacaccatt gttggaatta
961 ctctctgggg aggagaaatc ccaggagata cctgtgacaa gtatcatgag cagctaaagg
1021 ccaaaagaaa gttgtcaaaa atgatgatta ttggtgtcat gacatttgct atctgctggc
1081 tgccctatca tatttacttc attctactg caatctatca acaactaaat agatgaaat
1141 acatccagca ggtctacctg gctagctttt ggctggcaat gagctcaacc atgtacaatc
1201 ccatcatcta ctgctgtctg aataaaagat ttcgagctgg cttcaagaga gcatttcgct
1261 ggtgtccttt catcaaagtt tccagctatg atgagctaga gctcaagacc accaggttcc
1321 atccaaaccg gcaaagcagt atgtacaccg tgaccagaat ggagtccatg acagtcgtgt
1381 ttgaccccaa cgatgcagac accaccaggt ccagtcggaa gaaaagagca acgccaagag
1441 acccaagttt caatggctgc tctcgagga attccaaatc tgccctcgcc acttcaagtt
1501 tcataagctc accctatacc tctgtggatg aatattctta attccatttc ctgaggtaaa
1561 agattagtgt gagaccatca tgggtgccag ctaggacccc attctcctat ttatcagttc
1621 tgtcctatat accctctaga aacagaaagc aatttttagg cagctatggt caaattgaga
1681 aaggtagtgt ataaatgtga caaagacact aataacatgt tagcctccac ccaaaataaa
1741 atgggcttta aattt

```

## (2) INFORMATION FOR SEQ ID NO:2596:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1141 base pairs

(B) TYPE: nucleic acid



(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2596

```
1 atgggggacct gtgacattgt gactgaagcc aatatctcat ctggccctga gagcaacacc
61 acggggcatca cagccttctc catgcccagc tggcagctgg cactgtgggc accagcctac
121 ctggccctgg tgctggggc cgtgacgggt aatgccatcg tcatctggat catcctggcc
181 catcggagga tgcgcacagt caccaactac ttcacgtca atctggcgt ggctgacctc
241 tgcattggctg ccttcaatgc cgccttcaac tttgtctatg ccagccacaa catctgggtac
301 tttggccctg ccttctgcta cttccagaac ctcttcccca tcacagccat gtttgtcagc
361 atctactcca tgaccgccat tgctgcccag aggtacatgg ccatcgtcca ccccttccag
421 cctcggcttt cagctcccag caccaaggcg gttattgtg gcactgtggg ggtggctctc
481 gccctggcct cccctcagtg cttctactcc accgtcacca tggaccaggg tgccaccaag
541 tgcgtgggtg cctggcccga agacagcggg ggcaagacgc tctcctgta ccacctcgtg
601 gtgatcgccc tcatctactt cctgcccgtc gcggtgatgt ttgtagccta cagcgtcatc
661 ggcctcacgc tctggaggcg cgcagtgcc ggacatcagg cgcacgggtc caacctccgc
721 catctgcagg ccaagaagaa gtttgtgaag accatgggtc tgggtgggtc gacgtttgcc
781 atctgctggc tgccctacca cctctacttc atcctgggca gcttccagga ggacatctac
841 tgccacaagt tcatccagca agtctacctg gcactcttct ggttggccat gagctctacc
901 atgtacaatc ccatcatcta ctgctgtctc aaccacaggt ttcgctctgg gttccggctt
961 gccttccgct gctgcccatt ggctcacacc accaaggaag ataagctcga gctgactccc
1021 acgacctccc tctccacgag agtcaacagg tgtcacacta aggagacttt gttcatggct
1081 ggggacacag cccctccga ggctaccagt ggggaggcgg ggcgtcccca ggatggatca
1141 gggctatggt ttgggtatgg tttgcttggc cccacaaaaa ctcatgttga aatttga
```

(2) INFORMATION FOR SEQ ID NO:2597:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4083 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2597

```
1 atggataacg tctcccgtt ggactcagac ctctcccac aaatctccac taacacctcg
61 gaacccaatc agttcgtgca accagcctgg caaattgtcc ttggggcagc tgcttacacg
121 gtcattgttg tgacctctgt ggtgggcaac gtggtagtga tgggatcat cttagccac
181 aaaagaatga ggacagtga gaactatttt ctggtgaacc tggccttcgc ggagccctcc
241 atggctgcat tcaatacagt ggtgaacttc acctatgtg tccacaacga atggtactac
301 ggcctgttct actgcaagtt ccacaacttc ttcccctcgc ccgcttgctt cgccagtatc
361 tactccatga cggctgtggc ctttgatagg tacatggcca tcatacatcc cctccagccc
421 cggctgtcag ccacagccac caaagtgtc atctgtgtca tctgggtcct ggctctcctg
481 ctggccttcc cccagggcta ctactcaacc acagagacca tggccagcag agtcgtgtgc
541 atgatcgaat ggccagagca tccgaacaag atttatgaga aagtgtacca catctgtgtg
601 actgtgctga tctacttct cccctgtctg gtgattggct atgcatacac catagtggga
661 atcacactat gggccagrga gatccccggg gactcctctg accgtacca cgagcaagtc
721 tctgccaaagc gcaaggtggt caaaatgatg attgtcgtgg tgtgcacctt cgccatctgc
781 tggtgcccct tccacatctt cttcctcctg ccctacatca acccagatct ctacctgaag
841 aagtttatcc agcaggtcta cctggccatc atgtggctgg ccatgagctc caccatgtac
901 aaccccatca tctactgtg cctcaatgac aggttccgtc tgggcttcaa gcatgccttc
961 cgtgtgctgc cttcatcag cgcggcgac tatgaggggc tggaaatgaa atccaccgg
1021 tatctccaga cccaggcgag tgtgtacaaa gtcagccgcc tggagaccac catctccaca
1081 gtggtggggg cccacgagga ggagccagag gacggcccca aggccacacc ctctccctg
1141 gacctgacct ccaactgtc ttcacgaagt gactccaaga ccatgacaga gagcttcagc
1201 ttctcctcca atgtgtctc ctaggatcc
1 ctattgcagt atctttcagc ttccagtctt atctgaagac cccggcacca aagtgaccag
61 gaggcagaga agaacttcag aggagtctcg tcttgggctg cccgtgggtg agtgggaggg
121 tccgggactg cagaccggtg gcatggcca ctctcccagc agcagaaacc tggatagacg
181 ggggtggagg cgtgggtgca gacgccgtga acctgaccgc ctgctagct gccggggcgg
241 ccacgggggc agttgagact ggtggtgtgc aactgctgga ccaagctggc aacctctcct
301 cctccccttc cgcgtggga ctgctgtggt cttccccgc gccctcccag cctggggcca
361 acctcaccaa ccagttcgtg cagcgtcctt ggcgcatcgc gctctgttcc ctggcgtatg
421 gtgtgggtgt ggacgtggca gttttgggaa atctcatcgt catctggatc atcctggccc
481 acaagcgcag gaggactgtc accaactact tcttgtgaa cctggcttct tccgacgctt
541 ccatggccgc cttcaacacg ttggtcaatt tcatctacgc gtttcatagc gactgtgtat
601 ttggcgccaa ctactgccgc ttccagaact tctttcctat cacagctgtg ttcgccagca
661 tctactccat gacggccatt gcggtggaca ggtatatggc tattattgat cccttgaac
721 ccagactgtc tgctacagca accaagattg tcattggaag tatttggatt ctacgatttc
781 tacttgctct cctcagtggt ctttattcca aaaccaaagt catgccagc cgtactctct
841 gctttgtgca atggccagaa ggtcccaaac aacatttcac ttaccatatt atcgtcatta
901 tactggtgta ctgtttccca ttgctcatca tgggtattac ataccatt gttggaatta
961 ctctctgggg aggagaaatc ccaggagata cctgtgacaa gtatcatgag cagctaaagg
```

```

1021 ccaaa gaaa ggttggtcaaa atgatgatta ttgttggtcat gaatttggct atctgctggc
1081 tgccctatca tatttacttc attctcactg caatctatca acaactaaat agatggaaat
1141 acatccagca ggtctacctg gctagctttt ggctggcaat gagctcaacc atgtacaatc
1201 ccatcatcta ctgctgtctg aataaaagat ttcgagctgg cttcaagaga gcatttcgct
1261 ggtgtccttt catcaaagtt tccagctatg atgagctaga gctcaagacc accagggttc
1321 atccaaaccg gcaaagcagt atgtacaccg tgaccagaat ggagtccatg acagtcgtgt
1381 ttgaccccaa cgatgcagac accaccagggt ccagtcggaa gaaaagagca acgccaagag
1441 acccaagttt caatggctgc tctgcagga attccaaatc tgcctccgcc acttcaagtt
1501 tcataagctc accctatacc tctgtggatg aatattctta attccatttc ctgaggtaaa
1561 agattagtgt gagaccatca tgggtccagt ctaggacccc attctcctat ttatcagtcc
1621 tgctctatat accctctaga aacagaaagc aatttttagg cagctatggt caaattgaga
1681 aaggtagtgt ataaatgtga caaagacact aataacatgt tagcctccac caaaaataaa
1741 atgggcttta aattt
1 atggggacct gtgacattgt gactgaagcc aatatctcat ctggccctga gagcaacacc
61 acgggcatca cagccttctc catgcccagc tggcagctgg cactgtgggc accagcctac
121 ctggccctgg tgcgtgtggc cgtgacgggt aatgccatcg tcatctggat catcctggcc
181 catcgaggga tgcgcacagt caccaactac ttcactgtca atctggcgtt ggctgacctc
241 tgcattgctg ccttcaatgc cgccttcaac tttgtctatg ccagccacaa catctggtac
301 tttggccgtg ccttctgcta ctccagaac ctcttcccca tcacagccat gtttgtcagc
361 atctactcca tgaccgccat tgcgtccgac aggtacatgg ccactgtcca ccccttccag
421 cctcggcttt cagctccag caccagggc gttattgctg gcactgtggt ggtggctctc
481 gccctggcct cccctcagt cttctactcc accgtcacca tggaccaggg tgccaccaag
541 tgcgtggtgg cctggcccga agacagcggg ggcaagacgc tctcctgta ccactcgtg
601 gtgatcgccc tcatctactt cctgcccgtc gcggtgatgt ttgtagccta cagcgtcatc
661 ggccctacgc tctggaggcg cgcagtccc ggacatcagg cgcacgggtc caacctccgc
721 catctgcagg ccaagaagaa gtttgtgaag accatggtgc tgggtggtct gacgtttgcc
781 atctgtggc tgccctacca cctctacttc atcctgggca gcttccagga ggacatctac
841 tgccacaagt tcatccagca agtctactg gcactctct ggttggtccat gagctctacc
901 atgtacaatc ccatcatcta ctgctgtctc aaccacaggt ttcgtcttgg gttccggctt
961 gccttccgct gctgcccatt ggtcacacc accaaggaag ataagctcga gctgactccc
1021 acgacctccc tctccacgag agtcaacagg tgtcacacta aggagacttt gttcatggct
1081 ggggacacag cccctccga ggctaccagt ggggaggcgg ggcgtcccca ggatggatca
1141 gggctatggt ttgggtatgg tttgcttggc cccacaaaaa ctcatgttga aatttga

```

## (2) INFORMATION FOR SEQ ID NO:2598:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2598

```

1 ctccataagg cacaaacttt cagagacagc agagcacaca agcttctagg acaagagcca
61 ggaagaaacc accggaagga accatctcac tgtgtgtaaa catgacttcc aagctggccg
121 tggctctctt ggcagccttc ctgatttctg cagctctgtg tgaagggtga gttttgccaa
181 ggagtgtctaa agaacttaga tgtcagtga taaagacata ctccaaacct ttccacccca
241 aatttatcaa agaactgaga gtgattgaga gtggaccaca ctgcgccaac acagaaatta
301 ttgtaaagct ttctgatgga agagagctct gtctggaccc caaggaaaac tgggtgcaga
361 ggggtgtgga gaagtttttg aagagggctg agaattcata aaaaaattca ttctctgtgg
421 tatccaagaa tcagtgaaga tgccagtga acttcaagca aatctacttc aacacttcat
481 gtattgtgtg ggtctgttgt agggttgcca gatgcaatac aagattcctg gttaaatttg
541 aatttcagta aacaatgaat agtttttcat tgtaccatga aatatccaga acatacttat
601 atgtaaagta ttattttatt gaatctacaa aaaacaacaa ataattttta aatataagga
661 ttttccctaga tattgcacgg gagaatatac aaatagcaaa attgggccaa gggccaagag
721 aatatccgaa ctttaatttc aggaattgaa tgggtttgct agaattgtat atttgaagca
781 tcacataaaa atgatgggac aataaatttt gccataaagt caaatttagc tggaaatcct
841 ggattttttt ctgttaaate tggcaaccct agtctgctag ccaggatcca caagtccttg
901 ttccactgtg ccttggtttc tcttttattt ctaagtggaa aaagtattag ccaccatctt
961 acctcacagt gatgttgtga ggacatgtgg aagcacttta agttttttca tcataacata
1021 aattattttc aagtgttaact tattaacctt tttattattt atgtatttat ttaagcatca
1081 aatattttgt caagaatttg gaaaaataga agatgaatca ttgattgaat agttataaag
1141 atgttatagt aaattttatt tattttatag attaaatgat gttttattag ataaatttca
1201 atcagggttt ttagattaaa caaacaaaaa attgggtacc cagttaaatt ttcatctcag
1261 atatacaaca aataattttt tagtataagt acattattgt ttatctgaaa ttttaattga
1321 actaacaatc ctagtttgat actcccagtc ttgtcattgc cagctgtgtt ggtagtgtg
1381 tgttgaatta cggaataatg agttagaact attaaaacag ccaaaactcc acagtcaata
1441 ttagtaattt cttgctggtt gaaacttggt tattatgtac aaatagattc ttataatatt
1501 atttaaaatga ctgcattttt aaatacaagg ctttatattt ttaactttta aaaaaaccgg

```

## (2) INFORMATION FOR SEQ ID NO:2599:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1561 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2599

```

1 gaattctctc tccagcagcc ctgccagatg cccgcccagc ccctgcctca ggcggggagg
61 gcttcaggga agctcaccaa ggcagaaggg cgggagagat tgctcagagc ccagctggtg
121 tccagggact gaccgtgagc ctgggtgaaa gtgagttccc cgttgaggc aacagacgag
181 gagaggatgg aaggcctggc cccaagaat gagccctgag gttcagggag cggctggagt
241 gagccggccc cagatctccg tccagctgcg ggtcccagag gcctgggtta cactcgcagc
301 tcctggggga ggcccttgac gtgcctcagt tcccaaacag gaacctggg aaggaccaga
361 gaagtgccta ttgcgcagt agtgcccgac acagctgcat gtggccggtg tcacagggcc
421 ctgggtaaac tgaggcaggc gacacagctg catgtggccg gtatcacagg gccctgggtg
481 aactgaggca ggcgacacag ctgcatgtgg ccggtatcac agggccctgg gtaactgag
541 gcaggcgaca cagctgcatg tggccgtatc acagggccct gggtaaactg aggcaggtga
601 cacagctgca tgtggccggt atcacggggc cctggataaa cagaggcagg cgacacagct
661 gcatgtggcc ggtatcacgg ggcctgggtt aaactgaggc aggcgaggcc acccccatca
721 agtccctcag gtctaggttt ggcaggtttg gcaaaaacac agcaacgctc ggttaaactc
781 gaatttcggg taagtatatc ctgggcctca tttggaagag acttagatta aaaaaaac
841 gtcgagacca gcccgcccaa cacggtgaaa ccccgctctc actaaaaata caaaaaatta
901 gccaggcgca gtggtcacg cctgtgatcc cagcactctg ggaggctgag gcaggcggat
961 cacccgaggt cagatgttca agaccagcct ggccgacagg gcgaaacact gtctctacta
1021 caaatacaaa aattagccgg gagtgggtgg aggtgcctgt aatctcagct attcaggagg
1081 ctgaggcagg agaatacatt gaacctggga ggccgagggt gccgtgagcc gggatcacgc
1141 caccgcactc cagcctgggc gatagagcaa gactctgtct ccaaaaaaat aaattaaaaa
1201 acccacattg attatctgac atttgaatgc gattgtgcat cctgaatttt gtctggaggc
1261 cccaccgag ccaatccagc gtcttgtccc ccttctcccc cttttcatca acgcccctgtg
1321 ccaggggaga ggaagtggag ggcgctggcc ggccgtgggg caatgcaacg gcctccagc
1381 acagggttat aagaggagcc ggccggggcac ggaggggcag agaccccgga gccccagccc
1441 cccatgacc ctgcggccgc gactgcgctg tcttttctc gcctgtgtcc tgcggcctt
1501 gctgctgggg ggtgagtttt tgagtccaac ctcccgtgct tccctctgct ccgggttctg
1561 t

```

## (2) INFORMATION FOR SEQ ID NO:2600:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2600

```

1 agcttcatcc tggagtcaac agattgggtt tgaatcctgg ctctgtccct ttctagctgt
61 gtgttttggt gttactccac ctctctgagc cttaatttct tcatcagtaa aagtaattt
121 cacctcctag ggttgttggg agggagaata agaacttcta aagtaccgga acctagcaac
181 taggacacta tatttgcagg caagatgaag aggggtgggg aagtaatagg aaacagccca
241 aatcgagagc cataatagtc tctctttact tagtgccagt gcaggcctgt gattctgttc
301 ttaaaaacgt ctggggcaag ctgcaggaaa gacccgagat agcttatgtt ctaccataag
361 ccttaaggga ggaggactcc aggcaggagg acttaccatg gcacctctaa gagaaagcct
421 actgaccaga gagaggtcag tcatgtactc ccgtagcttc ttagaatttc tgatctgact
481 cgctgcctct agagttgttc aggtggaaat tggaaggcta tagaggaaat cggcagcata
541 cagtggctca cgtctgtaat ccaaaatcca agcatttttg aaggccaaag taggaggatc
601 acttaagccc aggagttaa gaccagccta ggcaaccgag tgagatccat ctccactaaa
661 aaattttaaa atttgccagg tatggtggtg tgcacctgta gcccagcta ctcaggagag
721 tcagagaatc ggcgcacccc ggagttcgag gttgcagtga gccatgatca cgccactgta
781 ctccagcctg ggtgacagag aagaccacct gtctcaaaaa acataaataa ataaataaat
841 aaataggccg tgcgcagcgg ctccagactg taattccaac attttagaag cgggaggcag
901 cggatcacct gaggtcagga gttcgggacc agcctgacca acgtggtgaa accccaactc
961 tactaaaaat acataaatta ggcggggcgt ggtggtggcc gcctgtaatc ccagctactc
1021 ggtaggctgc agcaggagaa tggtttgaa ccgggaggca gaggttcgag tgagccaaaa
1081 tcccctcact gcattccagc ctgagactaa aaaaaagagg cgatttccca catcggtgga
1141 aatttgagct gtttaaaactc tggatgcctt tttcagttct aatattccag atctccttgg
1201 tggataaaca cttcatttcc cttctcctga gcagagctcc tgagccctgg cccgctggaa
1261 cctgtcactt ctaaaaaagt tcgaggtccg gactgtctct cccggagcct tgaggctgat
1321 gagacggagc gagagagggg ccggggggcaa tggagtctac tcgcgggccc agggaggcgc
1381 cagaggggcc cggaaccgac cgcaagaata acttcttccc tcttccgcta acttcccggc
1441 agggctacgc tcagggtggg ggccccgagg gctggggcgt cggcttcccc ctggggatcc
1501 cccgcttcag agaagccaag cgttagcgca gccaaagccg gaggcagcga agctccggcc
1561 cggggtggcg ctgggtcagg gtacctctc ggcggtcccc tggccggccg aactcgcgcc

```

1621 tgggtgctctg tcaccccgct ccccgccctg agtgagcctg tccccctctca ggggcgcgcc  
1681 cgagtcgctc cgggttggtc gccaggtcca gagttaaact ttcagccaat gaaaaagggc  
1741 gcgagggctg acgcacggaa acgtcatggg aattcccccc tccggggggc cgagaagggg  
1801 ctttcccgcc cctgagccct gctggcaggc gaggtgtcgc gaccgggtccc aggtgggtcg  
1861 ggcgcggaga gaagccgcaa ccagagccgc cgccacggtg agtggctgga ttcagacccc  
1921 tgggtggccc ggacaagaga aaagagggag gagggccttt agcggacagc gcctggggct  
1981 ggagagcagc agctgcacac agccggaag gagcgcagc cgacgacact cggatccacg  
2041 tcgacaccgt tgtacaaaga tacgcggacc cgtacgtaca cctgtacctg tgtggcgca  
2101 cacacggcag cgtccgtgca gtcgactcg cacacacatg cacacggaga cgtgccacc  
2161 ggtgcactgg tgcctgcacc cacacccttc acgcacaaac tcaagatacg ctaccccggtg  
2221 tctgtacatc aagacaggcg ctgacacaca cccacactga gaagctcggg attcacctat  
2281 ctacacacat gctcgcttgc aactcatgt tgacgccatg gacacacaac atgcaaccaa  
2341 gcactacagc cgaacacacac ttgtggagct gtgatggaga cacactcttg tattaggtgg  
2401 gggggggggg ggagcgtgca gagatctccc tgtcgcctgc gcgccagaa ccggtgcggt  
2461 gtgggaccag ctgctgttgt gaggtttggg agagagagaa aaagagccca ctccgaggag  
2521 gagacacttt tcccgagcc ccagaatcgc gttctcgggg cagaaccccg gggcctccca  
2581 caggaaagag ccccgctac aggtgttcg aaggggaggc cgtccgacag caggaaatgtc  
2641 cccccaaaag ccccggggt ttatcagccg tggcctccct cctggcagaa aatcccaagg  
2701 ttgtccaga ccgggggagg ggagcgggag gcggacttg cccagactg ccagcctcct  
2761 ccggccgtg aaagaccctc ctgttccctg cctggaggg aggagggggc ttaaccacc  
2821 ggggcttccc ggattctcct agacctctgc ccgctgaaaa gcagcgggac gccgtagact  
2881 gtcgagggcc atcccgcctc tcccgctcgc agggcggggc cagtggcgtc atttccaggc  
2941 ccgccccctc cggccccgcc tccccttggg attttcggga ctttccctaa ctgctcctaac  
3001 tttcctgccc cttccccgcc aagcccaact ccggtatctg ctctccaccg gatctcacc  
3061 gccacaccgg gacaggcggc tggaggaggt cggaccctcc cccaaatctg ggcctccatt  
3121 ctcccgcaca ccccatctta gatctgacct cctccccac gccactcctc ccaactttag  
3181 gcgggctctt aaaattctgg gaagcagaac ctggccggag ccactagaca gagccgggac  
3241 tagccagag acatggagag ttgctacaac ccagtgaatc atgcccgtg cccctgacct  
3301 ggccggctag cccctcgtgt ctgtccacct gtctgcccga gcccctact gctgccttac  
3361 acctgtatgc ctgcagatg ctctcagcct gccagtctgt ccactctgtc gcaactctgc  
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3481 gaagatggga ggtggggcta gtgtggggg tgcgtgagag cggatgccac cccagctctg  
3541 tctccaaacc aggtcttga ttgtattatt gaatatgatg atttcaaatt gaactcctcc  
3601 attgtggaac ccaaggagcc agccccagaa acaggtcagc aagttcaata acctcccta  
3661 gtctaaagcg ggggaggagg agcatgtgcc ctctctctgg gggaggggtc tgggagatcg  
3721 tgtgtcagc aaggtctctc tgtcccgagc tgatggcccc tacctggtga tcgtggaaca  
3781 gcctaagcag gttgagtgag caaaaggagg ggtgtggaa tggcttcagc tttggggaca  
3841 aatggggtag ttagctggc tggcatggag gagcattgcc gaagaggccc acaggggatt  
3901 ggatggtcac tgcgtctgat cagagtgtg tagttttggg tcagggctac taccagcgac  
3961 tcgggtcact gctggcctgg gtgtcttcc ctgatcaca tgctactatg cccttgacct  
4021 tcagagaggc ttccgatttc gatatggctg tgaaggcccc tcccatggag gactgcccgg  
4081 tgcctccagt gagaagggcc gaaagacctc tccactgtc aaggtgkcc aggatggtgc  
4141 tggmgggtg gctaagtga cagcatgccc aaggccctga cgtgacagtc ccttgccctc  
4201 cctagatctg taactacgag ggaccagcca agatcgaggt ggacctggtg acacacagtg  
4261 acccacctcg tgctcatgcc cacagtctgg tgggcaagca atgctcggag ctggggatct  
4321 gcgcggtttc tgtggggccc aaggacatga ctgcccagta ggtgcccttc ttaacgcttg  
4381 gccccactg gtatgccskt cwtgccagtc ccaggcccca gccacctcca tatgatgta  
4441 gcatctgacc aaggggaaan gatgtaggtt ggcaccaaac ccaagggcct aagtagaaac  
4501 tccaatggct tccttgagg agtaaggctg agctgagcct ggcaatggga aaggtgcctg  
4561 gcaatgggaa aggtgcctca ggaagaaaga actgcatggc caaaggctcc cgattctctc  
4621 ttctcagatt taacaacctg ggtgtcctgc atgtgactaa gaagaacatg atggggacta  
4681 tgatacaaaa acttcagagg cagcggctcc gctctaggcc ccagggcctt acgggtatgg  
4741 gtgcaggggg tgggtcgggt atgggtgcag ggggtgggtg ggtcatggga ggtgtcatg  
4801 gaaggagcag ggagggagaa gccaggggtc acacatgtac ctactgcccc gagggcagc  
4861 agcgggagct ggagcaagag gccaaagaac tgaagaaggt gatggatctg agtatagtgc  
4921 ggctgcgctt ctctgccttc cttagagcca gtgatggctc cttctccctg cccctgaagc  
4981 cagtcacctc ccagccatc catgatagca gtgagtatcc tgattgcctg ggggtccagg  
5041 cctggtsgsa gaggtggcat gaggggtgac ctcaagctgt gcagtcacaa aagaccagg  
5101 tttcagaacc tgcstgcca catatgagct gagtgtacct gagcaagtca tttccccccc

## (2) INFORMATION FOR SEQ ID NO:2601:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3601 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2601

1 ggccaccgga gcggcccgcc gacgatcgt gacagcttc cctgcccttc ccgtcggctc  
61 ggccgccagc cgccgcagcc ctccggctgc acgcagccac cgccccgct cccggagccc

121 agcgccgccc agggccgcagc cgcccggcca gtaaggcgcc gccgcccgc gccaccgcgg  
181 gccctgccgt tccctccgcc gcgctgcgcc atggcgcgcc gctgactggc ctggcccggc  
241 cccgcccgcg tcccgtcgc cccgaccgc actcggggcc gccgggctc cggcctgccg  
301 ccgctcttc cttctccagc cggcaggccc cgccgcttag gaggagagc ccaccgcgc  
361 caggaggccg aacgcggact cgccaccgc cttcagaatg gcagaagatg atccatattt  
421 gggaaggcct gaacaaatgt ttcatttgga tccttctttg actcatacaa tatttaatcc  
481 agaagtattt caaccacaga tggcactgcc aacagatggc ccataccttc aaatattaga  
541 gcaacctaaa cagagaggat ttcgtttccg ttatgtatgt gaaggcccat cccatggtag  
601 actacctggt gcctctagt gaaagaacaa gaagtcttac cctcaggtca aaatctgcaa  
661 ctatgtggga ccagcaaagg ttattgttca gttggtcaca aatggaaaaa atatccacct  
721 gcatgcccac agcctggtgg gaaaacactg tgaggatggg atctgactg taactgctgg  
781 acccaaggac atggtggtcg gcttcgcaaa cctgggtata cttcatgtga caaagaaaaa  
841 agtatttgaa acactggaag cacgaatgac agaggcgtgt ataaggggct ataactcctg  
901 actcttggtg caccctgacc ttgcctattt gcaagcagaa ggtggagggg accggcagct  
961 gggagatcgg gaaaaagagc taatccgcca agcagctctg cagcagacca aggagatgga  
1021 cctcagcgtg gtgcggctca tgtttacagc ttttctccg gatagcactg ccagcttcac  
1081 aaggcgctg gaaccggtg tatcagacgc catctatgac agtaaaagccc ccaatgcac  
1141 caacttgaaa attgtaagaa tggacaggac agctggatgt gtgactggag gggaggaaat  
1201 ttatcttctt tgtgacaaag ttcagaaaga tgacatccag attcgatttt atgaagagga  
1261 agaaaatggt ggagtctggg aaggatttgg agatttttcc cccacagatg ttcatagaca  
1321 atttgccatt gtcttcaaaa ctccaaagta taaagatatt aatattacaa aaccagcctc  
1381 tgtgtttgtc cagcttcgga ggaatctga cttggaaact agtgaaccaa aacctttct  
1441 ctactatcct gaaatcaaag ataaagaaga agtgacagag aaacgtcaga agctcatgcc  
1501 caatttttcc gatagtctg gcggtggtag tggtgccgga gctggaggcg gaggcatgtt  
1561 tggtagtgcc ggtggaggag ggggactgg aagtacaggt ccagggtata gcttcccaca  
1621 ctatggattt cctacttatg gtggattac tttccatcct ggaactacta aatctaagtc  
1681 tgggatgaag catggaacca tggacactga atctaaaaag gaccctgaag gttgtgacaa  
1741 aagtgatgac aaaaacactg taaacctctt tgggaaagt attgaaacca cagagcaaga  
1801 tcaggagccc agcgaggcca ccgttgggaa tggtagggtc actctaactg atgcaacagg  
1861 aacaaaagaa gagagtgtcg gagttcagga taacctctt ctagagaagg ctatgcagct  
1921 tgcaaaagag catgccaatg cccttttcca ctacgcggtg acaggagagc tgaagatgct  
1981 gctggccgtc cagcgccatc tcaactgctg gcaggatgag aatggggaca gtgtcttaca  
2041 cttagcaatc atccaccttc attctcaact tgtgagggat ctactagaag tcacatctgg  
2101 tttgatttct gatgacatta tcaacatgag aaatgatctg taccagacgc ccttgcaact  
2161 ggcagtgatc actaagcagg aagatgtggt ggaggatttg ctgagggtcg gggccgacct  
2221 gagccttctg gaccgcttgg gtaactctgt tttgcaccta gctgccaaag aaggacatga  
2281 taaagtcttc agtatcttac tcaagcacia aaaggcagca ctacttctg accacccaa  
2341 cggggacggt ctgaatgcca tctatctagc catgatgagc aatagcctgc catgtttgct  
2401 gctgctggtg gccgctgggg ctgacgtcaa tgctcaggag cagaagtcgg ggcgcacagc  
2461 actgcacctg gctgtggagc acgacaacat ctcatggca ggctgcctgc tctggagggg  
2521 tgatgcccac gtggacagta ctacctacga tggaaaccaca ccctgcata tagcagctgg  
2581 gagagggtcc accaggctgg cagctcttct caaagcagca ggagcagatc ccctggtgga  
2641 gaactttgag cctctctatg acctggatga ctcttgggaa aatgcaggag aggatgaagg  
2701 agttgtgcct ggaaccacgc ctctagatat ggccaccagc tggcaggat ttgacatatt  
2761 aaatgggaàa ccatatgagc cagagtttac atctgatgat ttactagcac aaggagacat  
2821 gaaacagctg gctgaagatg tgaagctgca gctgtataag ttactagaaa ttcctgatcc  
2881 agacaaaaac tgggctactc tggcgagaa attaggtctg gggatactta ataatgcctt  
2941 ccggtctgagt cctgctcctt ccaaaacact tatggacaac tatgaggtct ctgggggtac  
3001 agtcagagag ctggtggagg ccctgagaca aatgggctac accgaagcaa ttgaagtgat  
3061 ccaggcagcc tccagcccag tgaagaccac ctctcaggcc cactcgtctc ctctctcgcc  
3121 tgctccaca aggcagcaaa tagacgagct ccgagacagt gacagtgtct gcgacaggg  
3181 cgtggagaca tccttccgca aactcagctt taccgagtct ctgaccagt gtgcctcact  
3241 gctaaactct aacaaaaatgc cccatgatta tgggcaggaa ggacctctag aaggcaaaat  
3301 ttgacctgct gacaatttcc cacaccgtgt aaaccaaagc cctaaaattc cactgcgttg  
3361 tccacaagac agaagctgaa gtgcatccaa aggtgctcag agagccggcc cgcctgaatc  
3421 attctcgatt taactcgaga ccttttcaac ttggcttctt ttcttggttc ataaatgaat  
3481 tttagtttgg ttcacttaca gatagtatct agcaatcaca aactggctg agcggatgca  
3541 tctggggatg aggttgctta ctaagctttg ccagctgctg ctggatcaca gctgctttct  
3601 gttgtcattg ctgttgcctc tctgc

## (2) INFORMATION FOR SEQ ID NO:2602:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1621 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2602

1 actttcctgc cccttccccg gccaaagccca actccggatc tcgctctcca ccggtatctca  
61 cccgccacac ccggacaggc ggctggagga ggcgggctc taaaattctg ggaagcagaa

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121 cctggccgga gccactagac agagccgggc ctagcccaga gacatggaga gttgctacaa
181 cccaggtctg gatggtatta ttgaatatga tgatttcaaa ttgaactcct ccattgtgga
241 acccaaggag ccagcccag aaacagctga tggcccctac ctggtgatcg tggaacagcc
301 taagcagaga ggcttccgat ttcgatattg ctgtgaaggc cctccccatg gaggactgcc
361 cgggtgcctcc agtgagaagg gccgaaagac ctatcccact gtcaagatct gtaactacga
421 gggaccagcc aagatcgagg tggacctggt aacacacagt gacccacctc gtgctcatgc
481 ccacagtctg gtgggcaagc aatgctcgga gctggggatc tgcgccgttt ctgtggggcc
541 caaggacatg actgccaat ttaacaacct ggggtgtcctg catgtgacta agaagaacat
601 gatggggact atgatacaaa aacttcagag gcagcggtc cgctctaggc cccagggcct
661 tacggaggcc gagcagcggg agctggagca agaggccaaa gaactgaaga aggtgatgga
721 tctgagtata gtgcggtgc gcttctctgc cttccttaga gccagtgatg gctccttctc
781 cctgcccctg aagccagtc cctcccagcc catccatgat agcaaactc cgggggcac
841 aaacctgaag atttctcgaa tggacaagac agcaggctct gtgcgggggtg gagatgaagt
901 ttatctgctt tgtgacaagg tgcagaaaga tgacattgag gttcgggtct atgaggatga
961 tgagaatgga tggcaggcct ttggggactt ctctcccaca gatgtgcata aacagtatgc
1021 catttgtgtc cggacacccc cctatcacaa gatgaagatt gagcggcctg taacagtgtt
1081 tctgcaactg aaacgcaagc gaggagggga cgtgtctgat tccaaacagt tcacctatta
1141 ccctctggtg gaagacaagg aagaggtgca gcggaagcgg aggaaggcct tgcccacctt
1201 ctcacagccc ttcgggggtg gctcccacat ggggtgaggc tctgggggtg cagccggggg
1261 ctacggagga gctggaggag gtgaggggtt actgatggag ggaggggtta aggtaagaga
1321 agctgtggag gaaaaaatc tgggggaggc cgggcgtggc ttgcacgcct gtaatccagc
1381 ctttgggagg ccaaggcagg cagttacctg agatcaggag ttcaagacca gcttgccaa
1441 cagcgtgaaa cctcgtctct actaaaaata caaacattag ctgggcatgg tggcaggcgc
1501 ctgtaatccc agctactcgg gaggttgagg caggagaatc gcttgaacct tgggagacaa
1561 gaggttgag taagctgaga tcacaccact gcactccagg ctgggcaata agagcgaac
1621 tccgtctcaa aaaaaaaaaa aaaaaaaaaa

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## (2) INFORMATION FOR SEQ ID NO:2603:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3061 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2603

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1 cacggtgagt ggctggattc agaccctcgt gtggccggga caagagaaaa gagggaggag
61 ggccttttagc ggacagcgcc tggggctgga gagcagcagc tgcacacagc cggaaagggc
121 gcgcaggcga cgacactcgg atccacgtcg acaccgttgt acaaagatac ggcggaccgc
181 gggcgctctaa aattctggga agcagaacct ggcggagcgc actagacaga gccgggccta
241 gccagagac atggagagtt gctacaacct aggtctggat ggtattattg aatatgatga
301 tttcaaattg aactcctcca ttgtggaacc caaggagcca gccccagaaa cagctgatgg
361 cccctacctg gtgatcgtgg aacagcctaa gcagagaggc ttccgatttc gatatggctg
421 tgaaggcccc tcccattggag gactgcccg tgcctccagt gagaagggcc gaaagacctc
481 tcccactgtc aagatctgta actacgaggg accagccaag atcgagggtg acctggtaac
541 acacagtac ccacctcgtg ctcatgcccc cagtctgggt ggcaagcaat gctcggagct
601 ggggatctgc gccgtttctg tggggcccaa ggacatgact gcccaattta acaactggg
661 tgtcctgcat gtgactaagg agaacatgat ggggactatg atacaaaac ttcagaggca
721 gcggctccgc tctaggcccc agggccttac ggaggccgag cagcgggagc tggagcaaga
781 ggccaaagaa ctgaagaagg tgatggatct gagtatagtg cggctgcgct tctctgcctt
841 ccttagagcc agtgatggct ccttctccct gcccctgaag ccagtcatct cccagcccat
901 ccatgacagc aaatctccgg gggcatcaaa cctgaagatt tctcgaatgg acaagacagc
961 aggtctctgt cgggggtggag atgaagttta tctgctttgt gacaagggtg agaaagatga
1021 cattgaggtt cggttctatg aggatgatga gaatggatgg caggcccttg gggacttctc
1081 tcccacagat gtgcataaac agtatgccat tgtgttccgg acaccccctt atcacaagat
1141 gaagattgag cggcctgtaa cagtgtttct gcaactgaaa cgcaagcgag gaggggacgt
1201 gtctgattcc aaacagttca cctattaccc tctggtggaa gacaaggaag aggtgcagcg
1261 gaagcggagg aaggccttgc ccaccttctc ccagcccttc ggggtgggt cccacatggg
1321 tggaggctct ggggtgtag ccgggggcta cggaggagct ggaggagggt gcagcctcgg
1381 tttcttcccc tctccctcgt cctacagccc ctaccagtc ggcgggggcc ccatgggctg
1441 ctacccggga ggcgggggag ggcgcagat ggcggccacg gtgcccagca gggactccgg
1501 ggaggaagcc gcggagccga gcgcccctc caggaccccc cagtgcagc cgcaggcccc
1561 ggagatgctg cagcgagctc gagagtacaa cgcgcgctg ttccgctcgg cgcagcgag
1621 cgcccagacc ctactcgact acggcgctac cgcggaccgg cgcgcgctgc tggcgggaca
1681 gcgccacctg ctgacggcgc aggacgagaa cggagacaca ccactgcacc tagccatcat
1741 ccacgggcag accagtgtca ttgagcagat agtctatgtc atccaccacg cccaggacct
1801 cggcgttgtc aacctcacca accacctgca ccagacgccc ctgcacctgg cggtgatcac
1861 ggggcagacg agtgtggtga gctttctgct gcgggtaggt gcagaccag ctctgctgga
1921 tcggcatgga gactcagcca tgcactggc gctgcgggca ggcgctgggt ctcctgagct
1981 gctgcgtgca ctgcttcaga gtggagctcc tgctgtgccc cagctgttgc atatgcctga
2041 ctttgaggga ctgtatccag tacacctggc ggtccgagcc cgaagccctg agtgcttga

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2101 tctgctggtg gacagtgggg ctgaagtgga ggccacagag cggcaggggg gacgaacagc  
2161 cttgcatcta gccacagaga tggaggagct ggggttggtc acccatctgg tcaccaagct  
2221 ccgggccaac gtgaacgctc gcacctttgc gggaaacaca cccctgcacc tggcagctgg  
2281 actggggtac ccgacctca cccgcctcct tctgaaggct ggtgctgaca tccatgctga  
2341 aaacgaggag cccctgtgcc cactgccttc acccctacc tctgatacg actcggactc  
2401 tgaaggccct gagaaggaca ccgaagcag cttccggggc cacacgcctc ttgacctcac  
2461 ttgcagcacc aaggtgaaga ccttgctgct aaatgctgct cagaacacca tggagccacc  
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## (2) INFORMATION FOR SEQ ID NO:2604:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13384 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2604

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2341 aaacgaggag cccctgtgcc cactgccttc accccctacc tctgatagcg actcggactc
2401 tgaaggccct gagaaggaca ccgaagcag cttccggggc cacacgcctc ttgacctcac
2461 ttgcagcacc aaggtgaaga ccttgcgtgt aaatgctgct cagaacacca tggagccacc
2521 cctgaccccg ccagcccag cagggccggg actgtcactt ggtgatacag ctctgcagaa
2581 cctggagcag ctgctagacg ggccagaagc ccagggcagc tgggcagagc tggcagagcg
2641 tctggggctg cgcagcctgg tagacacgta ccgacagaca acctcaccca gtggcagcct
2701 cctgcgcagc tacgagctgg ctggcgggga cctggcaggt ctactggagg cctgtctga
2761 catgggccta gaggagggag tgaggctgct gagggtcca gaaacccgag acaagctgcc
2821 cagcacaaca gaggtgaagg aagacagtgc gtacgggagc cagtcaaggc agcagaaggc
2881 agagaagctg ggcccccccc ctgagccacc aggggggtc tgcacgggc acccccagcc
2941 tcagggtcac tgacctgctg cctgccccca gcccccttc cggacccctt gtacagcgtc
3001 cccacctatt tcaaatctta tttaacacc cacaccacc cctcagttgg gacaaataaa
3061 ggattctcat gggaagggga ggacccctcc ttcccaactt aaaaaaaaaa aaa

```

## (2) INFORMATION FOR SEQ ID NO:2605:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2161 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2605

```

1' atgacagcaa aagattcttc aaaggaactt actgcttctg aacctgaggt ttgcataaag
61 acttttcaagg agcaaatgca tttagaactt gagcttccga gattaccagg aaacagacct
121 acatctccta aaatttctcc acgcagttca ccaaggaact caccatgctt tttcagaaag
181 ttactgtgta ataaaagcat tcggcagcgt cgtcgttca ctgtggctca tacatgcttt
241 gatgtggaaa atggcccttc cccaggtcgg agtccactgg atccccaggc cagctcttcc
301 gctgggtctg tacttcacgc cacctttcct gggcacagcc agcgcagaga gtcatttctc
361 tacagatcag acagcgacta tgacttgtca ccaaaggcga tgtcgagaaa ctcttctctt
421 ccaagcgagc aacacggcga tgacttgatt gtaactcctt ttgcccaggt ccttgccagc
481 ttgcgaagtg tgagaaacaa cttcactata ctgacaaacc ttcatggtag atctaacaag
541 aggtccccag ctgctagtca gcctcctgtc tccagagtca acccacaaga agaattctat
601 caaaaattag caatggaaac gctggaggaa ttagactggt gtttagacca gctagagacc
661 atacagacct accggtctgt cagtgaagtg gcttctaaca agttcaaaag aatgctgaac
721 cgggagctga cacacctctc agagatgagc cgatcaggga accaggtgtc tgaatacatt

```

```

781 tcaataactt tcttagacaa gcagaatgat gtggagatcc catctcctac ccagaaagac
841 agggagaaaa agaaaaagca gcagctcatg acccagataa gtggagttaa gaaattaatg
901 catagttaa gcctaaacaa tacaagcatc tcacgctttg gactcaacac tgaaaatgaa
961 gatcacctgg ccaaggagct ggaagacctg aacaaatggg gtcttaacat ctttaatgtg
1021 gctggatatt ctcaaatag acccctaaca tgcacatgt atgctatatt ccaggaaaga
1081 gacctcctaa agacattcag aatctcatct gacacattta taacctacat gatgacttta
1141 gaagaccatt accattctga cgtggcatat cacaacagcc tgcacgtgc tgatgtagcc
1201 cagtcgaccc atgttctcct ttctacacca gcattagacg ctgtcttcac agatttgag
1261 atcctggctg ccatttttgc agctgccatc catgacgttg atcatcctgg agtctccaat
1321 cagtttctca tcaacacaaa ttcagaactt gctttgatgt ataagtatga atctgtgttg
1381 gaaaatcatc accttgctgt gggtttcaaa ctgctgcaag aagaacactg tgacatcttc
1441 atgaatctca ccaagaagca gcgtcagaca ctcagggaaga tggttattga catgggttta
1501 gcaactgata tgtctaaaca tatgagcctg ctggcagacc tgaagacaat ggtagaaacg
1561 aagaaagtta caagttcagg cgttcttctc ctagacaact ataccgatcg cattcaggtc
1621 cttcgcaaca tggtagactg tgcagacctg agcaacccca ccaagtcctt ggaattgtat
1681 cggcaatgga cagaccgcat catggaggaa tttttccagc agggagacaa agagcggag
1741 aggggaatgg aaattagccc aatgtgtgat aaacacacag cttctgtgga aaaatcccag
1801 gttggtttca tcgactacat tgtccatcca ttgtgggaga catgggcaga ttgtgtacag
1861 cctgatgctc aggacattct cgatacctta gaagataaca ggaactggta tcagagcatg
1921 atacctcaaa gtccctcacc accactggac gagcagaaca gggactgcca gggctgatg
1981 gagaagtttc agtttgaact gactctcgat gaggaagatt ctgaaggacc tgagaaggag
2041 ggagaggagc acagctattt cagcagcaca aagacgcttt gtgtgattga tccagaaaac
2101 agagattccc tgggagagac tgacatagac attgcaacag aagacaagtc ccccggtgat
2161 aca

```

## (2) INFORMATION FOR SEQ ID NO:2606:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2606

```

1 tatcacaca gcatgcacgc agccgatgtt acccagacag tccattgctt cttgctccgc
61 acagggatgg tgcaactgct gtcggagatt gagctcctgg ccatcatctt tgctgcagct
121 atccatgatt atgagcacac gggcactacc aacagcttcc acatccagac caagtcagaa
181 tgtgccatcg tgtacaatga tcgttcagtg ctggagaatc accacatcag ctctgttttc
241 cgattgatgc aggatgatga gatgaacatt ttcataacc tcaccaagga tgagtttgta
301 gaactccgag ccctggtcat tgagatggtg ttggtacag atatggca

```

## (2) INFORMATION FOR SEQ ID NO:2607:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2607

```

1 atgacagcaa aagattcttc aaaggaactt actgcttctg aacctgaggt ttgcataaag
61 actttcaagg agcaaatgca tttagaactt gagcttccga gattaccagg aaacagacct
121 acatctccta aaattttctc acgcagttca ccaaggaact caccatgctt ttccagaaag
181 ttactgggtg ataaaagcat tcggcagcgt cgtcgcttca ctgtggctca tacatgcttt
241 gatgtggaaa atggcccttc ccaggctcgg agtccactgg atccccaggg cagctcttcc
301 gctgggctgg tacttcacgc cacccttctt gggcacagcc agcgcagaga gtcatttctc
361 tacagatcag acagcgacta tgacttgta ccaaaggcga tgtcgagaaa ctcttctctt
421 ccaagcgagc aacacggcga tgacttgatt gtaactcctt ttgcccaggt ccttgccagc
481 ttgcgaagtg tgagaaacaa ctctactata ctgacaaacc ttcatggtac atctaacaag
541 aggtccccag ctgctagtca gcctcctgtc tccagagtca acccacaaga agaattctat
601 caaaaattag caatggaaac gctggaggaa ttagactggt gtttagacca gctagagacc
661 atacagacct accggtctgt cagtgaatg gcttctaaca agttcaaaag aatgctgaac
721 cgggagctga cacacctctc agagatgagc cgatcagggg accaggtgtc tgaatacatt
781 tcaataactt tcttagacaa gcagaatgat gtggagatcc catctcctac ccagaaagac
841 agggagaaaa agaaaaagca gcagctcatg acccagataa gtggagttaa gaaattaatg
901 catagttaa gcctaaacaa tacaagcatc tcacgctttg gactcaacac tgaaaatgaa
961 gatcacctgg ccaaggagct ggaagacctg aacaaatggg gtcttaacat ctttaatgtg
1021 gctggatatt ctcaaatag acccctaaca tgcacatgt atgctatatt ccaggaaaga
1081 gacctcctaa agacattcag aatctcatct gacacattta taacctacat gatgacttta
1141 gaagaccatt accattctga cgtggcatat cacaacagcc tgcacgtgc tgatgtagcc
1201 cagtcgaccc atgttctcct ttctacacca gcattagacg ctgtcttcac agatttgag
1261 atcctggctg ccatttttgc agctgccatc catgacgttg atcatcctgg agtctccaat
1321 cagtttctca tcaacacaaa ttcagaactt gctttgatgt ataagtatga atctgtgttg

```

1381 gaaaatcatc accttgctgt gggtttcaaa ctgctgcaag aagaacactg tgacatcttc  
1441 atgaatctca ccaagaagca cgcgcagaca ctcaaggaaga tgggtattga catgggtgtta  
1501 gcaactgata tgtctaaaca tatgagcctg ctggcagacc tgaagacaat ggtagaaacg  
1561 aagaaagtta caagttcagg cgttcttctc ctagacaact ataccgatcg cattcaggtc  
1621 cttcgcaaca tggtagactg tgcagacctg agcaacccca ccaagtcctt ggaattgtat  
1681 cggcaatgga cagaccgat catggaggaa tttttccagc agggagacaa agagcgggag  
1741 aggggaatgg aaattagccc aatgtgtgat aaacacacag cttctgtgga aaaatcccag  
1801 gttgggttca tcgactacat tgtccatcca ttgtgggaga catgggcaga tttggtacag  
1861 cctgatgctc aggacattct cgatacctta gaagataaca ggaactggtg tcagagcatg  
1921 atacctcaaa gtccctcacc accactggac gagcagaaca gggactgcca gggctctgat  
1981 gagaagtttc agtttgaaact gactctcgat gaggaagatt ctgaaggacc tgagaaggag  
2041 ggagagggac acagctattt cagcagcaca aagacgcttt gtgtgattga tccagaaaac  
2101 agagattccc tgggagagac tgacatagac attgcaacag aagacaagtc ccccggtgat  
2161 aca  
1 tatcacaaca gcatgcacgc agccgatgtt acccagacag tccattgctt cttgctccgc  
61 acagggatgg tgcactgcct gtcggagatt gagctcctgg ccatcatctt tgctgcagct  
121 atccatgatt atgagcacac ggcactacc aacagcttcc acatccagac caagtccagaa  
181 tgtgccatcg tgtacaatga tcgttcagtg ctggagaatc accacatcag ctctgttttc  
241 cgattgatgc aggatgatga gatgaacatt ttcacacacc tcaccaagga tgagtttcta  
301 gaactccgag ccctggtcat tgagatggtg ttggctacag atatggca

## (2) INFORMATION FOR SEQ ID NO:2608:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2341 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2608

1 gggccgcccgt cggcgcgctg ggtgcgaggaa gggggctctg gatttcggtc cctccccttt  
61 ttcctctgag tctcggaacg ctccagctct cagaccctct tctcccagg taaaggccgg  
121 gagaggagg cgcattctct ttccaggcac cccaccatgg gcaatgcctc caatgactcc  
181 cagtctgagg actgcgagac gcgacagtgg cttccccagc gcgaaagccc agccatcagc  
241 tccgtcatgt tctcgccggg ggtgctgggg aacctcatag cactggcgct gctggcgcg  
301 cgctggcggg gggacgtggg gtgcagcgcc ggcgcagga gctcccctc cttgttccac  
361 gtgctggtga ccgagctggt gttcaccgac ctgctcggga cctgcctcat cagcccagtg  
421 gtactggctt cgtacgcgag gaaccagacc ctgggtggac tggcgcccga gagccgcg  
481 tgcacctact tcgctttcgc catgaccttc ttcagcctgg ccacgatgct catgctcttc  
541 gccatggccc tggagcgcta cctctcgatc gggcaccctt acttctacca gcgcccgcgc  
601 tcggcctccg ggggcctggc cgtgctgcct gtcattctat cagtctccct gctcttctgc  
661 tcgctgccgc tgcctggacta tgggcagtac gtccagtact gccccgggac ctgggtgcttc  
721 atccggcacg ggcggaccgc ttacctgcag ctgtacgcca cctgtgctg gcttctcatt  
781 gtctcggtgc tcgcctgcaa cttcagtgct attctcaacc tcatccgcat gcaccgccga  
841 agccggagaa gccgctgcgg accttccctg ggcagtggcc ggggcggccc cggggcccgc  
901 aggagagggg aaagggtgtc catggcggag gagacggacc acctcattct cctggctatc  
961 atgaccatca ccttcgcccgt ctgctccttg cctttcacga tttttgcata tatgaatgaa  
1021 acctcttccc gaaaggaaaa atgggacctc caagctctta ggtttttatc aattaattca  
1081 ataattgacc cttgggtctt tgccatcctt aggcctcctg ttctgagact aatgcgttca  
1141 gtcctctggt gtcggatttc attaagaaca caagatgcaa cacaaacttc ctgttctaca  
1201 cagtcagatg ccagtaaaaca ggtgcacctt tgaggtcagt agtttaaaag tctttagtta  
1261 tatagcatct ggaagatcat tttgaaattg ttcctggag aaatgaaaac agtgtgtaaa  
1321 caaaatgaag ctgccctaataaaaaaggagt atacaaacat ttaagctgtg gtcaaggcta  
1381 cagatgtgct gacaaggcac ttcattgtaaa gtgtcagaag gagctacaaa acctaccctc  
1441 aatgagcatg gtacttggcc tttggaggaa caatcgctg cattgaagat ccagctgcct  
1501 attgatttaa gctttcctgt tgaatgacaa agtatgtggt tttgtaattt gtttgaacc  
1561 ccaaacagtg actgtacttt ctattttaat cttgctacta ccgttatata catatagtgt  
1621 acagccagac cagattaaac ttcattgta atctctagga agtcaaatg tggaagcaac  
1681 caagcctgct gtcttgtgat cacttagcga acccttattt tgaacaatga agttgaaaat  
1741 cataggcacc ttttactgtg atgtttgtgt atgtgggagt actctcatca ctacagtatt  
1801 actcttaca gagtggactc agtgggttaa catcagtttt gtttactcat cctccaggaa  
1861 ctgcaggtca agttgtcagg ttattttatt tataatgtcc atatgctaag agtgatcaag  
1921 aagactttag gaatggttct ctcaacaaga aataatagaa atgtctcaag gcagttaatt  
1981 ctcatataata ctcttattat cctatttctg ggggaggatg tacgtggcca tgtatgaagc  
2041 caaatattag gcttaaaaaac tgaaaaatct ggttcattct tcagatatac tggaacctt  
2101 taaaagtga tattggggcc atgagtaaaa tagattttat aagatgactg tgtgtacca  
2161 aaattcatct gtctatattt tatttagggg aacatggttt gactcatctt atatgggaaa  
2221 ccatgtagca gtgagtcata tcttaataata tttctaaatg tttggcatgt aaatgtaaac  
2281 tcagcatcaa aatatttcag tgaatttgca ctgtttaatc atagttactg tgtaaaactca  
2341 tctgaaatgt taaaaaata aactataaaa ca

## (2) INFORMATION FOR SEQ ID NO:2609:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1321 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2609

```
1 gggggcgcca gggctgagcg gccggtgatg gggacccac atcccaggca gtgccggcac
61 ccctggcgcc tgacatgagc cettgcgggc ccctcaacct gagcctggcg ggcgaggcga
121 ccacatgcgc ggcgccttgg gtccccaaca cgtcgccgt gccgcctcg ggcgttcgc
181 ccgcgctgcc catcttctcc atgacgctgg gcgcctgttc caacctgctg gcgctggcgc
241 tctggcgcca ggccgcgggc cgctgcgac gccgcgctc ggccaccacc ttcctgtgt
301 tctgggccag cctgctggcc accgacctgg cgggccacgt gatccgggc gcgctggtgc
361 tgcgtctgta cactgcgggg cgctctccgg ccggcggggc ctgccacttc ctgggcggct
421 gcattggtctt ctccgctctg tgcgcgctgc tgcctgggtg tggcatggcc gtggagcgct
481 gcgtggcgct cagcgggcgc ctgctccacg ccgcgcgggt ctgcgtcgcc cgcgcgcgcc
541 tggcgctggc cgcggtggcc gcggtggcct tggcctggc gctgctggcc ctggcgcgcg
601 tgggcccgtc tgagctgcag taccgggcca cgtggtgctt catcgccctg ggtcccccg
661 gcgctggcg ccaggcactg cttgctggcc tcttcgccag cctcgccctg tgcgcgtcc
721 tcgcccgcgt ggtgtgcaac acgctcagcg gcctggccct gcacgcgcc cgctggcgac
781 gccgtcccg acggcctccc ccggcctcag gccccgacag ccggcgctgc tggggggcgc
841 acggaccccg ctccgctccc gcctcgctcc cctcgctccat cgcttcggcc tccaccttct
901 ttggcggtc tcggagcagc ggctcggcac gcagagctcg cggccacgac gtggagatgg
961 tgggccagct tgcgtgatac atggtggtgt cgtgcatctg ctggagccca atgctggtgt
1021 tgggtggcgt ggccgtcgcc ggctggagct ctacctccct gcagcgccca ggttcctgg
1081 ccgtgcgcct tgcctcctgg aaccagatcc tggacccttg ggtgtacatc ctactgcgcc
1141 aggcgctgct gcgccaactg ctccgctctt tggcccgag ggccggagcc aaggggcgcc
1201 ccgcggggct gggcctaaca ccgagcgctt gggaggccag ctgctgcgc agctcccgcc
1261 acagcgccct cagccacttc taagcacaac cagaggcca acgactaagc cagccacccc
1321 tgggctgggc ccaggtgcgc ggcgagagc ctttgggaat aaaaagccat tctgca
```

## (2) INFORMATION FOR SEQ ID NO:2610:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1021 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2610

```
1 atgggcaatg cctccaatga ctcccagtct gaggactgcy agacgcgaca gtggcttccc
61 ccaggcgaaa gccagccat cagctccgtc atgttctcgg ccggggtgct ggggaacctc
121 atagcactgg cgctgctggc gcgcccgttg ccgggggagc tggggtgcag cgccggccgc
181 aggagctccc tctccttgtt ccacgtgctg gtgaccgagc tgggtttcac cgacctgtc
241 gggacctgcc tcatcagccc agtggctact gcttcgtacg cgcggaacca gacctgtg
301 gcaactggcg ccgagagccg cgctgcacc tacttcgctt tcgccatgac cttcttcagc
361 ctggccacga tgcctatgct cttcgccatg gccctggagc gctacctctc gatcgggcac
421 cctacttctt accagcgccg cgtctcgccg tccgggggcc tggcctgctt gcctgtcatc
481 tatgcagtct ccctgctctt ctgctcgctg ccgctgctgg actatgggca gtacgtccag
541 tactgccccg ggacctgtg cttcatccgg cacgggcgga ccgcttacct gcagctgtac
601 gccaccctgc tgcctctctt cattgtctcg gtgctgcctt gcaacttcac tgtcattctc
661 aacctcatcc gcatgcaccg ccgaagccgg agaagccgct gcggaccttc cctgggcagt
721 ggcggggcg gcccgggggc ccgagaggaga ggggaaaggg tgtccatggc ggaggagagc
781 gaccacctca ttctcctggc tatcatgacc atcaccttcg ccgtctgctc cttgccttct
841 acgatttttg catatatgaa tgaaacctct tcccgaagg aaaaatggga cctccaagct
901 cttaggtttt tatcaattaa ttcaataatt gacccttggg tctttgccat ccttaggcct
961 cctgttctga gactaatgcy ttcagctctc tgtgtcgga tttcattaag aacacaagat
1021 gcaacacaaa cttcctgttc tacacagtca gatgccagta aacaggctga cctttga
```

## (2) INFORMATION FOR SEQ ID NO:2611:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1201 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2611

```
1 ctgcagatgg gaagaggttt ttccaggaat ttaaattgtg caataaggcc acacaatctt
61 acttaaaaaa aatggtgaag gggttttaat tacaccatga agttttacaa ttttttaggt
121 ttttagttct ggttttagaa aacagagtag aaggattaac agagaaaaac ttcaccatta
181 gacaagaagt caaatgatt ctaaggccg cgcaaacagg ctttccaaga attaatcatg
241 aggtggtgct tggagaattc ctttactcca gtgactttga aaccccttc tcacttcca
```

```

301 ctatgcttttc aaaggattca tgggtgaattg ggtctaacga gtataacacg gccggccgaa
361 cgtatgaagct cagcgtaccc ttccaggcgg gagaagttcc caggaggaag aatggagaaa
421 aagatcgagc ttaggcagtc ctcccaacct caccaaggct ccacctctct ccaaagccgc
481 aacgtgctgc cacctgcgcc gggagaggct gcaatcactg tctcctctct tttctttctc
541 tttttttttt ttcttttttt gcctgggggt cccgaccaag cgcagccgca gtctgggcac
601 tgccaactga ctccaactcc ttttatgggt agaggatgga ttcttcgtta tttccccgcc
661 caatctggta cccacccacc caccacacca ccacgtccgc tgggcgcacc caagtctaac
721 cccggggcgc acgccgtagc gcagacaccg tatttctcct cctttctcgg ccaacctag
781 gtagaatcct aaaacaactg cctctcttcc cagatctag atgttgccgc ccgcggacag
841 gaggttcaag aaatagtaca ctccgagcgg caggcagcga gagcgaaaac ggtcgcgggt
901 ttcagtgggt gccccactgg aagccgagtt caggagcggc taagcgtcgc cggggaaaagc
961 accggggcct cccagggtct cctccgagtt cccactccgc acctccagg gcgtgaaaac
1021 caggggagcc gcccgccccc cgcgccagc cccgccccag cccagacacc gccccccgc
1081 agtcttcctt gcggcgccca gggaggacgc cgtccgcccc cttccaatcc ggccaatggg
1141 cgccgggca gcgcgcggtt tgctccgcc tccgccaggg aaacttggag gaggagaaaa
1201 gtttgtacag aggggtgaaa ggccgcagca cgcgagctcc a

```

## (2) INFORMATION FOR SEQ ID NO:2612:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2612

```

1 agccccgcag cccgagagga agatgaacag cccagggcca gagcctctgc gagagtggac
61 cccgagccgc cccaggttag ccaggagcgg cctcagcggc agccgcaaac tccagtagcc
121 gcccgctgct gccgtgctgg ggcggagggc agccagagct ggggaccaag gctccgcgcc
181 acctgggcac agcctcacac ctgaacgctg tctcccgcga gacgagaccg gcgggcactg
241 caaagctggg actcgtcttt gaaggaaaaa aaatagcgag taagaaatcc agcaccattc
301 ttcactgacc catcccgctg cactcttctt ttcccaagtt tttgaaagct ggcaactctg
361 acctcggtgt ccaaaaatcg acagccactg agaccggctt tgagaagccg aagatttggc
421 agtttccaga ctgagcagga caaggtgaaa gcagggttga ggcgggtcca ggacatctga
481 gggctgaccc tgggggctcg tgaggctgcc accgctgctg ccgctacagg tgagatggcg
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601 ccaagagggg aagagcgccg tctccaaatt gctttttaa cttgttttca gtgagcattt
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1981 ccctgttttc cctctgagtc cttgggagtg aacgtgtcgc ctttaggtcg gggctgggat
2041 tcccacactg tttctcagag gaggcccaac ccctctttgg aagtcccaac cctaaccgga
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```

## (2) INFORMATION FOR SEQ ID NO:2613:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 781 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2613

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1 agcccatgac tgggttttct gaggcttatt atgtagcttc ctctttccct ggaacttgtt

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61 accagaaatg aaggcagctt cctaattattg ataaggtaga catagcattt atatgttttc  
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181 caaccagtta tatcagccaa gtttgaggcg agaagtcagt aaaaatccag atttgcaggc  
241 catccgaatt gcttctgtga accccatcct agacccttg atatatatcc tcctgagaaa  
301 gacagtgttc agtaaaagcaa tagagaagat caaatgcctc ttctgcccga ttggcgggtc  
361 ccgcaggag cgctccggac agcactgttc agacagtcaa aggacatctt ctgccatgtc  
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481 cctcctgcc aacctctcac tgcagacct cagtgaataat ggccttggag gcaggaattt  
541 gcttcagggt gtgctggca tgggctggc ccaggaagac accacctcac tgaggacttt  
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661 ggaatgaggt ggtggaagcg gcaggcgag gcctgccctt aaggggagct ccctgcaagt  
721 cacatttccc agtgaaacac tgaacttatc agaaaaatgt atataatagg caaggaaaaga  
781 aatacagtac tgtttctgga cccttataaa atcctgtgca atagacacat acatgtcaca

## (2) INFORMATION FOR SEQ ID NO:2614:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8766 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2614

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61 ttcctctgag tctcggaacg ctccagctct cagaccctct tctcccagg taaaggccgg  
121 gagaggagg cgcatctctt ttccaggcac ccaccatgg gcaatgcctc caatgactcc  
181 cagctctgag actgcgagac gcgacagtgg cttccccag gcgaaagccc agccatcagc  
241 tccgtcatgt tctcgcccg ggtgctggg aacctcatag cactggcgct gctggcgcg  
301 cgctggcg gggacgtgg gtgcagcgcc ggccgaggga gctccctctc cttgttccac  
361 gtgctggtga ccgagctggt gttcacggac ctgctcggga cctgcctcat cagccagtg  
421 gtactggctt cgtacgcgc gaaccagacc ctggtggcac tggcgcccga gagccgcgcg  
481 tgcacctact tgccttctgc catgacctt ttcagcctgg ccacgatgct catgctcttc  
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601 tccgctccg ggggctggc cgtgctgct gtcactatg cagtctccct gctcttctgc  
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2221 ccattgtagc gtgagtcata tcttaataata tttctaaatg tttggcatgt aaatgtaaac  
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## (2) INFORMATION FOR SEQ ID NO:2615:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4861 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2615

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1021 gttctgactt cagtaggggc aaagctgtgt ggtctccatg cagatctgtc agctgagggt  
1081 ggtgttagtg aatactacag ggatccttag aggccaacac tgtgggtatc tacagtggca  
1141 atgaggctgt tgaggttttc aattgtgaca agtccctcat atctctttt tccccacct  
1201 gggaggtcat gactgaggac atccctcttg gaattaggtc taacttgag gcctgctcct  
1261 ggtggtggtg aactggtgt ctgatgaaca gtgcccagtg agtgccaaag agccaaggcc  
1321 tgaagcatgg gcatgcatgg agggaccaca gcaccagatt caattgtagc aatggtacca  
1381 gtgcccaggc cacaggcata cttactatca cattgataat ggtgtgtaaa atgcaggtac

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1441 ttataaagca gctaaggagc cagggacttt actgcatgca tacgcagagc tacagtggct
1501 ccaggatcca ggggtgtggc tagctctcct tgggtgctga gctgggtgact agagcatgga
1561 caggcacaga gaaaccttga ctctaggacc caggggtgtc actagctcac tatagtgggtg
1621 gctctggtgt tggaggtgtg ggtgtgtgta gtacagcctc agagacaggg tctggagcgc
1681 aggtgtgcac attactacag cagctctgga gttgagaata tgggttacct ttctacagt
1741 gctgaactag tgtctggagc aaagactttc acagagagaa cttggcttgg ggtcccaggg
1801 tgagatctag ttcacaacag cagtgtactc agtgtctgag acatgaggag gtgcaactga
1861 gccacagagc cacagtccag agtgtgaata tctgtagagc agccacaact tttggggatc
1921 aggaacacac atagaattgt gagaggtggt aaccctggcc ccagtcctgg cgagtgaac
1981 aatagctgct tcttgggtgag ggggtgtgag gggtagtgca actgtgttcc cctttttaagc
2041 atcctgctat gggaatggct gttggacaaa agatgccagt gtcctctgtg gagcaggaca
2101 ctgggggctc cagtggctct gtgtcacatg actgacacag atagcctaca aatttcttta
2161 ttcgtagcta tctcctggtg tctcatatat gccagttcca ccggtgatcc ttctacatga
2221 atattctttc ttttctccat tgtgtgttcc caaattcttt aacaggctct tgagccccat
2281 cccccaactc cccacccttg tgagggtat tttggtttgt gtataactgt ctatgtttgt
2341 tttttgttg gggcataagg ctgacatctc ctactccacc atcttgctaa tgtcacctgc
2401 ataggaatct ttttatgctt tccttatatt cactaaaatt taacaatata aaacttaaaa
2461 acatatgata aattgaactt attaatatca aacttattat aaataagaaa ctaccaggct
2521 gggcatggtg gctcatgcct gtaatcccaa cattttggga ggctgagggt aaaggatcac
2581 ttgagcccag gaattcaaga ccagcctggg aaatatagag agaccctatc tctagagatt
2641 ttttttttta attagccagt agtgatggca cacatctata gtcccagcta ctccaggagc
2701 tgagggtgga gaattgcttg agcccaggag gtcaaggctg cagcaagcag taatcatgcc
2761 actgcaactc agcctggggc gcagagttag accctgtctc aaaaaagaa cctactagtc
2821 tacataccac acttcttcat ccccatctga gactatatat atttttcta acataggcca
2881 atgcaaaaaa gaggagctgg tgagtgaag taagaacaga aagacatgga ggcaagctct
2941 atagaataat agccaact taaacttaca cttaacagcg tgataggtat tgttccaaac
3001 acattaaatt catttaattg tccttcatg tctatgtatt tgggtgattat tatccttatt
3061 attcacattg ctgagtgtat tattctgttc tcatgatgct gatagagaca taccgagac
3121 tggataactt attaaaaaaa aaaagggtta atggactcac agttccacgt ggatggggag
3181 tcctcacat catggtagaa agcaaaagac acgtcttaca tggcagcagg gaagagagag
3241 aaatgagaac caaacaaga ggggttcccc ttataaaacc atcagcttca atgcaactta
3301 ttcactacca tgagaacagt atgggggaaa ccacccccat gattcaatga tctaccaggt
3361 gcctcccaca acctgtggga attatgggag ctacaattcc agatgagatt tgggtgggga
3421 cacagccaaa ccacatcact gaggaactg agttatagg agattagtaa cgcccaacac
3481 agctggtagg tgggtggagc aggcagctg actctagggt ctggactctg aactgcatca
3541 tgctgccaa gaggttcctc tttttctctc tctctaagtt tcccttattc ccttacagtc
3601 attccttcaa cagcatttcc ttcaccatct tttctacttc tactatataa ttaatttttt
3661 ctctctggtc ccaaaattca acgtgcaaat gcagccttat ataccctaac tcatctttac
3721 ctttagactt tcttccaatg tttctacttc attccatttt aaatttatcc atgagatgcc
3781 tattttacaag ctgtaaccat catgaagtga atgaagaata atacctacta ctgtacaata
3841 gaattccaag agtataaata ggagttatgg ctttctgact tgaaactaaa tacttgatac
3901 ttgattttgc tgtctgagat caatctgaaa agtaataata atcactaaca tttgttgagc
3961 atcaattgtg ggccaagtgt catttcaatc actctgtaca tattaactca tttcatccta
4021 caacaacccg gtgaggcaag ttctgttatt ctgttttaca gttgaggaaa cagaggcata
4081 gagagcttaa gtatgttgcc cagttagatg ccagaagagg agccaggatg ggtctcgggc
4141 agtttaacag cacagctgaa gtcttaacca ctatgccaac agctttttgg tcttacacat
4201 cccatgggaa gaggaaaata aaaaggatc tatttgtata cttttttatt tctgatataa
4261 gaagcagaat tcctttcaca tgacctatgt ctatttaata cgtcattttg aaacttacca
4321 ataaaaattc ccaagcgcca gaaaactgtt agtggctttt tccattcttc tctatttttt
4381 tttgtgctac taattttgct tctttccctc agaaggctgc cggaaatagta aacattcact
4441 gacatgtcat aattactgga aaatgggcac tggaaaatca cattgtaatt aattcaaagc
4501 atgttttcca aatgtactac tttaaattgg agcttatatc ataattcaag gaaacctttg
4561 tgtgtgtact gttccacat gtctcagcct gggatatcca ggagtaattc accttgccgc
4621 tgctccaga ccatttcca tgggaagggg tgacccttg cctcttgga accactattt
4681 ctaagctgcc aacattactc ttgcattatc aacattctaa cttcatggga agggctgtgg
4741 tgagtttctg gaatgtgaat aggaagttgt ttttctaaac agcctgacac tgaggggagg
4801 cagtgaagct gtaagcagtc tgggttgggc agaaggcaga aaaccagcag agtcacagag
4861 gagatg

```

## (2) INFORMATION FOR SEQ ID NO:2616:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 961 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2616

```

1 gtcgaggatc cctaaagtcc tttgaagctt tcatattctg taacttttgt gccaaagaagg
61 ccttacagtg agatgggagc ccagtattta ttgagtttcc tcattcataa aatggggata
121 ataatagtaa atgagttgac acgcgctaag acagtggaaat agtggctggc acagataagc

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181 cctcggtaaa tggtagccaa taatgataga gtatgctgta agatatcttt ctctccctct
241 gcttctcaac aagtctctaa tcaattattc cactttataa acaaggaaat agaactcaaa
301 gacattaagc acttttccaa aggtcgctta gcaagtaaat gggagagacc ctatgaccag
361 gatgaaagca agaaattccc acaagaggac tcattccaac tcatactctg tgaaaagggtt
421 cccaatgccc agctcagatc aactgcctca atttacagtg tgagtgtgct cactcctttt
481 ggggactgta tatccagagg accctcctca ataaaaacact ttataaataa catccttcca
541 tggatgaggg aaaggaggta agatctgtaa tgaataagca ggaactttga agactcagtg
601 actcagttag taataaagac tcagtgaact ctgactcctg cctaactgcc actccttggt
661 gtcccaagaa agcggcttcc tgctctctga ggaggacccc ttccctggaa ggtaaaacta
721 aggatgtcag cagagaaatt tttccacat tggtgcttgg tcaaagagga aactgatgag
781 ctcaactctag atgagagagc agtgaggagg agacagagac tcgaatttcc ggagctatct
841 cagttttctt ttccgttttg tgcaatttca cttatgatac cggccaatgc ttggttgcta
901 ttttggaac tccccttagg ggatgcccct caactggccc tataaagggc cagcctgagc
961 tgcagaggat caagacagca cgtggacctc gcacagcctc tcccacaggt accatg

```

## (2) INFORMATION FOR SEQ ID NO:2617:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1141 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2617

```

1 cctccgacag cctctccaca ggtaccatga aggtctccgc ggcacgcctc gctgtcatcc
61 tcattgctac tgccctctgc gctcctgcat ctgcctcccc atattcctcg gacaccacac
121 cctgctgctt tgccctacatt gcccgcacac tgcccctgac ccacatcaag gagtatttct
181 acaccagtgg caagtgtctc aaccagcag tcgtctttgt caccgaaag aaccgccaag
241 tgtgtgcca cccagagaag aaatgggttc gggagtacat caactcttgg gagatgagct
301 aggatggaga gtccttgaac ctgaacttac acaaatttgc ctgtttctgc ttgctcttgt
361 cctagcttgg gaggttccc ctcaactatc taccacccc gctccttga gggccagat
421 tctgaccacg acgagcagca gtacaaaaa ccttccccag gctggacgtg gtggctcagc
481 cttgtaatcc cagcactttg ggaggccaag gtgggtggat cacttgaggt caggagtctg
541 agacagcctg gccaacatga tgaaacccca tgtgtactaa aaatacaaaa aattagccgg
601 gcgtggtagc gggcgctgt agtcccagct actcgggagg ctgaggcagg agaattggcg
661 gaacccggga gcggagcttg cagtggcggc agatcgcgcc actgcacttc agcctggcgg
721 acagagcgag actccgtctc aaaaaaaaaa aaaaaataca aaaattagcc
781 gcgtggtggc ccacgcctgt aatcccagct actcgggagg ctaaggcagg aaaattgttt
841 gaacccagga ggtggaggct gcagttagct gagattgtgc cacttcactc cagcctgggt
901 gacaaagtga gactccgtca caacaacaac aacaaaaagc tcccccaact aaagcctaga
961 agagcttctg aggcgtgct ttgtcaaaag gaagtctcta ggttctgagc tctggctttg
1021 ccttggcttt gcaaggctc tgtgacaagg aaggaaagtc gcatgcctct agaggcaagg
1081 aaggaggaa cactgcactc ttaagcttcc gccgtctcaa cccctcacag gagcttactg
1141 gcaaacatga aaatcgggg

```

## (2) INFORMATION FOR SEQ ID NO:2618:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2618

```

1 gtcgaggatc cctaaagtcc ttgaagctt tcatactctg taacttttgt gccaaagagg
61 ccttacagtg agatgggagc ccagtattta ttgagtttcc tcattcataa aatggggata
121 ataatagtaa atgagttgac acgcgctaag acagtggaat agtggctggc acagataagc
181 cctcggtaaa tggtagccaa taatgataga gtatgctgta agatatcttt ctctccctct
241 gcttctcaac aagtctctaa tcaattattc cactttataa acaaggaaat agaactcaaa
301 gacattaagc acttttccaa aggtcgctta gcaagtaaat gggagagacc ctatgaccag
361 gatgaaagca agaaattccc acaagaggac tcattccaac tcatactctg tgaaaagggtt
421 cccaatgccc agctcagatc aactgcctca atttacagtg tgagtgtgct cactcctttt
481 ggggactgta tatccagagg accctcctca ataaaaacact ttataaataa catccttcca
541 tggatgaggg aaaggaggta agatctgtaa tgaataagca ggaactttga agactcagtg
601 actcagttag taataaagac tcagtgaact ctgactcctg cctaactgcc actccttggt
661 gtcccaagaa agcggcttcc tgctctctga ggaggacccc ttccctggaa ggtaaaacta
721 aggatgtcag cagagaaatt tttccacat tggtgcttgg tcaaagagga aactgatgag
781 ctcaactctag atgagagagc agtgaggagg agacagagac tcgaatttcc ggagctatct
841 cagttttctt ttccgttttg tgcaatttca cttatgatac cggccaatgc ttggttgcta
901 ttttggaac tccccttagg ggatgcccct caactggccc tataaagggc cagcctgagc
961 tgcagaggat caagacagca cgtggacctc gcacagcctc tcccacaggt accatg
1 cctccgacag cctctccaca ggtaccatga aggtctccgc ggcacgcctc gctgtcatcc
61 tcattgctac tgccctctgc gctcctgcat ctgcctcccc atattcctcg gacaccacac

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121 cctgctgctt tgcctacatt gcccgccac tgccccgtgc ccacatcaag gagtatttct
181 acaccagtg gcaagtgtcc aaccagcagc tegtctttgt caccgaaaag aaccgccaag
241 tgtgtgccaa cccagagaag aaatgggttc gggagtacat caactctttg gagatgagct
301 aggatggaga gtccttgaac ctgaacttac acaaatttgc ctgtttctgc ttgctcttgt
361 cctagcttgg gaggttccc ctcactatcc taccacccc gctccttgaa gggcccagat
421 tctgaccacg acgagcagca gttacaaaaa ccttccccag gctggacgtg gtggctcagc
481 cttgtaatcc cagcactttg ggaggccaag gtgggtggat cacttgaggt caggagttcg
541 agacagcctg gccaacatga tgaacccca tgtgtactaa aaatacaaaa aatttagccg
601 gcgtggttagc gggcgctgt agtcccagct actcgggagg ctgaggcagg agaattggcg
661 gaacccggga gcggagcttg cagtgaagcg agatcgcgcc actgcactcc agcctgggag
721 acagagcgag actccgtctc aaaaaaaaaa aaaaaaaaaa aaaaaataca aaaattagcc
781 gcgtggtggc ccacgcctgt aatcccagct actcgggagg ctaaggcagg aaaattgttt
841 gaacccagga ggtggaggtc gcagtgaagc gagattgtgc cacttcactc cagcctgggt
901 gacaaagtga gactccgtca caacaacaac aacaaaaagc ttccccaact aaagcctaga
961 agagcttctg aggcgtctg ttgtcaaaag gaagtctcta ggttctgagc tctggctttg
1021 ccttggcttt gcaagggtc ttgtgacaag aaggaagtca gcatgcctct agaggcaagg
1081 aagggaggaa cactgcactc ttaagcttcc gccgtctcaa cccctcacag gagcttactg
1141 gcaaacatga aaaatcgagg

```

## (2) INFORMATION FOR SEQ ID NO:2619:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3961 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2619

```

1 attaaacctc tcgccgagcc cctccgcaga ctctgcgccg gaaagtttca tttgctgtat
61 gccatcctcg agagctgtct aggttaacgt tcgcactctg tgtatataac ctcgacagtc
121 ttggcaccta acgtgctgtg cgtagctgct cctttgggtg aatccccagg cccttgttgg
181 ggcacaaggt ggcaggatgt ctcagtgtga cgaacttcag cagcttgact caaaattcct
241 ggagcaggtt caccagcttt atgatgacag ttttcccatg gaaatcacag agtacctggc
301 acagtgggta gaaaagcaag actgggagca cgctgccaat gatgtttcat ttgccaccat
361 ccgttttcat gacctcctgt cacagctgga tgatcaatat agtcgctttt ctttggagaa
421 taacttcttg ctacagcata acataaggaa aagcaagcgt aatcttcagg ataattttca
481 ggaagaccca atccagatgt ctatgatcat ttacagctgt ctgaaggaa aaaggaaaaat
541 tctggaaaac gccagagat ttaatcaggc tcagtcgggg aatattcaga gcacagtgat
601 gttagacaaa cagaaagagc ttgacagtaa agtcagaaat gtgaaggaca aggttatgtg
661 tatagagcat gaaatcaaga gcctggaaga tttacaagat gaatatgact tcaaatgcaa
721 aaccttgtag aacagagaac acgagaccaa tgggtgtggc aagagtgatc agaacaaga
781 acagctgtta ctcaagaaga tgtatttaat gcttgacaat aagagaaagg aagtagttca
841 aaaaataata gagttgctga atgtcactga acttaccagg aatgccctga ttaattgtga
901 actagtggag tggaagcggg gacagcagag cgctgtattt gggggggccc ccaatgcttg
961 cttggatcag ctgcagaact ggttcactat agttgcggag agtctgcagc aagttcggca
1021 gcagcttaaa aagttggagg aattggaaca gaaatacacc tacgaacatg accctatcac
1081 aaaaaacaaa caagtgttat gggaccgcac cttcagctct tccagcagc tcattcagag
1141 ctctgtttgt gtggaaagac agcctgcat gccaacgcac cctcagaggg cgctggctct
1201 gaagacaggg gtccagttca ctgtgaagtt gagactgttg gtgaaattgc aagagctgaa
1261 ttataatttg aaagtcaaag tcttatttga taaagatgtg aatgagagaa atacagtaaa
1321 aggatttagg aagttcaaca ttttgggcac gcacacaaaa gtgatgaaca tggaggagtc
1381 caccaatggc agtctggcgg ctgaatttcg gcacctgcaa ttgaaagaac agaaaaatgc
1441 tggcaccaga acgaatgagg gtctctctcat cgttactgaa gagcttcact cccttagttt
1501 tgaaccccaa ttgtgccagc ctggtttggg aattgacctc gagacgacct ctctgccgt
1561 tgtggtgatc tccaacgtca gccagctccc gagcggttgg gcctccatcc tttggtacaa
1621 catgctgggt gcggaaccca ggaatctgtc cttcttctct actccaccat gtgcacgatg
1681 ggctcagctt tcagaagtgc tgagttggca gttttcttct gtcacaaaaa gaggtctcaa
1741 tgtggaccag ctgaacatgt tgggagagaa gcttcttggg cctaaccgca gccccgatgg
1801 tctcattccg tggacgaggt tttgtaagga aaatataaat gataaaaaat ttcccttctg
1861 gctttggatt gaaagcatcc tagaactcat taaaaaacac ctgctccctc tctggaatga
1921 tgggtgcatc atgggcttca tcagcaagga gcgagagcgt gccctgttga aggaccagca
1981 gccggggacc ttctgtctgc ggttcagtga gagctcccgg gaaggggcca tcacattcac
2041 atgggtggag cggtcccaga acggaggcga acctgacttc catgcggttg aaccttacac
2101 gaagaaagaa ctttctgtct ttactttccc tgacatcatt cgcaattaca aagtcatggc
2161 tgctgagaat attcctgaga atcccctgaa gtatctgtat ccaaatattg acaaaagacca
2221 tgccctttgga aagtattact ccaggccaaa ggaagcacca gagccaatgg aacttgatgg
2281 ccctaaagga actggatata tcaagactga gttgatttct gtgtctgaag ttcaccttct
2341 tagacttcag accacagaca acctgctccc catgtctcct gaggagtttg acgaggtgtc
2401 tcggatagtg ggctctgtag aattcgacag tatgatgaac acagtataga gcatgaattt
2461 ttttcatctt ctctggcgac agtttctctt ctcatctgtg attccctcct gctactctgt

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2521 tccttcacat cctgtgtttc tagggaaatg aaagaaaggc cagcaaattc gctgcaacct
2581 gttgatagca agtgaatttt tctctaactc agaaacatca gttactctga agggcatcat
2641 gcatcttact gaaggtaaaa ttgaaaggca ttctctgaag agtgggtttc acaagtgaag
2701 aacatccaga tacacccaaa gtatcaggac gagaatgagg gtccctttggg aaaggagaa
2761 ttaagcaaca tctagcaaat gttatgcata aagtcagtgc ccaactgtta taggttgttg
2821 gataaatcag tggttattta gggaaactgct tgacgttaga acggtaaaatt tctgtgggag
2881 aattcttaca tgttttcttt gctttaagtg taactggcag ttttccattg gtttacctgt
2941 gaaatagtgc aaagccaagt ttatatacaa ttatatcagt cctctttcaa aggtagccat
3001 catggatctg gtagggggaa aatgtgtatt ttattacatc tttcacattg gctattttaa
3061 gacaaagaca aattctgttt cttgagaaga gaattattgc tttactgttt gttatggctt
3121 aatgacacta gctaatatca atagaaggat gtacatttcc aaattcaciaa gttgtgtttg
3181 atatccaaag ctgaatacat tctgctttca tcttggtcac atacaattat ttttacagtt
3241 ctcccaaggg agttaggcta ttcacaacca ctcattcaaa agttgaaatt aaccatagat
3301 gtagataaac tcagaaattt aattcatggt tcttaaatgg gctactttgt cctttttgtt
3361 attagggtgg tatttagtct attagccaca aaattgggaa aggagttaga aaagcagtaa
3421 ctgacaactt gaataatata ccagagataa tatgagaatc agatcatttc aaaactcatt
3481 tcctatgtaa ctgcattgag aactgcata ttttcgctga tatatgtgtt tttcacattt
3541 gcgaatggtt ccattctctc tctgtactt tttccagaca cttttttgag tggatgatgt
3601 ttcgtgaagt atactgtatt tttacctttt tcttccctta tcaactgacac aaaaagttaga
3661 ttaagagatg ggtttgacaa ggttcttccc ttttacatac tgctgtctat gtggctgtat
3721 cttgtttttc cactactgct accacaacta tattatcatg caaatgctgt attcttcttt
3781 ggtggagata aagatttctt agtttttgtt ttaaaattaa agctaaagta tctgtattgc
3841 attaaatata atatcgacac agtgctttcc gtggcactgc atacaatctg aggcctctc
3901 tctcagtttt tatatagatg gcgagaacct aagtttcagt tgattttaca attgaaatga
3961 ctaaaaaaca aagaagacaa cattaataaac aatattgttt cta

```

## (2) INFORMATION FOR SEQ ID NO:2620:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2581 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2620

```

1 attaaacctc tcgccgagcc cctccgcaga ctctgcgcgc gaaagtttca tttgctgtat
61 gccatcctcg agagctgtct aggttaacgt tcgcactctg tgtatataac ctcgacagtc
121 ttggcaccta acgtgctgtg cgtagctgct cctttggttg aatccccagg ccctgtgttg
181 ggcacaaggt ggcaggatgt ctcatgtgta cgaacttcag cagcttgact caaaattcct
241 ggagcaggtt caccagcttt atgatgacag ttttcccatg gaaatcagac agtacctggc
301 acagtgtgta gaaaagcaag actgggagca cgctgccaat gatgtttcat ttgccacctt
361 ccgttttcat gacctcctgt cacagctgga tgatcaatat agtcgctttt ctttggagaa
421 taacttcttg ctacagcata acataaggaa aagcaagcgt aatcttcagg ataattttca
481 ggaagaccca atccagatgt ctatgatcat ttacagctgt ctgaaggag aaaggaaaat
541 tctggaaaac gccagagat ttaatcaggc tcagtcgggg aatattcaga gcacagtgat
601 gttagacaaa cagaaagagc ttgacagtaa agtcagaaat gtgaaggaca aggttatgtg
661 tatagagcat gaaatcaaga gcctggaaga tttacaagat gaatatgact tcaaatgcaa
721 aaccttgtag aacagagaac acgagaccaa tgggtgtggca aagagtgtac agaacaaga
781 acagtgttta ctcaagaaga tgtatttaat gcttgacaat aagagaaagg aagtgtttca
841 caaaataata gagttgctga atgtcactga acttaccag aatgcctga ttaattatga
901 actagtggag tggaaagcga gacagcagag cgctgtattt ggggggcccgc ccaatgcttg
961 cttggatcag ctgcagaact ggttcaactat agttgcggag agtctgcagc aagttcggca
1021 gcagcttaaa aagttggagg aattggaaca gaaatacacc tacgaacatg accctatcac
1081 aaaaaacaaa caagtgttat gggaccgcac ctacagcttt ttccagcagc tcattcagag
1141 ctcgtttgtg gtggaaagac agccctgcac gccaacgcac cctcagaggc cgtgtgtctt
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1261 ttataatttg aaagtcaaa tcttatttga taaagatgtg aatgagagaa atacagttaa
1321 aggttttagg aagttcaaca ttttgggcac gcacacaaaa gtgatgaaca tggaggagtc
1381 caccaatggc agtctggcgg ctgaatttcg gcacctgcaa ttgaaagaa agaaaaatgc
1441 tggcaccaga acgaatgagg gtctctctcat cgttactgaa gagcttcaat cccttagttt
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1621 catgctggtg gcggaaccca ggaatctgtc cttcttctct actccaccat gtgcacgatg
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1981 gccggggacc ttcctgctgc ggttcagtga gagctcccgg gaaggggcca tcacattcac
2041 atgggtggag cggtcccaga acggaggcga acctgacctc catgcggttg aacctacac
2101 gaagaaagaa ctttctgctg ttactttccc tgacatcatt cgcaattaca aagtcatggc

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2161 tgctgagaat attcctgaga atccccgtgaa gtatctgtat ccaaatattg acaaagacca  
2221 tgccttttga aagtattact ccaggccaaa ggaagcacca gagccaatgg aacttgatgg  
2281 ccctaaagga actggatata tcaagactga gttgatttct gtgtctgaag tgtaagtga  
2341 cacagaagag tgacatgttt acaaacctca agccagcctt gctcctggct ggggcctgtt  
2401 gaagatgctt gtattttact tttccattgt aattgctatc gccatcacag ctgaacttgt  
2461 tgagatcccc gtgttactgc ctatcagcat tttactactt taaaaaaaaa aaaaaaagcc  
2521 aaaaaccaa tttgtattta aggtatataa attttccaa aactgatacc ctttgaaaaa  
2581 gtataaataa aatgagcaaa agttgaa

## (2) INFORMATION FOR SEQ ID NO:2621:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2621

1 ttactaagat gattattgtt ttatagcaat tgaaagaaca gaaaaatgct ggcaccagaa  
61 cgaatgaggt gagagtgggt tatgttgtga atgggcc

## (2) INFORMATION FOR SEQ ID NO:2622:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2622

1 acgacctctc tgcccgttgt ggtgatctcc aacgtcagcc agtccccgag cggttgggcc  
61 tccatccttt ggtacaacat gctggtgtg gcggaaccca gggataggaa aacacatttg  
121 ctttggtccc aggttttaag cagagacccc acgctctcgc tgctgcatct cgctgtgca  
181 tctctgaaat agcccaat

## (2) INFORMATION FOR SEQ ID NO:2623:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2623

1 ggtctcaatg tggaccagct gaacatgttg ggagagaagc ttcttggtat atgcatatta  
61 acttggtatg tttataaaaa ttgaaattca taaaaatc

## (2) INFORMATION FOR SEQ ID NO:2624:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2624

1 ctgatcagta gaaaacatgt ttacatcttt gttgtagt tatagagcat gaaatcaaga  
61 gcctggaaga tttacaagat gaatatgact tcaaatgcaa aaccttgag aacagaggta  
121 aggttcaca actgaagtgg tgcccgttg

## (2) INFORMATION FOR SEQ ID NO:2625:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6966 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2625

1 attaaacctc tcgccgagcc cctccgaga ctctgcgcg gaaagtcca tttgtgtat  
61 gccatcctcg agagctgtct aggttaactg tcgcactctg tgtatataac ctgcacagtc  
121 ttggcaccta acgtgctgtg cgtagctgct cctttggttg aatccccagg cccttggtg  
181 ggcacaaggt ggcaggatgt ctcatgtgta cgaacttcag cagcttgact caaaattcct  
241 ggagcagggt caccagcttt atgatgacag tttcccatg gaaatcagac agtacctggc  
301 acagtgggta gaaaagcaag actgggagca cgctgccaat gatgtttcat ttgccaccat  
361 ccgttttcat gacctcctgt cacagctgga tgatcaatat agtcgctttt ctttgagaa  
421 taactttctg ctacagcata acataaggaa aagcaagcgt aatcttcagg ataatttca  
481 ggaagacca atccagatgt ctatgatcat ttacagctgt ctgaaggag aaaggaaaaat  
541 tctggaaaac gccagagat ttaatcaggc tcagtcgggg aatattcaga gcaagtgtat  
601 gttagacaaa cagaaagagc ttgacagtaa agtcagaaat gtgaaggaca aggttatgt  
661 tatagagcat gaaatcaaga gcctggaaga tttacaagat gaatatgact tcaaatgcaa

721 aaccttgcag aacagagaac acgagacca tgggtgtggca aagagtgtatc agaaacaaga  
781 acagctgtta ctcaagaaga tgtatttaac gcttgacaat aagagaaagg aagtagttca  
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901 actagtggag tgaagcggg gacagcagag cgcctgtatt gggggggccc ccaatgcttg  
961 cttggatcag ctgcagaact ggttcactat agttgaggag agtctgcagc aagttcggca  
1021 gcagcttaaa aagttggagg aattggaaca gaaatacacc tacgaacatg accctatcac  
1081 aaaaaacaaa caagtgttat gggaccgcac cttcagtcct ttccagcagc tcattcagag  
1141 ctctgttgtg gtggaagac agccctgcat gccaacgcac cctcagaggc cgctggtctt  
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1261 ttataatttg aaagtcaaa gctttattga taaagtgtg aatgagagaa atacagttaa  
1321 aggatttagg aagttcaaca ttttgggcac gcacacaaaa gtgatgaaca tggaggagtc  
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1561 tgtggtgatc tccaacgtca gccagctccc gagcggttg gctccatcc tttggtacaa  
1621 catgctggtg gcggaaccca ggaatctgtc cttcttcttg actccaccat gtgcacgatg  
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1981 gccggggacc ttctgctgct ggttcagtga gagctcccgg gaaggggcca tcacattcac  
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2221 tgcttttga aagtattact ccaggccaaa ggaagcacca gagccaatgg aacttgatgg  
2281 ccctaaagga actggatata tcaagactga gttgatttct gtgtctgaag ttcaccttc  
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2761 ttaagcaaca tctagcaaat gttatgcata aagtcagtc ccaactgtta taggttggtg  
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2881 aattcttaca tgttttctt gctttaagtg taactggcag ttttccattg gtttacctgt  
2941 gaaatagttc aaagccaagt ttatatcaa ttatatcagt cctctttcaa aggtagccat  
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3421 ctgacaactt gaataataca ccagagataa tatgagaatc agatcatttc aaaactcatt  
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3541 gcgaatggtt ccattctctc tctgtactt tttccagaca cttttttgag tggatgatgt  
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3661 ttaagagatg ggtttgacaa ggttcttccc ttttacatac tgctgtctat gtggctgtat  
3721 cttgtttttc cactactgct accacaacta tattatcatg caaatgctgt attcttctt  
3781 ggtggagata aagatttctt gaggtttgtt ttaaaattaa agctaaagta tctgtattgc  
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3961 ctaaaaaaca aagaagacaa cattaaaaac aatattgttt cta  
1 attaaacctc tcgccgagcc cctccgcaga ctctgcgccg gaaagtttca tttgctgtat  
61 gccatcctcg agagctgtct aggttaacgt tcgactctg tgtatataac ctgcagagtc  
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241 ggagcaggtt caccagcttt atgatgacag ttttccatg gaaatcagac agtaccctggc  
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121 ctttggccc aggttttaag cagagacccc acgctctcgc tgctgcatct cgctgctgca  
181 tctctgaaat agcccaat  
1 ggtctcaatg tggaccagct gaacatgttg ggagagaagc ttcttggtat atgcatatta  
61 attgttatg ttataaaaa ttgaaattca taaaaatc  
1 ctgtacgta gaaaacatgt ttacatcttt gttgtagtg tatagagcat gaaatcaaga  
61 gcctggaaga ttacaagat gaatatgact tcaaatgcaa aacctgagc aacagaggta  
121 agggttcaca actgaagtgg tgcccggttg

## (2) INFORMATION FOR SEQ ID NO:2626:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18601 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2626

1 tcaagatcag cctgggcaac atggcgaaac cccgtctcta caataaatac aaaaaaatta  
61 tcttgccgga gttatgcag ttgtagtccc aactacctgg gaggtgagg cgggagaatc  
121 acctgagcct gggaggctga ggctgcagc agccgagatc ggccgctgca ttccagcctg  
181 ggtgacagag cgagaccatg tctcaaaaaa taaaaattaa aaaaaaattg ttttcattac  
241 ctacagccctc ctcttctat cccaaggcgt cgaaattccg gtcccacccc ttcccatgga  
301 gcccttgccg tctccaggct cctcaagcta gtttcggttc cgggctcacg cgggggttct  
361 cgaaaaatcag ctgtttcagt cttgggctag tccactaatt ggactcctcc cctcgtagaa  
421 agtgcctact tgaacttctc caccaatcgc tgaagctgca ggtgtggttt cggtcagct  
481 tgtcccgccc tggcggaggg gcggagtgtc ggccgcgcca gtgagctcgc agtctgggaa  
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2581 aaaaaaaaaa aagaaaaaaa aaagcttcag agccagcagg gatcatgctg taataatac  
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2701 acataaatgc aaaataaatg aattagggag atagatgaaa taagattgtg gaaatagtaa  
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16261 ccgcctcagc ctcccaagt gcttggtatc caggtgtgag ccacctggcc tgagagtta  
16321 ttatgcgcca ggcactaggc aaatggtttg catttatttt ctattttat tgaatctaca  
16381 aaatagctct gtgaagtaaa cactgttact gttttcagct aaggaaactg atttagagta  
16441 gtcaagtttt gtacctagg tacgtggcta atgatacagg totgttagat tccgtagccc  
16501 tgattttaac caccctactg cctctcaaga attactaggt attgttctca tttatagatg  
16561 ataaatctga ggctcagaaa agttaggcca ctgacctag gtccccagc caggattcaa  
16621 actccaggag gcctgattcc aaacctatgc tctttagccc tccgcctac tgccttctta  
16681 gactagcttc tgcttattct accattcctg atttcatttg aaccactgag cctgcccct  
16741 ttgtctgtct ttgggtatcc aggcagggtg atgaactgca acaaccgctg gagcttaagc  
16801 cagagccaga gctggagtca ttagagctgg aactagggtt ggtgccagag ccagagctca  
16861 gcctggactt agagccactt ctgaaggcag ggtggtatct ggggccagag ctgagctctg  
16921 tgetggagtc cactctggag cctgtgatag agcccacact atgcatggta tcacaaacag  
16981 tgccagagcc agaccaagga cctgtatcac agccagtgc agagccagat ttgcccgtg  
17041 atctgagaca tttgaacact gagccaatgg aaagtaagt atgagatgga gtggcacaca  
17101 ttccctttcc tactcttctt cctctccca ttacagaaaa agctgaactc caagctctc  
17161 attggagaga ggtccatctg tgattccttt ttttaggaat tacacatgcc tccccacc  
17221 tccctgctct ttcatccac aagttccac tcaggctctt cccaggcctt tccctgcatc  
17281 ctccctccct tgggtgctg ggttgggaac tctaactaa gatcggggcc tcaattttct  
17341 ctctggatta cctagtctc agaaactgtg taaagattga agaaatcatg ccgaatggtg

17401 acccactgtt ggctggccag aacaccgtgg atgaggttta cgtctcccgc cccagccact  
17461 tctacactga tggacccttg atgccttctg acttctagga accacatttc ctctgttctt  
17521 ttcatactct tttgcccttc ctactcctca tagcatgata ttgttctcca aggatgggaa  
17581 tcaggcatgt gtcccttcca agctgtgtta actgttcaaa ctcaggcctg tgtgactcca  
17641 ttgggggtgag aggtgaaagc ataacatggg tacagagggg acaacaatga atcagaacag  
17701 atgctgagcc ataggtctaa ataggatcct ggaggctgcc tgctgtgctg ggaggtatag  
17761 gggtcctggg ggcaggccag ggcagttgac aggtacttgg agggctcagg gcagtggett  
17821 ctttccagta tggaaggatt tcaacatttt aatagttggt taggctaaac tgggtgcatac  
17881 tggcattggc ctggttggg agcacagaca caggatagga ctccatttct tcttccatt  
17941 ccttcattgtc taggataact tgctttcttc tttcctttac tcttggtcca agccctgaat  
18001 ttcttctttt cctgcagggg ttgagagctt tctgccttag cctaccatgt gaaactctac  
18061 cctgaagaaa gggatggata ggaagtagac ctcttttctt taccagtctc ctcccctact  
18121 ctgcccccta agctggctgt acctgttctt cccccataaa atgatcctgc caatctaatg  
18181 tgagtgtgaa gtttgacacac tagtttatgc tacctagtct ccactttctc aatgcttagg  
18241 agacagatca ctccctggagg ctggggatgg taggattgct ggggattttt ttttttttaa  
18301 agaggggtctc actctgttgc ccaggctaga gtgcaatggt gcaatcacag ctactgcag  
18361 cctcaacctc ctgggttcaa gcaatctccc tacctcagcc tctgggttag ctagcaccat  
18421 ggcacgcca ccatgcccta tttttttttt ttaaagacag ggtcttgcta tattgccag  
18481 gctggtcttg aactgggctc aagtgtacct cacgccttgc ctcccaaagt gctgggatta  
18541 taggcatgag ccactgtgct tggccaggat tttttttttt ttttttttga gatggagttt  
18601 ctctcttgtt gtccaggctg gagtgcgaat gtgtgatccg gggaattc

## (2) INFORMATION FOR SEQ ID NO:2627:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2761 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2627

1 cagctggaat tcggggcgcc ggcgcagact gggaggggga gccgggggtt ccgacgtcgc  
61 agccgaggga acaagcccca accggatcct ggacaggcac cccggcttgg cgctgtctct  
121 cccctcggc tcggagagc ccttcggcct gagggagcct cgcgcgccgt ccccggcaca  
181 cgcgcagccc cggcctctcg gcctctgccg gagaaacagg atggcccaat ggaatcagct  
241 acaggagctt gacacacggt acctggagca gctccatcag ctctacagt acagcttccc  
301 aatggagctg cggcagtttc tggcccttg gattgagagt caagattggg catatgcggc  
361 cagcaaagaa tcacatgcc a tttgtgtt tcataatctc ctgggagaga ttgaccagca  
421 gtatagccgc ttcttgcaag agtcgaatgt tctctatcag cacaatctac gaagaatcaa  
481 gcagtttctt cagagcaggt atcttgagaa gccaatggag attgcccga ttgtggccc  
541 gtgcctgtgg gaagaatcac gcctctaca gactgcagcc actgcccgcc agcaaggggg  
601 ccaggccaac caccacacag cagccgtggt gacggagaag cagcagatgc tggagcagca  
661 ccttcaggat gtccggaaga gactgtcagga tctagaacag aaaatgaaag ttgtagagaa  
721 tctccaggat gactttgatt tcaactataa aacctcaag agtcaaggag acatgcagaa  
781 tctgaatgga aacaaccagt cagtaccag gcagaagatg cagcagctgg aacagatgct  
841 cactgcgctg gaccagatgc ggagaagcat cgtgagttag ctggcggggc tttgtcagc  
901 gatggagtac gtgcagaaaa ctctacagga cgaggagctg gctgactgga agaggcggca  
961 acagattgcc tgcattggag gcccgcccaa catctgccta gatcggctag aaaactggat  
1021 aacgtcatta gcagaatctc aacttcagac ccgtcaacaa attaaagaaac tggaggagtt  
1081 gcacaaaaaa gtttcttaca aaggggaccc cattgtacag caccggccga tgctggagga  
1141 gaggatcgct gagctgttca gaaacttaat gaaaagtgc tttgtgttg agcggcagcc  
1201 ctgcatgccc atgcacctcg accggccctt cgctcatcag accggcgctc agttcactac  
1261 taaagtcagg ttgtgtgtca agttccctga gttgaattat cagcttaaaa ttaaagtgtg  
1321 cattgacaaa gactctgggg acgttgagc tctcagagga tcccggaaat ttaacattct  
1381 gggcacaac acaaaagtga tgaacatgga agaattcaac aacggcagcc tctctgcaga  
1441 attcaaacac ttgaccctga gggagcagag atgtgggaat gggggccgag ccaattgtga  
1501 tgcttccctg attgtgactg aggagctgca cctgatcacc tttgagaccg aggtgtatca  
1561 ccaaggtctc aagattgacc tagagacca ctcttgta gttgtgttg tctccaacat  
1621 ctgtcagatg ccaaatgcct gggcgcccat cctgtgttac aacatgtcga ccaacaatcc  
1681 caagaatgtg aacttcttca ctaagccgcc aattggaacc tgggaccaag tggccgaggt  
1741 gctcagctgg cagttctcgt ccaccaccaa gcgggggctg agcatcgagc agctgacaac  
1801 gctggctgag aagctcctag ggcctggtgt gaactactca ggtgtcaga tcacatgggc  
1861 taacttctgc aaagaaaaca tggctggcaa ggcttctcc tactgggtct ggctagacaa  
1921 tatcatcgac cttgtgaaaa agtatatctt ggcccttgg aatgaagggt acatcatggg  
1981 tttcatcagc aaggagcggg agcgggccat ctgagcact aagccccag gcaccttct  
2041 gctgcgcttc agtgaaagca gcaaaagaag agcgctcact ttcacttggg tggagaagga  
2101 catcagcggg aagacccaga tccagtcctg ggaaccatac acaaagcagc agctgaacaa  
2161 catgtcattt gctgaaatca tcatgggcta taagatcatg gatgctacca atatcctgtt  
2221 gtctccactt gtctatctct atcctgacat tcccaaggag gaggcattcg ggaagtattg  
2281 tcggccagag agccaggagc atcctgaagc tgaccaggt agcgtgccc catacctgaa  
2341 gaccaagttt atctgtgtga caccaacgac ctgcagcaat accattgacc tggcgatgct

2401 ccccccgcgt ttagattcat tgatgcagtt tggaaataat ggtgaagggtg ctgaaccctc  
 2461 agcaggaggg cagtttgagt ccctcacctt tgacatggag ttgacctcg agtgcgctac  
 2521 ctcccccatg tgaggagctg agaacggaag ctgcagaaag atacgactga ggcgccctacc  
 2581 tgcattctgc caccctcac acagccaaac cccagatcat ctgaaactac taactttgtg  
 2641 gttccagatt ttttttaatc tcctacttct gctatctttg agcaatctgg gcacttttaa  
 2701 aaatagagaa atgagtgaat gtgggtgatc tgcttttatt taaatgcaaa taaggatgtg  
 2761 ttctctgaga cccatgatca ggggatg

## (2) INFORMATION FOR SEQ ID NO:2628:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2628

1 cgacagcgac cagatcaagg aggaactgcc ggagcccttt gagcatcttc tgcagagaat  
 61 cgcccggaga cccaagcctc agcagttctt tggattaatg ggcaaacggg atgctggaca  
 121 tggccagatc tctcacaaaa gacataaaac agattccttt gttggactaa tgggcaaaag  
 181 agcttttaaat tctgtggctt atgaaaggag tgcaatgca

## (2) INFORMATION FOR SEQ ID NO:2629:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2629

1 gagagtgcgg agcgaccacg tgcgctcgga ggaaccagag aaactcagca ccccgcgga  
 61 ctgtccgtcg caaaatccaa catgaaaatc ctctgtggct tggcagtctt ttttcttgc  
 121 tccactcagc tgtttcgaga agaaatagga gccaatgatg atctgaatta ctggctccgac  
 181 tggtagcaga gcgaccagat caaggaggaa ctgccggagc cttttgagca tcttctgcag  
 241 agaattcgccc ggagacccaa gcctcagcag ttctttggat taatgggcaa acgggatgct  
 301 gattcctcaa ttgaaaaaca agtggccctg ttaaaggctc tttatggaca tggccagatc  
 361 tctcacaaaa gacataaaac agattccttt gttggactaa tgggcaaaag agcttttaaat  
 421 tctgtggctt atgaaaggag tgcaatgcag aattatgaaa gaagacgtta ataaactacc  
 481 taacattatt tattcagctt cattttgtgc aatgggcaat gacaggtaaa ttaagacatg  
 541 cactatgagg aataattatt tatttaataa caattgttta gggttgaaaa ttcaaaaagt  
 601 gtttattttt catattgtgc caatatgtat tgtaaacatg tgttttaatt ccaatatgat  
 661 gactccctta aaatagaaat aagtgtttat ttctcaacaa agcacagtgt taaatgaaat  
 721 tgtaaaacct gtcaatgata cagtccttaa agaaaaaaa tcattgcttt gaagcagttg  
 781 tgtcagctac tgcggaaaag gaaggaaact cctgacagtc ttgtgctttt cctatttgtt  
 841 ttcattgtga aaatgtactg agatttttgt attacactgt attgtatct ctgaagcatg  
 901 tttcatgttt tgtgactata tagagatgtt tttaaaagt tcaatgtgat tctaattgtc  
 961 tcatttcatt gtatgatgtg ttgtgatagc taacatttta aataaaagaa aaaatatctt  
 1021 g

## (2) INFORMATION FOR SEQ ID NO:2630:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2581 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2630

1 ggcgcgcaag gcaactgagca ggcgaaagag cgcgctcgga cctccttccc ggcggcagct  
 61 accgagagtg cggagcgacc agcgtgcgct cggaggaaac agagaaactc agcaccctgc  
 121 gggactgtcc gtcgcaaaat ccaacatgaa aatcctcgtg gccttggcag tctttttct  
 181 tgtctccact cagctgtttg cagaagaaat aggagccaat gatgatctga attactggtc  
 241 cgactggtag gacagcgacc agatcaagga ggaactgccg gagccctttg agcatcttct  
 301 gcagagaatc gcccggagac ccaagcctca gcagttcttt ggattaatgg gcaaacggga  
 361 tgctgattcc tcaattgaaa aacaagtggc cctgttaaag gctctttatg gacatggcca  
 421 gatctctcac aaaagacata aaacagattc ctttgttggg ctaatgggca aaagagcttt  
 481 aaattctgtg gcttatgaaa ggagtgcatt gcagaattat gaaagaagac gtttaataac  
 541 tacctaacat tattttattc gtttcatttg tgtcaatggg caatgacagg taaattaaga  
 601 catgactat gaggaataat tattttatta ataacaattg tttggggttg aaaattcaaa  
 661 aagtgtttat ttttcatatt gtgccaatat gtattgtaaa catgtgtttt aattccaata  
 721 tgatgactcc cttaaaatag aaataagtgg ttatttctca acaaagcaca gtgttaaatg  
 781 aaattgtaaa acctgtcaat gatacagtc ctaaagaaaa aaaatcattg ctttgaagca  
 841 gttgtgtcag ctactgcgga aaaggaagga aactcctgac agtcttgtgc ttttcttatt  
 901 tgttttcatg gtgaaaatgt actgagattt tggatttaca ctgtatttgt atctctgaag  
 961 catgtttcat gttttgtgac tatatagaga tgtttttaaa agtttcaatg tgattcctaat

1021 gtcttcattt cattgtatga tgtgttgta tagctaacaat tttaaataaa agaaaaaata  
1081 tcttgaaaaa aaaaaaaaaa aa

## (2) INFORMATION FOR SEQ ID NO:2631:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2631

1 cgacagcgac cagatcaagg aggaactgcc ggagcccttt gagcatcttc tgcagagaat  
61 cgcccgga cccaagcctc agcagttctt tggattaatg ggcaaacggg atgctggaca  
121 tggccagatc tctcacaata gacataaac agattccttt gttggactaa tgggcaaaag  
181 agctttaaat tctgtggctt atgaaaggag tgcaatgca  
1 gagagtgcgg agcgaccacg tgcgctcgga ggaaccagag aaactcagca ccccgcgga  
61 ctgtccgtcg caaatccaa catgaaaatc ctggtggcct tggcagttt ttttctgtc  
121 tccactcagc tgtttgcaga agaaatagga gccaatgatg atctgaatta ctggtccgac  
181 tggtagcaga gcgaccagat caaggaggaa ctgccggagc ctttgagca tcttctgcag  
241 agaatcgccc ggagaccacg gcctcagcag ttctttggat taatgggcaa acgggatgct  
301 gattcctcaa ttgaaaaaca agtggccctg ttaaaggctc tttatggaca tggccagatc  
361 tctcacaata gacataaac agattccttt gttggactaa tgggcaaaag agctttaaat  
421 tctgtggctt atgaaaggag tgcaatgcag aattatgaaa gaagacgtta ataaactacc  
481 taacattatt tattcagctt catttgtgtc aatgggcaat gacaggtaaa ttaagacatg  
541 cactatgagg aataattatt tattaataa caattgttta ggggtgaaaa ttcaaaaagt  
601 gtttattttt catattgtgc caatatgtat tgtaaacatg tgttttaatt ccaatatgat  
661 gactccctta aaatagaaat aagtgttat ttctcaaca agcacagtgt taaatgaaat  
721 tgtaaaacct gtcaatgata cagtccttaa agaaaaaaa tcattgcttt gaggcagttg  
781 tgtcagctac tgcggaaaag gaaggaaact cctgacagtc ttgtgctttt cctatttgtt  
841 ttcatgggtg aaatgtactg agattttggt attacactgt atttgtatct ctgaagcatg  
901 tttcatgttt tgtgactata tagagatgtt tttaaaagtt tcaatgtgat tctaattgtc  
961 tcatttcatt gtatgatgtg ttgtgatagc taacatttta aataaaagaa aaaatatctt  
1021 g  
1 gcgcccgaag gcactgagca ggcgaaagag cgcgctcgga cctccttccc ggcggcagct  
61 accgagagtg cggagcgacc agcgtgctgt cggaggaacc agagaaactc agcaccctgc  
121 gggactgtcc gtgcgaaaat ccaacatgaa aatcctcgtg gccttggcag tttttttct  
181 tgtctccact cagctgtttg cagaagaaat aggagccaat gatgatctga attactggtc  
241 cgactggtac gacagcgacc agatcaagga ggaactgccg gagccctttg agcatcttct  
301 gcagagaatc gcccgagac ccaagcctca gcagttcttt ggattaatgg gcaaacggga  
361 tgctgattcc tcaattgaaa aacaagtggc cctgttaaag gctctttatg gacatggcca  
421 gatctctcac aaaagacata aaacagattc ctttgttga ctaatgggca aaagagcttt  
481 aaattctgtg gcttatgaaa ggagtgcatt gcagaattat gaaagaagac gtaataaac  
541 tacctaaccat tatttattca gcttcatttg tgtcaatggg caatgacagg taaattaaga  
601 catgcactat gaggaataat ttttattta ataacaattg tttggggttg aaaattcaaa  
661 aagtgtttat tttcatatt gtgccaatat gtattgtaaa catgtgtttt aattccaata  
721 tgatgactcc cttaaaatag aaataagtgg ttatttctca acaaagcaca gtgttaaatg  
781 aaattgtaaa acctgtcaat gatacagtc ctaaagaaaa aaatcattg ctttgaagca  
841 gttgtgtcag ctactgcgga aaaggaagga aactcctgac agtcttgtgc ttttctatt  
901 tgttttcatt gtgaaaatgt actgagattt tggatttaca ctgtatttgt atctctgaag  
961 catgtttcat gttttgtgac tatatagaga tgtttttaa agtttcaatg tgattcta  
1021 gtcttcattt cattgtatga tgtgttgta tagctaacaat tttaaataaa agaaaaaata  
1081 tcttgaaaaa aaaaaaaaaa aa

## (2) INFORMATION FOR SEQ ID NO:2632:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2632

1 gaaaaagcct tccacctcc tgtctggctt tagaaggacc ctgagcccca ggcgccagca  
61 caggactctg ctgcagaggg ggggtgtgta cagatagtag ggctttaccg ctagcttctg  
121 aaatggataa cgtcctcccg gtggactcag acctctcccc aaacatctcc actaacacct  
181 cggaacccaa tcagttcgtg caaccagcct ggcaaatgtt cctttgggca gctgcctaca  
241 cggtcattgt ggtgacctct gtggtgggca acgtggtagt gatgtggatc atcttagccc  
301 acaaaaagaat gaggacagtg acgaactatt ttctggtgaa cctggccttc gcggaggcct  
361 ccattggctg attcaatata gtggtgaact tcacctatgc tgtccacaac gaatgggtact  
421 acggcctgtt ctactgcaag ttccacaact tcttccccat gcgcgctgtc ttcgccagta  
481 tctactccat gacggctgtg gcctttgata ggtacatggc catcatacat cccctccagc



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541 cccggtgtgc agccacagcc accaaagtgg tcatctgtgt catctgggtc ctggtctctc
601 tgctggcctt cccccagggc tactactcaa ccacagagac catgcccagc agagtcgtgt
661 gcatgatcga atggccagag catccgaaca agatttatga gaaagtgtac cacatctgtg
721 tgactgtgct gatctacttc ctccccctgc tgggtgattg ctatgcatac accgtagtgg
781 gaatcacact atgggcccagt gagatccccg gggactcctc tgaccgctac caccagcaag
841 tctctgccaa gcgcaaggtg gtcaaaatga tgattgtcgt ggtgtgcacc ttcgccatct
901 gctggctgcc cttccacatc ttcttctctc tgccctacat caaccagat ctctacctga
961 agaagtttat ccagcaggtc tacctggcca tcatgtggct ggccatgagc tccacctagt
1021 acaaccccat catctactgc tgcctcaatg acaggttcct tctgggcttc aagcatgcct
1081 tccgggtgtg ccccttcac agcgccggcg actatgaggg gctggaaatg aaatccaccc
1141 ggtatctcca gaccagggc agtgtgtaca aagtcagccg cctggagacc accatctcca
1201 cagtgggtgg ggcccacgag gaggagccag aggacggccc caaggccaca ccctgtctcc
1261 tggacctgac ctccaactgc tcttcacgaa gtgactccaa gacctgaca gagagcttca
1321 gcttctctc caatgtgtc tcttaggcca cagggccttt ggcaggtgca gccccactg
1381 cctttgacct gctcctctc atgcatggaa attccttca tctggaacca tcagaaacac
1441 cctcacactg ggacttgcaa aaagggctag tatgggttag ggaaaacatt ccatccttga
1501 gtcaaaaaat ctcaattctt ccctatcttt gccaccctca tgtgtgtga ctcaaaccaa
1561 atcactgaac tttgtgagc ctgtaaaata aaaggtcgga ccagcttttc ccaaaagccc
1621 attcattcca ttctggaagt gactttggct gcatgcgagt gctcatttca ggat

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## (2) INFORMATION FOR SEQ ID NO:2633:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2633

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1 aattcagagc caccgcgggc aggcgggcag tgcattccaga agcgtttata ttctgagcgc
61 cagttcagct ttcaaaaaga gtgctgcca taaaaagcct tccaccctcc tgtctgcttt
121 agaaggacc tgagccccag gcgccagcca caggactctg ctgcagaggg gggttgtgta
181 cagatagtag gctttacgcc tagcttcgaa atggataacg tcctcccggt ggaactcagac
241 ctctcccaa acatctccac taacacctcg gaacccaatc agttcgtgca accagcctgg
301 caaattgtcc tttgggcagc tgctacacg gtcattgtgg tgacctctgt ggtgggcaac
361 gtggtagtga tgtggtcat cttagccac aaaagaatga ggacatgct gaactatttt
421 ctggtgaacc tggccttcgc ggaggcctcc atggtgcat tcaatacagt ggtgaacttc
481 acctatgctg tccacaacga atggtactac ggcctgttct actgcaagtt ccacaacttc
541 tttcccatcg ccgctgtctt cgccagtatc tactccatga cggctgtggc ctttgatagg
601 tacatggcca tcatacatcc cctccagccc cggctgtcag ccacagccac caaagtggtc
661 atctgtgtca tctgggtcct ggctctctct ctggccttcc cccagggcta ctactcaacc
721 acagagacca tgcccagcag agtcgtgtgc atgatcgaat ggccagagca tccgaacaag
781 atttatgaga aagtgtacca catctgtgtg actgtgctga tctacttctt cccctgtctg
841 gtgattggct atgcatacac cgtagtggga atcacactat gggccagtga gatccccggg
901 gactcctctg accgctacca cgagcaagtc tctgccaaag gcaaggtggg caaaatgatg
961 attgtcgtgg tgtgcacctt cgccatctgc tggctgccct tccacatctt ctctctctg
1021 ccctacatca acccagatct ctacctgaag aagtttatcc agcaggtcta cctggccatc
1081 atgtggctgg ccatgagctc caccatgtac aaccccatca tctactgctg cctcaatgac
1141 aggttccgctc tgggcttcaa gcatgccttc cgggtgctgc cttcatcag cgccggcgac
1201 tatgagggcg tggaaatgaa atccaccgg tatctccaga cccagggcag tgtgtacaaa
1261 gtcagccgcc tggagaccac catctccaca gtgggtgggg ccacagagga ggagccagag
1321 gacggcccca aggccacacc ctgctcctg gacctgacct ccaactgtct ttcacgaagt
1381 gactccaaga ccatgacaga gagcttcagc ttctcttcca atgtgtctct ctaggccaca
1441 gggcctttgg caggtgcagc ccccactgcc tttgacctgc ctcccttcat gcatggaaat
1501 tcccttcac tggaaccatc agaaacaccc tcacactggg acttgcaaaa agggtcagta
1561 tgggttaggg aaaacattcc atccttgagt caaaaaatct caattcttcc ctatctttgc
1621 caccctcatg ctgtgtgact caaaccaaat cactgaactt tgtgagcct gtaaaataaa
1681 aggtcggaac agcttttctt caagagccca atgcattcca tttctggaag tgactttggc
1741 tgcattgcag tgcatttcc aggatg

```

## (2) INFORMATION FOR SEQ ID NO:2634:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2634

```

1 gaaaaagcct tccaccctcc tgtctggctt tagaaggacc ctgagcccca ggcggccagc
61 caggactctg ctgcagaggg gggttgtgta cagatagtag ggctttaccg cctagctctg
121 aaatggataa cgtctctccc gtggactcag acctctcccc aaacatctcc actaacacct
181 cggaacccaa tcagtctgtg caaccagcct ggcaaatgt cctttgggca gctgcctaca

```



241 cggtcattgt ggtgacctct gtgggtgggca acgtggtagt gatgtggatc atcttagccc  
 301 acaaaagaat gaggacagt acgaactatt ttctggtaga cctggccctc gcggaggcct  
 361 ccattggctgc attcaataca gtgggtgaact tcacctatgc tgtccacaac gaatggtagt  
 421 acggcctgtt ctactgcaag ttccacaact tcttcccat cgccgcgtgc ttgcgcagta  
 481 tctactccat gacggctgtg gcctttgata ggtacatggc catcatacat cccctccagc  
 541 cccggctgtc agccacagcc accaaagtgg tcatctgtgt catctgggtc ctggctctcc  
 601 tgctggcctt cccccagggc tactactcaa ccacagagac catgcccagc agagtcgtgt  
 661 gcatgatcga atggccagag catccgaaca agatttatga gaaagtgtac cacatctgtg  
 721 tgactgtgct gatctacttc ctcccctgc ttggtattgg ctatgcatac accgtagtgg  
 781 gaatcacact atgggccagt gagatccccg gggactcctc tgaccgctac cagagcaag  
 841 tctctgcaa gcgcaagggt gtcaaaatga tgattgtcgt ggtgtgcacc ttgcctatct  
 901 gctggctgcc cttccacatc ttcttctctc tgccctacat caaccagat ctctacctga  
 961 agaagtttat ccagcaggtc tacctggcca tcatgtggct ggccatgagc tccaccatgt  
 1021 acaaccccat catctactgc tgcctcaatg acaggtgagg atcccaaccc catgagctct  
 1081 ccaggggcca caagaccatc tacatacaca gtggccaagc ggcatcctaa atgagtaaac  
 1141 ccagctgtga gacaagaggg acaagtggg actgcagcta acttatcacc acacaactca  
 1201 gcctggctga ttatcacat ccaggaatgg gagcccgag tagactgatt ttctttttt  
 1261 cttttcca

## (2) INFORMATION FOR SEQ ID NO:2635:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2635

1 atgtgagaa aggtagctgc caaaccttga ctgcaataac aataacaaaa attaaaaacc  
 61 taataataata agtatatcat actgaccttt cctgtttacc ttgctgtagg taccacatct  
 121 gtgtgactgt gctgatctac ttcttcccc tgctggtgat tggctatgca tacaccgtag  
 181 tgggaatcac actatgggcc agtgagatcc cggggactc ctctgaccgc taccacgagc  
 241 aagtctctgc caagcgcaag gtgagcaggg gacaggcaga actaacccac cctggcacag  
 301 acaacaggct gtcgagaagg gatggcacac ttgtgagccc cagaggcagc tagcacaana  
 361 tatccccagg tat

## (2) INFORMATION FOR SEQ ID NO:2636:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2636

1 ggatccaatt ttgcccggc ataagtgtat agtaaatttc ccagccttaa agcacttccc  
 61 gagagatgct ttgagcgctc gcgggtaccag tgcgtaaacg ccgctcccg gctggcgcg  
 121 gtgtgcgcca actccaacct gcgcgcaagt ctgccgtgc gcgctccagt cccacagctc  
 181 cgagtcctccg cagtgaagg agggggcggt gcaccgggt agatgggccc ctgaggactc  
 241 ccgggggttca gttttccgcg gctgccaaga gggccaagt ggacagtggc agggctctga  
 301 agcagatcag caacaaccgc aagtgtctca gccccaggtc ctacagacag gaggaaaacg  
 361 acaagaggcg gacacacaac gtcttggaa gtcagaggag gaacgagctg aagcgcagct  
 421 tttttgccct gcgtgaccag atccctgaat tggaaaacaa cgaaaaggcc cccaaggtag  
 481 tgatcctcaa aaaagccacc gcctacatcc tgtccattca agcagacgag cacaagctca  
 541 cctctgaaaa ggacttattg aggaacagac gagaacagtt gaaacacaaa ctcgaacagc  
 601 ttcgaaactc tggtagcata actgacctaa ctgaggagg agctggaaac tctcgtgaga  
 661 gtaaggagaa cggttccttc tgacagaact gatgcgctgg aattaaaatg catgctcaaa  
 721 gcctaaccctc acaaccttgg ctggggcttt gggactgtaa gcttagagac tgtcacttcc  
 781 cagggtgaatc agctagccag gtaactgagc tagatatatt gtgggggtgt ttccctaaaca  
 841 cagcctcagg aaagtgtgtt tcgggacacc tggaccagg agtcgtcgcc tctggcttct  
 901 cggtagctgg agcgcggccc ggagcgcggc gctggcacat cgccccaca catgaccgtt  
 961 tcccattgac acaggcaagc cgcctctgca gactgtctc agggctcttg gcttcattcc  
 1021 ctggaagttg attgtcctcc actccagctg ttcccaaat ccttccctcc tcccagcacc  
 1081 cctcgtgcac gcagattcc agctgcggac cgcactgtgt tcagttactt ccaagccacc  
 1141 tactgcccc tcgcggagt gctggggctc ccggctcgca gactccacg gcaagtagca  
 1201 agcagcaaaa ggcgtggtag ctgcggcggt ggaatgagac agttgtcaac agctggcgca  
 1261 cgtgccgccc tgcgcaccgg gactggcgag tacgcagccc aggtactgcc ccttcccagt  
 1321 gacgtctctg cagggggtta taaaagctc gtgcgcagct aactcgcag ctgagcaacc  
 1381 cgaaccgaga ggtgcccgcg aaactgcagg cggcggcagc ggcagcaaaa gagaaggaaa  
 1441 aatctccagc tggatacgaa gctccagaat cctggccata ggctcagaac ttttacaggt  
 1501 cgcgtgcaa tgggccccca cttcgtcct aagtcctcac gcagcacagg gctttgcctt  
 1561 tccctgcgga ggaaggagaa ataggagttg caggcagcag caggtgcata aatgcggggg  
 1621 atctcttgct tccagaact gtgaccggtg gaatttcttt cccttttca gtttaccgca

```

1681 agagagatgc tgtctccaga cttctgaact caaacgtctc ctgaagcttg aaagtggagg
1741 aattcagagc caccgcgggc aggcgggcag tgcattccaga agcgtttata ttctgagcgc
1801 cagttcagct ttcaaaaaga gtgctgccca gaaaaagcct tccaccctcc tgtctggctt
1861 tagaaggacc ctgagcccca ggcgccagcc acaggactct gctgcagagg ggggttgtgt
1921 acagatagta gggctttacc gcctagcttc gaaatggata acgtcctccc ggtggactca
1981 gacctctccc caaacatctc cactaacacc tcggaaccca atcagttcgt gcaaccagcc
2041 tggcaaatg tcttttgggc agctgcctac acggtcattg tggtgacctc tgtggtgggc
2101 aacgtggtag tgatgtggat catcttagcc cacaaaagaa tgaggacagt gacgaactat
2161 tttctggtga acctggcctt cgcggaggcc tccatggctg cattcaatac agtggtgaaac
2221 ttcacctatg ctgtccacaa cgaatggtag tacggcctgt tctactgcaa gtccacaaac
2281 ttcttcccca tcgccgctgt cttgccagct atctactcca tgacggctgt ggcctttgat
2341 aggtgagatt agcctttgtg aaaaggcgag aaagtgtcga tagaggacca tggcattgct
2401 gtgaggtttg gaactgggtg gggatatggg caagtggag attggccact ctgaggggtt
2461 ttttactgat ca

```

## (2) INFORMATION FOR SEQ ID NO:2637:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2637

```

1 agaatatgga aaaggaattg gaaaataatt gtacaaatca tcaggaatca aagggtttct
61 atgaattttc ttattggcag gaaaaatatg gaattcttga tacagatttt ggtgaccaga
121 tcagaacttt gttctttctt ctctgttcca ggtacatggc catcatacat cccctccagc
181 cccggctgtc agccacagcc accaaagtgg tcatctgtgt catctgggtc ctggctctcc
241 tgctggcctt cccccagggc tactactcaa ccacagagac catgccagc agagtcgtgt
301 gcattgatga atggccagag catccgaaca agatttatga gaaagtgtga gtagagatga
361 ctccccatgc caaagaaacg atggtgcagg ctgccttctt ggccttctt tttctttct
421 ttctttccat attcttttgt tggtagagat ttaattgtga tctgcaagca tttctcacat
481 ataccctcat atcaggttga tatgtccaca gttgtcagg gactatagta tcccaaatc
541 tattctgagc attgaaagat aatttttgaa gtgtaagatc tagatcctgt tata

```

## (2) INFORMATION FOR SEQ ID NO:2638:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: - base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2638

```

1 gagggggatg tgctggtggt ctacactgtc tcacctctt gccaggtggt caaatgatg
61 attgtcgtgg tgtgcacctt cgccatctgc tggctgccct tccacatctt ctctctctg
121 ccctacatca acccagatct ctacctgaag aagtttatcc agcaggtcta cctggccatc
181 atgtggctgg ccatgagctc caccatgtac aaccccatca tctactgctg cctcaatgac
241 aggtgaggat cccaacccca tgagctctcc aggggccaca agaccatcta catacacagt
301 ggccaagcgg catctaaatg agtaaaccca gctgtgagac aagagggaca agtggggact
361 gcagctaact t

```

## (2) INFORMATION FOR SEQ ID NO:2639:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2639

```

1 ccgtcccaaa ggtcacctct tcatctgtc gctctccagg ttccgtctgg gcttcaagca
61 tgccctccgg tgctgccctt tcatcagcgc cggcgactat gaggggctgg aaatgaaac
121 caccgggtat ctccagaccc aggcagtggt gtacaaagtc agccgcttg agaccacct
181 ctccacagtg gtggggggccc acgaggagga gccagaggac ggccccaagg ccacacctc
241 gtccctggac ctgacctcca actgctcttc acgaagtgc tccaagacca tgacagagag
301 cttcagcttc tctccaatg tgctctcta ggccacaggg cctttggcag gtgcagcccc
361 cactgccttt gacctgcctc cttcatgca tggaaattcc cttcatctgg aaccatcaga
421 aacacctca cactgggact tgcaaaaagg gtcagtatgg gttagggaaa acattccatc
481 cttgagtcga aaaatctcaa ttcttcccta tctttgccac cctcatgctg tgtgactcaa
541 accaaatcac tgaactttgc tgagcctgta aaataaaagg tcggaccagc ttttcccaaa
601 agccattca ttccattctg gaagtgaact tggctgcatg cgagtgtcta ttccaggatg
661 aattctgcag cacagctgcg gacccggaag actcattttc ctggagcccc gtgttacttc
721 aataaagtta tctcagatta gcctcctgca gctggaggct cctatcacc cagcctacgc
781 ttgacagggt gaacaaaaga aggcaccaca taacatctaa atgaaaaatt tagccctgtc
841 ttctaagcat ctgtgaaaag aaacatatgt attcccctt ttggcatctc agtatttcag

```

901 tacatttata catcatgaga ttgagaacct cgggcttcca cattatgtcc ccggtgactg  
961 tcctgagcag ccgacgcaag cagaatatgt ccactgatac ctgctagtcc tcttacagac  
1021 caggaattgg gagacttgca ctacatttaa tgtgtagtgg accctctttt cctacttgta  
1081 aacaagggga ctgaactaga taatctaagt gttccttoga atcttaacat cccgtgggtc  
1141 aaggattgta tgagtttttt gtttgtttta caaaaaaaa caaacgaag aataaaagaa  
1201 tagaaaagaa taggagcagt gagtcttgta actaatccc agttcctgga gatgtagcaa  
1261 ctgctaaggc catctgtaac tatccatctc agacattctc cgatttatct taaaatcctg  
1321 agtacattcc ttctcatgga aggttttggc ttttgacaga gcagaggact tcatgccaa  
1381 gcctgcatcc atccagcttt agcaggcaga atttcatagc tgcagaacac tgtcagagaa  
1441 gacaaatgtg ggctccctgc tttaaccttt tgggtatttt aggggtgggg ccctaacctt  
1501 cattcttagt ttacactag catcgtgctc atatgtgcga caagcaagaa ggctgcactt  
1561 tgcaagctgca cttctgggaa gagggcatct tgcattctcc cttcagactc tctgaatgtc  
1621 tcctccctgc tccatggctt tgccagcttc ctgtctctaa ggggtagaat gactcatcaa  
1681 ccctaaagga cagtcagtct tccaagagcc atgaactgaa tgctttatat cctaatttag  
1741 atttagagtt tcagaagggt gagcatgcag ttttgttttg ttttttttc tgtctccaa  
1801 atctgtgttt tttccagata tggctggaag cagaagcttc atgtaacata aggggagaat  
1861 ctctggtagt ttgcataat ggatgcacat gtgcgcgcatc cataacatta aggggagaat  
1921 aatgcatggt ttacagcctt tgccagccct gctggctcta attctaccag ggcattccaa  
1981 ggccctgggg aagaagaaac agtataagcc agaaaacctc aagaactaca ttctctaaag  
2041 cagcatggaa agttttaaat aaactaagtg aagccagatc attgcagata tataaatgga  
2101 agacaaaatt tagaagcaac aaaagttagt gccctaagca ttagtcatac ttccaataga  
2161 gaatcttgct gtgtatggat tactcacttt ggaagaatgt aaagagctaa catgattatg  
2221 agaagtacct gagaagatgg tgtcaagaag ttggggacac cccatctatg gaagagaagg  
2281 ttagagttga gctcaacgag gattaactga gtgcctctc tggactttgc cctgaactgg  
2341 gaacacacag cccctgcagc tcttgaagag cctacottat tggccatcac taactaactc  
2401 accagtccta gtgagtctaa gctgcccagc agtcttggag gcattctgaga ggacagattc  
2461 tccacagaat tctaaaacc cacactcaac atgggcagtc aagcaaaagc tgggaccttt  
2521 ggagagcctc tggaatgaga gttctctggg gtacttccaa agggagctgg cagtcagtc  
2581 aggggacctc aaggaatttg gttgaacagt atcatctctg tgcatagtaa gagggaatgt  
2641 tgggtggtcc gggcagtttc caatatggca aagcatctgc ttggacagtg ccagcaagcc  
2701 ttcctctgac ccagctctca atgtccacta acttataaaa atgtcatcaa ctcccacatg  
2761 tgagaaacac catgatttgt actgtgcatg ggtcacattc ttattctaga aatgcattac  
2821 cctgtgttta tccaagtgtg tttacttggg gtaatgtcca gtagtaatag aatatgaaat  
2881 atcaaggaac catctttgtt acgtgacttc caaatgtga gatctcattg ctgtcactgt  
2941 gatatttgta ttgtgtgaat ctcttctctc tcttctctct catgctttct caggaggag  
3001 cctgatgta tatcatgaac tcacagttcc tagaccacag taattgaggg gcggtggggg  
3061 ggcctttatc ggagaagcta gagaacaaga gtccttctcc tcttatccc ccaacaggac  
3121 actaagagac aaggactgag tggaaatcctg gagaaagggg actcaggaac tgacctcatt  
3181 ggccgtgatt gtgaggagag gagtataagt ggagaggggc cattcctgag gtttccgtgt  
3241 tttccagcct ggtctcctgg aaagaatctt tatacagaaa taaagtatgt gtttactct  
3301 ctctgtcctc tgtctcttct ctaggggtcc taaacatcct ataggatgct aaatgggatg  
3361 gtactagaaa ccctaataac ttgcatagct agaaggatgg aatcaatgtt cagtaaaactc  
3421 ttgactctgt gatgaaatgg gttgggaaga tgtgggaaca gttcccaggt tgagatctgg  
3481 gaagggaggt gggattatgc gaaatcacag tgatgttgcc tatgaataaa gctgtgtcag  
3541 gatgcagaca caacagagtt ataagcaca gggagtttct gtaggacag aggttggggg  
3601 gaataacatc tgagaaagac aaaggggaaa gaaagcagaa gtactcaggg acagccttca  
3661 gaccaccatg ccaatctgac acctgggaaa aaaggggtgg ttaggaagag cctcagactg  
3721 tgggtcagct cccagcccaa cacgtgcaaa gattgcccag agagacattg cacgttaaca  
3781 gaatggccag gcctgatgcc ctgcccgtgt cagccgctgg ctggggctct ctagggaaag  
3841 tgttctgtgt ttgaacacca tgggtgatgc tgaagccctg cagctggagg ctgtcagcca  
3901 agtgcctctg agttcttctt aaagaggga

## (2) INFORMATION FOR SEQ ID NO:2640:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2640

1 gaaaaagcct tccacctcc tgtctggctt tagaaggacc ctgagcccc ggcgccacga  
61 caggactctg ctgcagaggg gggttgtgta cagatagtag ggctttaccg cctagcttctg  
121 aatggataa cgtcctcccg gtggactcag acctctccc aaacatctcc actaacacct  
181 cggaacccaa tcagttctgt caaccagcct ggcaaattgt ctttgggca cctgcctaca  
241 cggtcattgt ggtgacctct gtgggtggga acgtggtagt gatgtgcatc atcttagccc  
301 acaaaagaat gaggacagt acgaactatt ttctggtgaa cctggccttc gcggaggcct  
361 ccatgctgct attcaataca gtgggtgaact tcacctatgc tgtccacaac gaatggtact  
421 acggcctgtt ctactgcaag ttccacaact tcttcccat cgccgctgtc ttcccgagta  
481 tctactccat gacggctgtg gcctttgata ggtacatggc catcatacat cccctccagc  
541 cccggctgtc agccacagcc accaaagtgg tcatctgtgt catctgggtc ctggctctcc

601 tgctggcctt cccccagggc tactactcaa ccacagagac catgcccagc agagtcgtgt  
661 gcatgatcga atggccagag catccgaaca agatttatga gaaagtgtac cacatcgtg  
721 tgactgtgct gatctacttc ctccccctgc tgggtattgg ctatgcatac accgtagtgg  
781 gaatcacact atgggccagt gagatccccg gggactcctc tgaccgctac cacgagcaag  
841 tctctgccaa gcgcaagggt gtcaaaatga tgattgtcgt ggtgtgcacc ttcgccatct  
901 gctggctgcc ctccacatc ttcttctccc tgccctacat caaccagat ctctacctga  
961 agaagtttat ccagcaggtc tacctggcca tcatgtggct ggccatgagc tccaccatgt  
1021 acaaccccat catctactgc tgcctcaatg acaggttccg tctgggcttc aagcatgcct  
1081 tccggtgctg ccccttcctc agcgcggcg actatgaggg gctggaaatg aaatccaccc  
1141 gttactctca gaccagggc agtgtgtaca aagtcagccg cctggagacc accatctcca  
1201 cagtgggtgg ggccacagag gaggagccag aggacggccc caaggccaca cctcgtctcc  
1261 tggacctgac ctccaactgc tcttcacgaa gtgactccaa gaccatgaca gagagcttca  
1321 gcttctcttc caatgtgctc tcttaggcca cagggccttt ggcaggtgca gccccactg  
1381 cctttgacct gcctcccttc atgcatggaa attcccttca tctggaacca tcagaaacac  
1441 cctcacactg ggacttgcaa aaagggtcag tatgggttag ggaaaacatt ccatccttga  
1501 gtcaaaaaat ctcaattctt ccttatcttt gccaccctca tgctgtgtga ctcaaaccaa  
1561 gttactgaac ttgtctgagc gcttaaaata aaaggctcga ccagcttttc ccaaaagccc  
1621 attcattcca ttctggaagt gactttggct gcatgcgagt gctcatttca ggat  
1 aattcagagc caccgcgggc aggcgggag tgcattccaga agcgtttata ttctgagcgc  
61 cagttcagct ttcaaaaaga gtgtgcccc taaaaagcct tccaccctcc tgtctgcttt  
121 agaaggaccc tgagcccccag ggcgagcca caggactctg ctgcagaggg ggggtgtgta  
181 cagatagtag gctttacgcc tagcttcgaa atggataacg tcctcccggt ggactcagac  
241 ctctcccaa acatctccac taacacctcg gaacccaatc agttcgtgca accagcctgg  
301 caaattgtcc tttgggcagc tgcctacacg gtcattgtgg tgacctctg ggtgggcaac  
361 gtggtagtga tgtggatcat cttagccca aaaagaatga ggacagtgc aactatttt  
421 ctggtgaacc tggccttcgc ggaggcctcc atggctgcat tcaatacagt ggtgaacttc  
481 acctatgctg tccacaacga atggtactac ggcctgttct actgcaagtt ccacaacttc  
541 ttcccatcg ccgctgtctt cgccagtatc tactccatga cggctgtggc ctttgatagg  
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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2641

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3181 ccccccgcac cccaaccccc actcccaggc ctgttcggcg agcgctgacc tctgaccttc  
3241 ccagggcgac tctggagggc cctggtgtg caagtgaaat ggcacctggc tacaggcggg  
3301 cgtggtcagc tgggacgagg gctgtgccc gcccacccg cctggcatct acaccgtgt  
3361 cacctactac ttggactgga tccaccacta tgtcccaaaa aagccgtgag tcaggcctgg  
3421 ggtgtccacc tgggtcactg gagagccagc ccctcctgtc caaaacacca ctgcttcta  
3481 cccagggtgc gactgcccc cacaccttcc ctgccccgtc ctgagtgcct cttctgtcc  
3541 taagccccc gctctcttct gagcccttcc cctgtcctg aggaccttc cccatcctga  
3601 gcccccttcc ctgtcctaag cctgacgcct gcaactgggc ctccggccct cccctgccc  
3661 ggcagctggt ggtgggcgct aatcctcctg agtgcctgac ctcataaag tgcattgaaa  
3721 tcaactggtg gcacgcgtg gtttctggtt gtggatgtca ctgggagaga aggggtccag

```

3781 gtgtgtgag gacacctgcc acagtgcgag gtcctagccc tcaaggcaca gccagtcacc
3841 gtgggacggg gcctcctggg cagccctggt ccccgggggt ggcttctccc cacacgatgc
3901 atccagcatt cgggtcacac agagccactc gggcaactca gttgattata aaggacagcc
3961 aagtccctgc aaccgggtca agacagagaa tggctgcggg gagccccagg gctgccccatc
4021 acgagccctc accccacgct tcccacgagc tcttctcccg gccctctgtt ccaactgttg
4081 tgctttgccc tagttgtttg ctttgagaca ggatctcgct gtgtcatcca ggctgaagtg
4141 cagtgggtg atcagggctc actgtagcct tgaactcctg ggctcaagcg atcctcccat
4201 cttggcctcc catatagctg ggccacagga gtgagccacc acgcccagtt aatttttgta
4261 ttttcagtag agatggggtt tcgccatggt ggccagctct gtctcgaact cctgacctca
4321 agtgcctgag ccgcctcggc ctcccaagt gctgggatga caggcgtgag ccaccgcacc
4381 cagcctgagt ttgacatttt caaattcatt ttgaggtctt tctctacatc aatacatgag
4441 ccctccgctg ccggcgagtg ttgcatttta tcccgggctc ttgtttgcat tttatatttg
4501 aacatgatta cattcaggaa tgaaatgcgg ggctgttctg gttgaaaaca actctctaaa
4561 gaaacattca ctctttcctt ccaactgtca gatgcagaga tgtgcattta gtctctccaa
4621 tctctgcaaa tgacctctgt cctcacaagg ggtggactcg acttccagcg ccctctccag
4681 ccccacgtga cctctgcctc tgcagccctc gaaggcccat ccctcggctc ctgttctgca
4741 ggcccagcgt cttgtctatg aagatggacc tggaaactcg gccctccttc ctccctctgg
4801 cccatcccac cttctaggga tcacagagac agcacggggt gacccccagg gaacactgag
4861 cccctagaag cacttccaca cgccactgg aggttttgcg ggggtggagt cggagggatg
4921 agaccccgaa gggaagcaag acggccctc aggcagggc tgcgggtgta aggaaaggtg
4981 gacagcaggg gccggctact ggggtgaggg ggagggcagg ctccagcccc agagcttccc
5041 aaattagatc taagatccct gggaagctca gtgaagctca gcgcagtgc actggcagat
5101 gtgagcgtca gcttcagcag gaagggtctc tcaggacgtg acaggcagcg tgctggccag
5161 ggctgcagcc acctgcgttt tgactgggac gggggcacct gatccaaggt caccacgtg
5221 gctgccggca ggaggccctg gttccccgtc acaagggggt gtgaggggga aggccaaagt
5281 gtggccacan ggttncacc gagagggaca gtgccaagt tggccaagcc accctnggac
5341 aagaacaat nccaagtctt nccaaggtcc ttggacaaca aggagaancc cccccagctt
5401 ggggcnatt aaccaagggc cangncctcc cttcccggtt c

```

## (2) INFORMATION FOR SEQ ID NO:2642:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2642

```

1 tggaccaccc ccggtccccc cgtccagct tccattcttc accccacaat ctgtagcccc
61 cagccctgcc ctgtgaggcc cggccaggcc cagcatgctc ctcttgctc cccagatgct
121 gaatctgctg ctgtggcgcc tgcccgtcct ggcgagccgc gcctacgcgg cccctggtga
181 gtcccagccg gggctccacc tgcccctcac cacattccac aggtcagggc ctgggtgggt
241 tctggggagg ccgggctggc cccacacagc ggaagggctg ggcccaggcc tggggctgct
301 tctgggtcct gactggcac ctgcccagc ccaggccag gccctgcagc gagtgggcat
361 cgttgggggt caggaggccc ccaggagc

```

## (2) INFORMATION FOR SEQ ID NO:2643:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2643

```

1 cagatcggag cggacatcgc cctgctggag ctggaggagc cggatgaaggt ctccagccac
61 gtccacacgg tcacctgcc cctgcctca gagaccttcc ccccggggat gccgtgctgg
121 gtactggtc ggggcgatgt ggacaatgat ggtgggtctg gggacagtgg aggtggggcc
181 agggctttag ccacagccca gcccctgggc tccctctggg ctccaggtgg gggttgcccg
241 gcccctcct gaggtgcac cctcttccc acctgcagag gcctccac cgccatttcc
301 tctgaagcag gtgaaggtcc ccataatgga aaaccacatt tgtgacgcaa aataccacct
361 tggcgccctac acgggagacg acgtccgcat cgtccgtgac gacatgctgt gtgcccggaa
421 cacccgagg gactcatgcc aggtgggccc cgcgtgtccc ccgcccccg caccacaacc
481 cccactccca ggctgttcg gcgagcgtg acctctgacc ttcccagggc gactccggag
541 ggcccctggt gtgcaagtg aatggcact ggctgcaggc gggcgtggtc agctggggcg
601 agggctgtgc ccagcccaac cggcctggca tctacaccg gtgcacctac tacttggaact
661 ggatccacca ctatgtcccc aaaaagccgt gagtcaggcc tgggttgccc acctgggtca
721 ctggaggacc aaccctgct gtccaaaaca cactgcttc ctaccagggt ggcgactgcc
781 cccacacact tccctgcccc gtcctgagtg ccccttctg tctaagccc cctgctctct
841 tctgagcccc tccccctgtc ctgaggaccc ttccccatcc tgagccccct tccctgtcct
901 aagcctgacg cctgcactgg gccctccggc cctcccctgc ccaggcagct ggtgggtggc
961 gctaactctc ctgagtgtg gacctatta aagtgcattg aaatcactgg tgtgcatcgc
1021 tgtgtttctg gttgtggatg tcaactgggag agaaggggtc cagggtgtgt gaggacacct

```



1081 gccacagtgt gagtcctag ccctcaaggc acaagccagt caccgtggga cggggcctct  
1141 gggcagccct ggtccccgag ctggctt

## (2) INFORMATION FOR SEQ ID NO:2644:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2644

1 ccaggatgct gaatctgctg ctgctggcgc tgcccgtcct ggcgagccgc gcctacgcgg  
61 cccctgcccc aggccaggcc ctgcagcgag tgggcatcgt tgggggtcag gaggccccc  
121 ggagcaagtg gccctggcag gtgagcctga gaggccacgg ccctacttgg atgcacttct  
181 gggggggctc cctcatccac cccagtgagg tgctgaccgc agcgacttgc gtgggaccgg  
241 acgtcaagga tctggccgac ctccaggtgc aactgcggga gcagcacctc tactaccagg  
301 accagctgct gccggtcagc aggatcatcg tgcaccaca gttctacacc gccagatcg  
361 gagcggacat cgccctgctg gagctggagg agccggtgaa ggtctccagc caggtccaca  
421 cggtcaccct gcccctgccc tcagagacct tcccccgagg gatgcctgac tgggtcactg  
481 ctggggcgca tgtggacaat gatgagcgcc tcccaccgac atttcctctg aagcaggtga  
541 aggtcccat aatggaaaac cacatttctg acgcaaaata ccaccttggc gcctacacgg  
601 gagacgacgt ccgcatcgtc cgtgacgaca tgctgtgtgc cgggaacacc cggagggact  
661 catgccaggg cgactccgga gggcccctgg tgtgcaaggc gaatggcacc tggctgcagg  
721 cgggctggtg cagctggggc gagggtctgt cccagcccaa ccggcctggc atctacacc  
781 gtgtcaccta ctacttgac tggatccacc actatgtccc caaaaagccg tgagtcaggc  
841 ctgggtgtgc cacctgggtc actggaggac caaccctgac tgtccaaaac accactgctt  
901 cctaccaggg tggcgactgc ccccacacc ttccctgccc cgtcctgagt gcccttctc  
961 gtccaaagcc ccctgtctc ttctgagccc cttccctgt cctgaggacc cttcccatc  
1021 ctgagccccc ttccctgtcc taagcctgac gcctgactg ctccggccct cccctgccc  
1081 ggcagctggt ggtgggcgct aatcctcctg agtgctggac ctcatataag tgcattgaaa  
1141 tca

## (2) INFORMATION FOR SEQ ID NO:2645:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2645

1 ggccaggatg ctgaatctgc tgctgctggc gctgcccgtc ctggcgagcc gcgcctacgc  
61 ggcccctgccc ccaggccagg ccctgcagcg agtgggcatc gttgggggtc aggaggcccc  
121 caggagcaag tggccctggc aggtgagcct gagagtccac ggccatact ggatgcactt  
181 ctgcgggggc tccctcatcc acccccagtg ggtgctgacc gcagcgact gcgtgggacc  
241 ggagctcaag gatctggccg ccctcagggt gcaactgcgg gagcagcacc tctactacca  
301 ggaccagctg ctgccggtca gcaggatcat cgtgcaccca cagttctaca ccgcccagat  
361 cggagcggac atcgccctgc tggagctgga ggagccggtg aaggtctcca gccacgtcca  
421 cacggtcacc ctgcccctg cctcagagac cttccccccg gggatgccc gctgggtcac  
481 tggctggggc gatgtggaca atgatgagcg cctcccaccg ccatttcctc tgaagcaggt  
541 gaaggtcccc ataatggaaa accacattt tgacgcaaaa taccacctt ggcgcctacac  
601 gggagacgac gtccgcatcg tccgtgacga catgctgtgt gccgggaaca cccggaggga  
661 ctcatgccag ggcgactccg gagggccctt ggtgtgcaag gtgaatggca cctggtgca  
721 ggcggggcgt gtcagctggg gcgagggtg tgcccagccc aaccggcctg gcattctcac  
781 ccgtgtcacc tactacttgg actggatcca ccactatgtc cccaaaaagc cgtgagtcag  
841 gcctgggttg gccacctggg tcaactggagg accaaccctt gctgtccaaa acaccactgc  
901 ttctaccaca ggtggcgact gcccaccaca ccttccctgc cccgtcctga gtgcccctc  
961 ctgtcctaag cccctgtctc tcttctgagc ccttccctt gtccctgagga ccttcccca  
1021 tcttgagccc ccttccctgt cctaagcctg acgctgcac cgggccctcc ggcctcccc  
1081 tgcccaggca gctggtggtg ggcgctaata ctcctgagtg ctggacctca ttaaagtga  
1141 tggaa

## (2) INFORMATION FOR SEQ ID NO:2646:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2646

1 tgaatctgct gctgctggcg ctgcccgtcc tggcgagccg gcgcctacgc gccctgccc  
61 caggccaggc cctgcagcga gtgggcatcg tcgggggtca ggaggcccc aggagcaagt  
121 ggccctggca ggtgagcctg agagtccacg gccatactg gatgcacttc tgcgggggct  
181 cctcatcca ccccagtggt gtgctgaccg cagcgactg cgtgggaccg gacgtcaagg

```

241 atctggcgc cctcaggggtg caactgcggg agcagcacct ctactaccag gaccagctgc
301 tgccgggtcag caggatcatc gtgacccac agttctacac cgccagatc ggagcggaca
361 tcgcccctgct ggagctggag gagccggtga acgtctccag ccacgtccac acggtcacc
421 tgccccctgc ctcagagacc ttcccccg ggatgccgtg ctgggtcact ggctggggcg
481 atgtggacaa tgatgagcgc ctccaccgc catttcctct gaagcagggtg aaggtcccca
541 taatggaaaa ccacatttgt gacgcaaaat accaccttgg cgcctacacg ggagacgacg
601 tccgcacatcgt ccgtgacgac atgctgtgtg ccgggaacac ccggaggagac tcatgccagg
661 gcgactccgg agggcccctg gtgtgcaagg tgaatggcac ctggctgcag gcgggctgtg
721 tcagctgggg cgagggtgtg gccagccca accggcctgg catctacacc cgtgtcacct
781 actacttggg ctggatccac cactatgtcc ccaaaaagcc gtgagtcagg cctgggttgg
841 ccacctgggt cactggagga ccaaccctg ctgtccaaa caccactgct tctaccacg
901 gtggcgactg cccccacac ctccctgcc ccgtcctgag tgcccttcc tgtcctaagc
961 cccctgctct cttctgagcc cttcccctg tcttgaggac cttccctat cctgagcccc
1021 cttccctgtc ctaagcctga cgcctgcacc gggccctcca gccctcccct gccagatag
1081 ctgggtgggtg gcgctaattc tctgagtgcc tggacctcat taaagtgcac ggaaate

```

## (2) INFORMATION FOR SEQ ID NO:2647:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2647

```

1 accagctgac aggtggagct gccagtctcc agtgctcagc cctcagcggg gcctgcctgg
61 cagccccaca cacagagggc atcggggttg cgggggcacg tgttacacgg gggccctggg
121 tctgagtcac ccacttcctc cgagtctgga tgggaggacc cagcgcctc cctccgcccc
181 ctccctgatc ggaaggataa atggggaggg gagagccact gggtagaagg aacaggaggt
241 ggccagggtg agtccccact ctcagagacc ctgacatcag cgtcacctgg agcagagtgg
301 cccagcctca gactcagagc accaagaccc agggccgcag gcctggaccc acccgggtcc
361 ccccgctcca gctccattct tcacccaca atctgtagcc cccagccctg ccctgtgagg
421 cccggccagg cccacgatgc tcctccttgc tccccagatg ctgaatctgc tgcctgtggc
481 gctgcccgtc ctggcgagcc gcgcctacgc ggcccctggt gactcccagc cggggtccac
541 cctgcccctc accacattcc acaggtcagg gcctgggtgg gttctgggga ggtcgggtcg
601 gccccccaca cagggaaggc ctggggaggg gcctgggggt gcttctggtt cctgacctgg
661 cacctgcccc agccccaggc caggccctgc agcagtgagg catcgctggg ggtcagagtgg
721 cccccaggag caagtggccc tggcagggtg gcctgagagt ccacggccca tactggatgc
781 acttctgcgg gggctccctc atccacccc agtggtgct gaccgcagcg cactgcgtgg
841 gaccgtgagt ctcccggggc ctggaggggg ggggaagggc tggatgtgag ccctgggtcc
901 cgggtgctcc tgggggtgct ccaggggcct gagggtgagc ctccgctgcc caggagctc
961 aaggatctgg ccgcccctag ggtgcaactg cgggagcagc acctctacta ccaggaccag
1021 ctgctgcccg tcagcaggat catcgtgcac ccacagttct acaccgcca gatcggagcg
1081 gacatcgccc tgctggagct ggaggagccg gtgaacctct ccagccacgt ccacacggtc
1141 accctgcccc ctgcctcaga gaccttcccc ccggggatgc cgtgctgggt cactggctgg
1201 ggcgatgtgg acaatgatgg tgggtctggg gacagtggag gtggggccag ggtcttagcc
1261 acagcccagc ccctgggtcc ctctgggtc cagggtgggg ttgcccggcc cctcctgag
1321 gctgcaccct cttccccacc tgcagagcgc ctcccacgc catttcctct gaagcaggtg
1381 aaggtcccca taatggaaaa ccacatttgt gacgcaaaat accaccttgg cgcctacacg
1441 ggagacgagc tccgcacgt ccgtgacgac atgctgtgtg ccgggaacac ccggaggagc
1501 tcatgccagg tgggcccgcg ctgtcccgcg cccccgcg ccacaacccc actcccaggc
1561 ctgttcggcg agcgtgacc tctgaccttc ccagggcgac tccggagggc ccctggtgtg
1621 caaggtgaat ggcacctggc tgcaggcggg cgtggtcagc tggggcgagg gctgtgcccc
1681 gccaaccggc cctggcatct acaccgtgt cacctactac ttggactgga tccaccacta
1741 tgtcccaaaa aagccgtgag tcaggcctgg gttggccacc tgggtcactg gaggaccaac
1801 ccctgctgtc caaaacaçca ctgcttccca cccagggtgg gactgcccc cacccttcc
1861 ctgcccctgc ctgagtggcc ctctctgtcc taagccccct gctctcttct gagecccttc
1921 ccctgtcctg aggaccttcc cctatctga gcccccttc ctgtcctaag cctgacgcct
1981 gcaccgggccc ctccagccct cccctgccc gatactgggt ggtgggctgt aatcctctg
2041 agtgctggac ctcattaaag tgcattgaaa tcaactggtg gcatcgctgt gtttctggtt
2101 gtggatgtca ctgggagaga aggggtccag gtgtgctgag gacacctgcc acagtgtgag
2161 gtcctagccc tcaaggcaca gccagtcacc gtgggac

```

## (2) INFORMATION FOR SEQ ID NO:2648:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2648

```

1 ggaattccgt ggccaggatg ctgagcctgc tgctgctggc gctgcccgtc ctggcgagcc

```

```

61 ggcctacgc ggccctgcc ccagtccagg ccctgcagca agcgggtatc gtcgggggtc
121 aggagggccc caggagcaag tggccctggc aggtgagcct gagagtccgc gaccgatact
181 ggatgcactt ctgcgggggc tccctcatcc acccccagtg ggtgctgacc gcggcgcaact
241 gcctgggacc ggacgtcaag gatctggcca ccctcagggg gcaactgcgg gagcagcacc
301 tctactacca ggaccagctg ctgccagtca gcaggatcat cgtgcaccca cagttctaca
361 tcatccagac tggagcggat atcgccctgc tggagctgga ggagcccgtg aacatctcca
421 gccgcgtcca cagggtcatg ctgcccctg cctcggagac cttccccccg gggatgccgt
481 gctgggtcac tggctggggc gatgtggaca atgatgagcc cctccaccg ccatttcccc
541 tgaagcaggt gaaggtcccc ataatggaaa accacatttg tgacgcaaaa taccaccttg
601 ggcctacac gggagacgac gtccgcatca tccgtgacga catgctgtgt gccgggaaca
661 gccagaggga ctctgcaag ggcactctg gaggggccct ggtgtgcaag gtgaatggca
721 cctggctaca gggggcgctg gtcagctggg acgagggtg tgcccagccc aaccggcctg
781 gcattacac ccgtgtcacc tactacttgg actggatcca ccactatgtc cccaaaaagc
841 cgtgagtcag gcctgggtgt gccacctggg tcaactggag accaaccctt gctgtccaaa
901 acaccactgc ttctaccca ggtggcgact gccccccaca cttccctgc cccgtcctga
961 gtgccccctc ctgtcctaag cccctgtctc tcttctgagc cccttccct gtcctgagga
1021 cccctcccca tctgagccc ccttccctgt cctaagcctg acgcctgcac tgctccggcc
1081 ctcccctgcc caggcagctg gtgtggggc ctaatcctcc tgagtgtgtg acctcattaa
1141 agtgcattga aatc

```

## (2) INFORMATION FOR SEQ ID NO:2649:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2649

```

1 gctgccgctc ctggcgagcc ggcctacgc ggccctgcc ccaggccagg ccctgcagcg
61 agtgggcatc gttgggggtc aggagggccc caggagcaag tggccctggc aggtgagcct
121 gagagtccgc gaccgatact ggatgcactt ctgcgggggc tccctcatcc acccccagtg
181 ggtgctgacc gcagcgcaact gcgtgggacc ggacgtcaag gatctggccc ccctcagggg
241 gcaactgcgg gagcagcacc tctactacca ggaccagctg ctgccggtca gcaggatcat
301 cgtgcaccca cagttctaca cgcgccagat cggagcggac atcgccctgc tggagctgga
361 ggagccggtg aaggtctcca gccacgtcca caggtcacc ctgcccctg cctcagagac
421 cttccccccg gggatgccgt gctgggtcac tggctggggc gatgtggaca atgatgagcg
481 cctccaccg ccatttctc tgaagcaggt gaaggtcccc ataatggaaa accacatttg
541 tgacgcaaaa taccaccttg ggcctacac gggagacgac gtccgcatc tccgtgacga
601 catgctgtgt gccgggaaca cccggaggga ctcatgccag ggcgactccg gaggggccct
661 ggtgtgcaag gtgaatggca cctggctgca ggcggcgctg gtcagctggg gcgagggtg
721 tgcccagccc aaccggcctg gcattacac ccgtgtcacc tactacttgg actggatcca
781 ccactatgtc cccaaaaagc cgtgagtcag gcctgggtg tccacctggg tcaactggag
841 accagccct cctgtccaaa acaccactgc ttctaccca ggcggcgact gccccccaca
901 ccttccctgc cccgtcctga gtgcccctc ctgtcctaag cccctgtctc tcttctgagc
961 cccttccct gtcctgagga cccttcccca tctgagccc ccttccctgt cctaagcctg
1021 acgcctgcac cgggccctcc ggccctccc tgcccaggca gctggtggtg ggcgctaate
1081 c

```

## (2) INFORMATION FOR SEQ ID NO:2650:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2650

```

1 atctggaagc ataatgggg aggggagagc ccactgggta gaaggaacag ggagcggcca
61 gggtaagtcc ccactctcag agaccctgac atcagcgtca cctggagcag agtggcccag
121 cttcagactc agagcaccaa gaccaggcc tgcaggcctg gaccacccc ggtccccccg
181 tcccagctcc attcttcacc ccacaatctg tagccccag ccctgcccgt tgaggcccgg
241 ccaggccac gatgtcctc ctgtctccc agatgttgaa tctgtgtgt ctggcgctgc
301 ccgtcctggc gagcgcgcc tacgcggccc ctggtgagtc ccagccggg tccacctgc
361 ccctcaccac attccacagg tcaggccctg ggtgggttct ggggaggtg ggtggccc
421 cacacaggga agggctggg ccaggcctgg ggctgcttcc tggctcctgac ctggcacctg
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## (2) INFORMATION FOR SEQ ID NO:2651:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2651

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(2) INFORMATION FOR SEQ ID NO:2652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2652

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## (2) INFORMATION FOR SEQ ID NO:2653:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2653

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## (2) INFORMATION FOR SEQ ID NO:2654:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: \_ base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2654

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 15181 aggactagat gatggattga tgggtgggag atgtagatag tgggagagaa gcaggattct  
 15241 gatggatgga aaaactaaaa aattctattt tgggtgtggt aagtctaagt ctattagaca  
 15301 tgcaagtaga gatgtcactg ggcagatata catctggatt tcaggggcaa ggtccaagct  
 15361 agagaaagaa acctgggcat ggtcagcatg aggatggtgt ttaaagccat ggaacttatc  
 15421 ttgtgcatcc ctataagacc cctttgaggc acttgtttcc cctcacaatg gatgcagtgc  
 15481 atcttccatt ctgaattcca gaggaacaaa cctcctgctc ctagaagcta aactctccag  
 15541 acttagtctt ctgaattccc actgggattt aacctccctg gattcaattc cctacccac  
 15601 aaggaccctt ctaccaatcc atttcacaat atttgggtga actcttcaca ttttcaaatc  
 15661 ctgtcttcta tgtttgaaag cattttctc tgggcatttt gaaacctggc tttccctaa  
 15721 tgatgctact cctctctgtg gtgaagggtg ctctttcttc gactccatca ctaggggaat  
 15781 gaaggcagaa gagaggggtc gttatcccct cccccccagg accactgata aactcctcct  
 15841 catctcccaa agcagctgcc ttctggatct gccatgctct cctgccttc acagcacaat  
 15901 cttatccatc aaaatattta ttatgctctt aacaacttgt ataactagct cagtctttct  
 15961 ccacatctta tccctaccat catcctgtt tgtttgttt ttgagacaag gtattgctct  
 16021 gtcaccaggc ctggagtgc gtggcgtgat cttggctcac tgcagcctcg acctcctggg  
 16081 ctcaagtgat cctcccagct cagcctcctg agtagctagg actacaggcg cataccacca  
 16141 tgcccggtca agttttgtat ttttttttt ttccagagat agggttttgc tatgttgcct  
 16201 aggtgtgtct tgaactcctg agctcaagca atccaccgc ctacgcctcc caaagtgtcg  
 16261 ggattacagg catgaccac ccgacccggc ctctaccac catctttagt

## (2) INFORMATION FOR SEQ ID NO:2655:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2655

1 aattcgataa ttcaaaatga tttttagtg gggacaaggc caaacatata tatgtgcttt  
 61 atgctactaa taaaagggtt aaaccgaaca agttcaaaga caaaactcag tagtacttta  
 121 tttagacagg ttagtctaaa tctgttaacc ttatacttgc aactctgac attcattaat  
 181 tctgcaaat ttaataaatg ctttatttta agctaaatgc tgagatgaaa aaatgaaacc  
 241 atatgagtta gcaaatgaga aaatataggc atattaatca gtaaatgcag aatgataaat  
 301 gctccatcaa tatgcacttg ttgtagttag gccaccgagg aggtgtcaat cctctcaacc  
 361 tgggaggagc aggtaggact tcagatgtca tccaactcaa agatatagtg agggacttga  
 421 tcaaacattt gccaagacca ctatgagtta aatgaataga ttaggcattt ctccaattgt  
 481 gcaagcttcg aatcatatcc aaactcagaa caacatagct tggtcataat gatcccaagg  
 541 atcctatttg ccattgtctt tgagcctcaa aggaacatat taaaactcca taataccctt  
 601 ttgatctatt ctgaagttaa gtatgtgaatt tacatgatga tgacacaaac actgtaaagg

661 acctctgggt tacttggtta taagctagta ttctctgaat caatttttct gatccctaga  
721 tatttggttag gtgaagtcac acctatatat cccacacccc tagaacagca tctccaactt  
781 ttttttccct ccttgctctt tagtgggagc cacatcagta tccaaggagg agatccagaa  
841 gcctctccaa ccaggtaggg acagttagat attccagacc tcagctatgg cctttgttac  
901 agagtacaaa tgttatatag tacaagttta ttgtacacat cccattgagt ccttgagctt  
961 tagaattttt ttgtagaatt taacagtttt ttcatgccgt atttacatat tattgctagt  
1021 atttagaatt ttcttctcca aatgtataac gtttattatt gcattttttg tatccactaa  
1081 gtgaaaaatc atgcattaga tattgtagaa gtagatacaa caatgaacaa gaactgggtc  
1141 tgaccatgag aggaactgat gatccaatgg gggagataga cctgcacgtg tttataaaaa  
1201 ggaagtggct attccgggtt ctttttgatg ggcaagcatt ttgcaaggcc ttgggctatg  
1261 tgtgtgcaag gctaagccag ttagttaatt gggatttttt taaaaaggca cttcactggg  
1321 gggaaaagga acatagagtt ggttattgtc cccttgccca taataaaaaa ctattatttt  
1381 taatttttta actgggtttg cggttaaatc tcacagccca agagatttgc cacttcagat  
1441 ggattccata cacttgcat taagtatgca aaaaaattcc aattatccag caatttaacc  
1501 aaattatttg taacttttct aaaaacaaaa aaaattgttt cccttgtttt ggagcaatt  
1561 tcagttacag tcttttactt tctactcaag aaaatagttt caaaaagttg atgtttgttg  
1621 ctaaaagaac tatttttatg aataaatata aaactaagaa gttatggtgt ccctttttta  
1681 aaaaatgact catcaaaaga aataactttt tcctttctct tgtaagagaa aaaaattaat  
1741 ctcttttaga attgcaaaac tatttccttg atggagaaaa tcaattcaca tggcatagtc  
1801 gttatttatc cagttcaaaa accagagtag aatttactac tctgtctcca ttttttctct  
1861 cccacccccc ttaaccacac ttggattcag aaagcttcat tctgcaatca gcattgtcct  
1921 ttatctttcc agtaaaagata gccttttgga gtcgaagatg aggaaaagcc tgtattttat  
1981 agtcttgga gtgtcttctt ttgccaggac agagagagga gcttcagcag tgagagcaac  
2041 tgaaggggtt aatagtgga cttggctggg tgtctgttaa acttttttcc ctggctctgc  
2101 cctgggtttc cccttgaagg gatttccctc cgcctctgca acaagacctt ttataaagca  
2161 cagactttct atttcactcc gcggtatctg catcgggcct cactggcttc aggagctgaa  
2221 taccctccca ggcacacaca ggtgggacac aaataagggt tttggaacca ctattttctc  
2281 atcacgacag caacttaaaa tgcctgggaa gatggtcgtg atccttggag cctcaaatat  
2341 actttggata atgtttgcag cttgtaagtt atttcccttc atctgtttca aatgtt

## (2) INFORMATION FOR SEQ ID NO:2656:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2656

1 atgcctggga agatggctgt gatccttggga gcctcaata tactttggat aatgtttgca  
61 gcttctcaag cttttaaaat cgagaccacc ccagaatcta gatatcttgc tcagattgggt  
121 gactccgtct cattgacttg cagcaccaca ggctgtgagt cccattttt ctcttggaga  
181 acccagatag atagtccact gaatgggaag gtgacgaatg aggggaccac atctacgtg  
241 acaatgaatc ctgttagttt tgggaacgaa cactcttacc tgtgcacagc aacttgtgaa  
301 tctaggaaat tggaaaaagg aatccagggt gagatctact cttttcctaa ggatccagag  
361 attcatttga gtggccctct ggaggctggg aagccgatca cagtcaagtg ttcagttgct  
421 gatgtatacc catttgacag gctggagata gacttactga aaggagatca tctcatgaag  
481 agtcaggaa ttctggagga tgcagacagg aagtccctgg aaaccaagag tttggaagta  
541 acctttactc ctgtcattga ggatatttga aaagtctctg tttgccgagc taaattacac  
601 attgatgaaa tggattctgt gcccacagta aggcaggctg taaaagaatt gcaagtctac  
661 atatcaccac agaatacagt tatttctgtg aatccatcca caaagctgca agaagttggc  
721 tctgtgacca tgacctgttc cagcgagggt ctaccagctc cagagatttt ctggagtaag  
781 aaattagata atgggaatct acagcacctt tctggaaatg caactctcac cttaattgct  
841 atgaggatgg aagattctgg aatttatgtg tgtgaaggag ttaatttgat tgggaaaaac  
901 agaaaaagag tggaaattaat tgttcaagag aaaccattta ctgttgagat ctccccctga  
961 ccccgattg ctgctcagat tggagactca gtcattgtga catgtagtgt catgggctgt  
1021 gaatccccar ctttctctct gagaaccacg atagacagcc ctctgagcgg gaaggtgagg  
1081 agtgagggga ccaattccac gctgacctg agccctgtga gttttgagaa cgaacactct  
1141 tatctgtgca cagtgacttg tggacataag aaactggaaa agggaatcca ggtggagctc  
1201 tactcattcc ctagagatcc agaaatcgag atgagtgggt gcctcgtgaa tgggagctct  
1261 gtcactgtaa gctgcaaggt tcctagcgtg taccctcttg accggtgga gattgaatta  
1321 ctttaagggg agactattct ggagaatata gatttttttg aggatacga tatgaaatct  
1381 cttagagaac aaagtttgga aatgaccttc atccctacca ttgaagatac tggaaaagct  
1441 cttgtttgtc aggctaagtt acatattgat gacatggaat tcgaacccaa acaaaggcag  
1501 agtacgcaaa cactttatgt caatgttgcc cccagagata caaccgtctt ggtcagccct  
1561 tctccatcc tggaggaagg cagttctgtg aatatgacat gcttgagcca gggctttcct  
1621 gtcctgaaaa tctgtggag caggcagctc cctaaccggg agctacagcc tctttctgag  
1681 aatgcaactc tcaccttaat ttctacaaaa atggaagatt ctggggttta tttatgtgaa  
1741 ggaattaacc aggtggaag aagcagaaag gaagtggaat taattatcca agttactcca  
1801 aaagacataa aacttacagc ttttcttct gagagtgtca aagaaggaga cactgtcatc  
1861 atctcttgta catgtggaaa tgttccagaa acatggataa tctgaagaa aaaagcggag

1921 acaggagaca cagtactaaa atctatagat ggcgccctata ccatccgaaa ggcccagttg  
1981 aaggatgcgg gagtatatga atgtgaatct aaaaacaaag ttggtccaca attaagaagt  
2041 ttaacacttg atgttcaagg aagagaaaac aacaaagact atttttctcc tgagcttctc  
2101 gtgctctatt ttgcatcctc cttaataata cctgccattg gaatgataat ttactttgca  
2161 agaaaagcca acatgaaggg gtcatatagt cttgtagaag cacagaaatc aaaagtgtag

## (2) INFORMATION FOR SEQ ID NO:2657:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2657

1 aattcgataa ttcaaaatga tatttcagtg gggacaaggc caaacatat tatgtgcttt  
61 atgctactaa taaaaaggtt aaaccgaaca agttcaaaga caaaactcag tagtacttta  
121 ttcagacagg ttagtctaaa tctgttaacc ttatacttgc aactctgac attcattaat  
181 tctgcaaatt ttaataaatg ctttatttta agctaaatgc tgagatgaaa aaatgaaacc  
241 atatgagtta gcaaagtaga aaatataggc atattaatca gtaaattgcag aatgataaat  
301 gctccatcaa tatgcacttg ttgtagttag gccaccgagg aggggtgcaat cctctcaacc  
361 tgggaggagc aggtaggact tcagatgtca tccaactcaa agatatagtg agggacttga  
421 tcaaacattt gccaaagaca ctatgagtta aatgaataga ttaggcattt ctccaatggt  
481 gcaagcttcg aatcatatcc aaactcagaa caacatagct tgggtcataat gatcccaagg  
541 atcctatttg ccattgtctt tgagcctcaa aggaacatat taaaactcca taataccctt  
601 ttgatctatt ctgaagttaa gtagtgaatt tacatgatga tgacacaaac actgtaaagg  
661 acctctgggt tacttgttta taagctagta ttctctgaat caatttttct gatccctaga  
721 tatttggtag gtgaagtcac acctatatat cccacacacc tagaacagca tctccaactt  
781 ttttttccct ccttgtcttt tagtgggagc cacatcagta tccaaggagg agatccagaa  
841 gcctctccaa ccaggtaggg acagttatag attccagacc tcagctatgg cctttgttac  
901 agagtacaaa tgttatatag tacaagttta ttgtacacat cccattgagt ctctgagctt  
961 tagaattttc ttgtagaatt taacagtttt ttcatgccgt atttacctat tattgtagt  
1021 atttagaatt ttcttctcca aatgtataac gtttattatt gcattttttg tatccactaa  
1081 gtggaaaatc atgcattaga tattgtagaa gtagatacaa caatgaacaa gaactggtcc  
1141 tgaccatgag aggaactgat gatccaatgg gggagataga cctgcacgtg tttataaaaa  
1201 ggaagtggct attccgggtt ctttttgatg ggcaagcatt ttgcaaggcc ttgggctatg  
1261 tgtgtgcaag gctaagccag ttagttaatt gggatttttt taaaaaggca cttcactggg  
1321 gggaaaagga acatagagtt ggttattgtc ccttgccta taataaaaa ctattatttt  
1381 taatttttta actgggtttg cggttaaatc tcacagccca agagatttgc cacttcagat  
1441 ggattccata cacttgcatt taagtatgca aaaaaattcc aattatccag caatttaacc  
1501 aaattatttg taacttttct aaaacaaaaa aaaattgttt ccttgtttt ggcagcaatt  
1561 tcagttacag tcctttactt tctactcaag aaaatagttt caaaaagttg atgtttgttg  
1621 ctaaaagaac tatttttatg aataaatata aaactaagaa gttatgggtt cctttttta  
1681 aaaaatgact catcaaaaga aataactttt tcttttctct tgaagagaa aaaaattaat  
1741 ctctttttaga attgcaaaaca tatttccttg atggagaaaa tcaattcaca tggcatagtc  
1801 gttattttatc cagttcaaaa accagagtag aatttactac tctgtctcca tttttctct  
1861 cccaccccc ttaaccaca ttggattcag aaagcttcat tctgcaatca gcattgtcct  
1921 ttatctttcc agtaaagata gccttttggg gtcgaagatg aggaaaagcc tgtattttat  
1981 agtcttggaa gtgtcttctt ttgccaggac agagagagga gtttcagcag tgagagcaac  
2041 tgaagggtt aatagtggaa cttggctggg tgtctgttaa acttttttcc ctggctctgc  
2101 cctgggttcc ccttgaagg gatttcctc cgctctgca acaagacct ttataaagca  
2161 cagactttct atttcactcc gcggtatctg catcggcct cactggcttc aggagctgaa  
2221 taccctccca ggcacacaca ggtgggacac aaataagggt tttggaacca ctattttctc  
2281 atcacgacag caacttaaaa tgctgggaa gatggctgtg atccttggag cctcaaatat  
2341 acttttgata atgtttgcag cttgtaagtt atttcccttc atctgtttca aatgtt  
1 atgcctggga agatggctgt gatccttggg gcctcaaata tactttggat aatgtttgca  
61 gcttctcaag cttttaaaat cgagaccacc ccagaatcta gatattctgc tcagattggg  
121 gactccgtct cattgacttg cagcaccaca ggctgtgagt cccattttt ctcttggaga  
181 acccagatag atagtcact gaatgggaag gtgacgaatg aggggaccac atctacgctg  
241 acaatgaatc ctgttagttt tgggaacgaa cactcttacc tgtgcacagc aacttgtgaa  
301 tctaggaaat tggaaaaagg aatccagggt gagatctact cttttcttaa ggatccagag  
361 attcatttga gtggcctct ggaggctggg aagccgatca cagtcaagtg ttcagttgct  
421 gatgtatacc catttgacag gctggagata gacttactga aaggagatca tctcatgaag  
481 agtcaggaat ttctggagga tgcagacagg aagtcccttg aaaccaagag tttggaagta  
541 acctttact ctgtcattga ggatattgga aaagtcttg tttgccgagc taaattacac  
601 attgatgaaa tggattctgt gccacagta aggcaggctg taaaagaatt gcaagtctac  
661 atatcaccca agaatacagt tatttctgtg aatccatcca caaagtgcga agaaggtggc  
721 tctgtgacca tgacctgttc cagcagggtt ctaccagctc cagagatttt ctggagtaag  
781 aaattagata atgggaatct acagcacctt tctggaaatg caactctcac ctttaattgt  
841 atgaggatgg aagattctgg aatttatgtg tgtgaaggag ttaatttgat tgggaaaaac  
901 agaaaagagg tgaattaat tgttcaagag aaaccattta ctgttgagat cttccctgga

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961 ccccgattg ctgctcagat tggagactca gtcattgtga catgtagtgt catgggctgt
1021 gaatcccat cttctcctg gagaaccag atagacagcc ctctgagcgg gaaggtgagg
1081 agtgagggga ccaattccac gctgaccctg agccctgtga gttttgagaa cgaacactct
1141 tatctgtgca cagtgaactg tggacataag aaactggaaa agggaaatcca ggtggagctc
1201 tactcattcc ctgagatcc agaaatcgag atgagtgggt gcctcgtgaa tgggagctct
1261 gtcactgtaa gctgcaaggt tcctagcgtg taccctcttg accggctgga gattgaatta
1321 cttaaagggg agactattct ggagaatata gatttttgg aggatacggg tatgaaatct
1381 ctgagagaaca aaagtgttga aatgaccttc atccctacca ttgaagatac tggaaaagct
1441 cttgtttgtc aggctaagt acatattgat gacatggaat tcgaacccaa acaaaaggcag
1501 agtacgcaaa cactttatgt caatgttgcc ccagagata caaccgtctt ggtcagccct
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1621 gctccgaaaa tcctgtggag caggcagctc cctaacgggg agctacagcc tcttctgag
1681 aatgcaactc tcaccttaat ttctacaaa atggaagatt ctggggttta tttatgtgaa
1741 ggaattaac aggtggaag aagcagaag gaagtggat taattatcca agttactcca
1801 aaagacataa aacttacagc tttccttct gagagtgtca aagaaggaga cactgtcatc
1861 atctcttgta catgtggaaa tgttccagaa acatggataa tcctgaagaa aaaagcggag
1921 acaggagaca cagtactaaa atctatagat ggcgcctata ccacccgaaa ggcacgttg
1981 aaggatgcgg gagtatatga atgtgaatct aaaaacaaag ttggctcaca attaagaagt
2041 ttaacacttg atgttcaagg aagagaaaac aacaaagact attttctcc tgagcttctc
2101 gtgctctatt ttgcatctc cttataataa cctgccattg gaatgataat ttactttgca
2161 agaaaagcca acatgaagg gtcataatag cttgtagaag cacagaaatc aaaagtgtag

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(2) INFORMATION FOR SEQ ID NO:2658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2658

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1 gcaggaacag tgctagtatt gctcgagccc gagggctgga ggtagggga tgaaggtctg
61 cttccacgct ttgactgaa ttagggttag aattggggat ggggtaggg gcgcattcct
121 tcgggagccg aggtctaagt cctcggggtc ctgtactcga tgccgtttct cctatctctg
181 agcctcagaa ctgtcttcag tttccgtaca agggtaaaaa ggcgctctct gccccatccc
241 ccccgacctc gggaacaagg gtccgcattg aaccaggtgc gaatgttctc tctcattctg
301 cgccgttccc gcctccctc cccagccgc ggcctccgca tcccccgca ctgcaccctc
361 ggtgttggtt gcagcccgcg agcagttccc gtcaatccct ccccccctac acaggatgtc
421 catattagga catctgcgtc agcaggtttc cacggccttt ccctgtagcc ctggggggag
481 ccatcccgga aaccctcat cttggggggc ccacgagacc tctgagacag gaactgcgaa
541 atgctcacga gattaggaca cgcgcaagg cgggggcagg gagctgcgag cgctggggac
601 gcagccgggc ggccgcagaa gcgcccagg ccgcgcgcca cccctctggc gccaccgtgg
661 ttgagcccggt gacgtttaca ctcatccta aaacgcttgt tataaaagca gtggtgcgg
721 cgctctgtac tccaaccgca tctgcagcga gcaactgaga agccaagact gagccggcgg
781 ccgcgccgca gcgaacgagc agtgaccgtg ctccctacca gctctgcttc acagcgccca
841 cctgtctccg cccctcgccc cctcgccggg ctttgccctaa ccgccacgat gatgttctcg
901 ggcttcaacg cagactacga ggcgtcatcc tcccgtgca gcagcgctc cccggccggg
961 gatagcctct cttactacca ctacccgca gactccttct ccagcatggg ctgcctgtc
1021 aacgcgcagg taagctggc tcccgtcg cgcggggcgg ggggcttggg gtcgaggagg
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1261 ctggtctgca ctccaggacg gatctctgac attagctgga gcagacgtgt cccaagcaca
1321 aactcgctaa ctgagcctg gcttcttcgg ggaggtggca gaaagcggca atccccctc
1381 ccccgccagc ctggagcagc gaggaggat gaggaggag ggtgcagcgg gcgggtgtgt
1441 aaggcagttt cattgataaa aagcagttc attctggaga ctccggagcg gcgctgcgt
1501 cagcgagac gtcagggata tttataacaa acccccttcc aagcaagtga tgctgaagg
1561 ataacgggaa cgcagcgga ggatggaaga gacaggcact gcgctgcgga atgcctggga
1621 ggaaaagggg gagacctttc atccaggatg agggacattt aagatgaaat gtccgtggca
1681 ggatcgtttc tcttcaactg tgcagcggc actgggaact cggccacct gtgtccggaa
1741 cctgctcgtc cagctcggtt ttcccttct gttttgttct aggacttctg cagcgacctg
1801 gccgtctcca gtgccaactt cattcccacg gtcactgcca tctcgaccag tccggacctg
1861 cagtggctgg tcagcccg cctcgtctcc tctgtggccc catcgagac cagagccct
1921 caccctttcg gactccccgc cccctcgtc ggggcttact ccagggtg cgttgtgaag
1981 accatgacag gaggccgagc gcagagcatt ggcaggagg gcaagggtga acaggtgagg
2041 aactctagcg tactcttctt gggaatgtgg gggctgggtg ggaagcagcc ccggagatgc
2101 aggagcccag tacagaggat gaagccactg atggggctgg ctgcacatcc gtaactggga
2161 gccctggctc caagcccat ccacccaac tcagactctg agtctcacc taagaagtac
2221 tctcatagtt tcttccctaa gtttcttacc gcatgcttcc agactgggct cttcttgg
2281 ctcttgctga ggtcttatt ttaaagcaa gtcacaccta ttctgcaact gcaggtcaga

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2341 aatgggtttca cagtggggtg ccaggaagca gggaagctgc aggagccagt tctactgggg  
2401 tgggtgaatg gaggtgatg cagacacttt tactgaatgt cggctctttt ttgtgattat  
2461 tctagttatc tccagaagaa gaagagaaaa ggagaatccg aagggaagg aataagatgg  
2521 ctgcagccaa atgccgcaac cggaggaggg agctgactga tacactccaa gcggtaggta  
2581 ctctgtgggt tgctcctttt taaaacttaa gggaaagtgt gagattgagc ataaggccc  
2641 ttgagtaaga ctgtgtctta tgctttcctt tatccctctg tatacaggag acagaccaac  
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2761 aactagagtt catcctggca gctcaccgac ctgcctgcaa gatccctgat gacctgggct  
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2881 ccccgagtc tgaggaggcc ttccctctgc ctctcctcaa tgacctgag cccaagccct  
2941 cagtgaacc tgtcaagagc atcagcagca tggagctgaa gacctgagc ttgtatgact  
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3121 ggatggggcc catggccaca gagctggagc ccctgtgcac tccggtggtc acctgtactc  
3181 ccagctgcac tgcttacacg tcttctctcg tcttcacctt ccccgaggct gactccttcc  
3241 ccagctgtgc agctgcccac cgcaagggca gcagcagcaa tgagccttcc tctgactcgc  
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3361 acaagtgcc ctgccgagc tgggtcatta cagagaggag aaacacatct tccctaggag  
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3481 aaggacttga aagcatccat gtgtggactc aagtccttac ctcttccgga gatgtagcaa  
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3781 aatgaccaat attatactaa gaaaagatac gactttattt tctggtagat agaaataaat  
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3961 attgtgtttt taattttatt attaagatgg attctcagat atttataatt ttattttatt  
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4081 ttgtttgctt attgttccaa gacattgtca ataaaagcat ttaagttgaa tgcgaccaac  
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4981 aaaagttttc actaatgtgt acattttttt gtactctttt attctcgaaa gggaaggagg  
5041 gctattgccc tatcccttat taataaatgc attgtggttt ctggtttctc taataccata  
5101 tgcccttcat tcagtttata gtgggaggaa gtgggggaga aaaagtgtct cagaaatcaa  
5161 aagatatctc aaacagcaca aataatggct gatcgttctg caaacaataa gttacataat  
5221 agctcaagaa ggagaagtca acatgactct gaacaagctt taacttagaa actttatcat  
5281 cttaaggaag aacgtgacct ttgtccagga cgtctctggt aatggggcac ttacacacac  
5341 atgcacacgt acaaacaca gggaaaggag accgccttc tgccctgctc cgcgagtatc  
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5641 ctcttatatc acacaccact tggggtgctg tttctgctag acttgtgatg acagtggcct  
5701 taggatccct gtttctgtt caaagggcaa atattttata gccttttaaa atacctaaac  
5761 taaatacaga attaatataa ctaacaaaca cctggtctga aataacaagg tgatctaccc  
5821 tggaaaggaa ccagctgggtg ggccaggagc ggtgggtcac acctgtaatt ccagcacttt  
5881 gggaggtctg gacaggagga tcactggaat ccaggagttt gagaccagcc tgggcaacat  
5941 ggcaaaaccc agtgtgcttc tgttgtccca gctacactac tcaggaggct gaggcaggag  
6001 tatgacttga gcctgggagg gggaggttgc agagaactga tattgcacca ccactgcact  
6061 ccagcctggg tgacacagca aaacctatc tcaaaaaaaa aaaaaaaaaa aaggaaacca  
6121 gctggttccct gtaggtgtgc aataataaca accagaggaa gaaaaggaa acgatttccc  
6181 agatgaagaa ggcagctgg accttcggac

(2) INFORMATION FOR SEQ ID NO:2659:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: \_ base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2659

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1 gcagccgggc ggccgcagaa gcgcccaggc ccgcgcgcca cccctctggc gccaccgtgg
61 ttgagcccggt gacgtttaca ctcatccta aaacgcttgt tataaaagca gtggctgcgg
121 cgcctcgtac tccaaccgca tctgcagcga gcaactgaga agccaagact gagccggcgg
181 ccgcggcgca gcgaacgagc agtgaccgtg ctctaccca gctctgcttc acagcgccca
241 cctgtctccg cccctcggcc cctcgcccg ctttgcttaa ccgccacgat gatgttctcg
301 ggcttcaacg cagactacga ggcgtcatcc tcccgcgtga gcagcgcgct cccggccggg
361 gtagcctct cttactacca ctaccccgca gactccttct ccagcatggg ctgcctgtc
421 aacgcgcagg taaggctggc ttcccgctgc cgccggggcg ggggcttggg gtccgggagg
481 aggagacacc gggcgggacg ctccagtaga tgagtgggg gctcccttgt gcctggaggg
541 aggtctgcgt ggccggagcg gtgcgggctc gggggctcgg gacttgctct gagegcacgc
601 acgcttgcca tagtaagaat tggttccccc ttcgggaggc aggttcgttc tgagcaacct
661 ctggtctgca ctccaggacg gatctctgac attagctgga gcagacgtgt cccaagcaca
721 aactcgctaa ctagagcctg gcttcttcgg ggaggtggca gaaagcggca atccccctc
781 ccccgccagc ctggagcacg gaggaggat gaggaggagg ggtgcagcgg gcgggtgtgt
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961 ataacgggaa cgcagcggca ggatggaaga gacaggcact gcgctgcgga atgcctggga
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1081 ggatcgtttc tcttcaactg tgcagcgcg actgggaact cggccacact gtgtccggaa
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1381 accatgacag gaggcggagc gcagagcatt ggagggagg gcaaggtgga acaggtgagg
1441 aactctagcg tactcttctt gggaatgtgg gggctgggtg ggaagcagcc ccggagatgc
1501 aggagcccg tacagaggat gaagccactg atggggctgg ctgcacatcc gtaactggga
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2761 acaagtgcc ctgcccagc tgggtcatta cagagaggag aaacacatct tccctagagg
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3181 aatgaccaat attatactaa gaaaagatac gactttattt tctggtagat agaaataaat
3241 agctatatcc atgtactgta gttttcttc aacatcaatg ttcattgtaa tgttactgat
3301 catgcattgt tgaggtggtc tgaatgttct gacattaaca gttttccatg aaaacgtttt
3361 attgtgtttt taatttattt attaagatgg attctcagat atttatattt ttattttatt
3421 tttttctacc ttgaggtctt ttgacatgtg gaaagtgaat ttgaatgaaa aatttaagca
3481 ttgtttgctt attgttccaa gacattgtca ataaaagcat ttaagttgaa tgcgaccaac
3541 cttgtgctct tttcattctg gaagt
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(2) INFORMATION FOR SEQ ID NO:2660:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2660

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1 cctcagagtc gaagcttatt taaaagcata ttttccaatg cctgctttag ctgtggaaaa
61 ggaagactct ccgagggcaa atccaggagt catggaaaac aatgggcagg gcagcttggt
121 gctgtgactg gatgggtctt taagggtgtt tcccttgaat aaagaatgag ggaattccac
181 caggggaagg agagtagacc aaacatttgg tgaacagaaa gggagacaga gtcttttagt
241 ttattcccca aatattcctg gagagnccct tgagacacct ggtaggatta tagtgatcta
301 aagagggcatg gccatgtgac tgcttnggcc aatgatgtat gggcagaagt gatgtgtgcc
361 ataagtggat gctctgacag acatgatgtt ccgagttcct tccccacagn caggatagct
421 gtgaaaaggg gtatcaacac gaggcctcct tcagcctgag cccttttagt actacaatga
481 gcagagctac cctgccaacc tacaacggtc atgtagnaga aatgaccaac tttcactgga
541 ataagncaact gatatgttag gggtgnntgg tagggcagca taacactnnc tntcctgaca
601 gaactgggag tgagagataa ggctggagag agaaggaggt ggattgtgaa aahcccttc
661 tccaaggcat aggaatcgga actctcctga ttgtaaggaa aagccaatga aggtctccaa
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901 tgaacggagt tacagtcaga ggatcaggca agaaaatttc ttctatgcca caagcgctat
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2701 aaccaccct cgcccgacc cctggcccaa acaactggc caggttcctt cgtcccggt
2761 ccctgcatcc ccgcacccc cgtccgcagc cgtgaacttg agccccctc catcagaggt
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2881 cacaatgcac cggcggggc gggaaaaacg gccgggggag gggaccgggg aacagagggc
2941 cgagaggcgt gcggcagggg ggagggtagg agaaaagaag gcccgactgt aggagggcag
3001 cgagagcatta cctcatcccg tgagcctcgg .cgggcccaga gaagaatctt ctagggtgga
3061 gtctccatgg tgacggcgcg gcccgcccc ctgagagcga cgcgagccaa tgggaaggcc
3121 ttggggtgac atcatgggt atttttaggg gttgactggt agcagataag tgttgagctc
3181 gggttgata agggctca

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(2) INFORMATION FOR SEQ ID NO:2661:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: \_ base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2661

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1 cccggggagg ggaccgggga acagagggcc gagaggcgtg cggcaggggg gagggtagga
61 gaaagaagg cccgactgta ggagggcagc ggagcattac ctcattccgt gagcctccgc
121 gggcccagag aagaatcttc tagggtagg tctccatggt gacggggcgg cccgcccccc
181 tgagagcgac gcgagccaat gggaaggcct tggggtgaca tcatgggcta tttttagggg

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241 ttgactggtta gcagataagt gttgagctcg ggctggataa gggctcagag ttgactgag  
 301 tgtggctgaa gcagcgaggc gggagtgagg gtgcgcggag tcaggcagac agacagacac  
 361 agccagccag ccaggctggc agtatagtcc gaactgaaa tcttattttc ttttcacctt  
 421 ctctctaact gccagagct agcgctgtg gctcccgggc tgggtggttc ggagtgacca  
 481 gagagccttg tctccagccg gccccgggag gagagccctg ctgcccaggc gctgttgaca  
 541 gcggcggaaa gcagcggtag cccacgcgcc cgccggggga cgtcggcgag cggctgcagc  
 601 agcaaaagac tttcccggcg gggaggaccg gagacaagtg gcagagtcgc ggagcgaact  
 661 tttgcaagcc tttctgctg cttaggtctc tccacggcgg taaagaccag aaggcggcgg  
 721 agagccacgc aagagaagaa ggacgtgcgc tcagcttcgc tcgcaccggt tgttgaactt  
 781 gggcgagcgc gagccgcggc tgccggggcg cccctcccc tagcagcgga ggaggggaca  
 841 agtcgtcggg gtccggggcg ccaagaccgc ccgcccggcg gccactgcag ggtccgcact  
 901 gatcgcgtcc gcggggagag ccgctgctct gggaagtga ttcgctgcg gactccgagg  
 961 aaccgctgcg cccgaagagc gctcagtgag tgaccgcgac ttttcaaagc cgggtagcgc  
 1021 gcgcgagtcg acaagtaaga gtgcgggagg catcttaatt aacctgcgc tccctggagc  
 1081 gagctggtga ggagggcgca gcggggacga cagccagcgg gtgcgtgcgc tcttagagaa  
 1141 actttccctg tcaaaggctc cggggggcgc ggggtgcccc cgcttgccag agccctgttg  
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 1261 atgactgcaa agatggaaac gaccttctat gacgatgcc tcaacgcctc gttctccccg  
 1321 tccgagagcg gaccttatgg ctacagtaac cccaagatcc tgaacagag catgaccctg  
 1381 aacctggccg acccagtggg gagcctgaag ccgcacctcc gcgccaagaa ctccgacctc  
 1441 ctcacctcgc ccgacgtggg gctgctcaag ctggcgtcgc ccgagctgga gcgctgata  
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 1561 aagaacgtga cagatgagca ggaggggttc gccgagggtc tcgtgcgcgc cctggccgaa  
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 1861 cccagcagc agcagcagcc gccgcaccac ctgccccagc agatgcccgt gcagcaccg  
 1921 cggtgcagc ccctgaagga ggagcctcag acagtgcgc agatgcccgt cgagacaccg  
 1981 cccctgtccc ccctgcacat ggagtcccag gagcggatca aggcggagag gaagcgcag  
 2041 aggaaccgca tcgctgcctc caagtgccga aaaaggaagc tggagagaat cgcccggtg  
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## (2) INFORMATION FOR SEQ ID NO:2662:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2662

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3541 aacagatctt gaattgcttc cttttactac tttttgttc ccaagtata tactgaagtt  
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## (2) INFORMATION FOR SEQ ID NO:2663:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: \_ base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2663

1 cggccccaga aaacccgagc gagtaggggg cgccgcgcag gagggaggag aactgggggc  
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301 gctggggggac cgccggcgcg gccgcgcgct gccggggcgag aggctggggg gccggggccg  
361 gggccgtgcc ccggagcggg tcggaggccg gggccggggc cgggggacgg cggtccccg  
421 cgccgctcca gcggtcggg gatcccgcc gggccccgca gggaccatgg cagccgggag  
481 catcaccacg ctgcccgcct tgcccaggga tggcggcagc ggcgccttc cgcccgcca  
541 cttcaaggac cccaagcggc tgtactgcaa aaacgggggc ttcttcctgc gcatccacc  
601 cgacggccga gttgacgggg tccgggagaa gagcgaccct cacatcaagc tacaacttca  
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## (2) INFORMATION FOR SEQ ID NO:2664:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2664

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1 cagtgcagctg tgattgcacc actgcaattt agcctgagtg acagaatgaa aaaaaaattt
61 ttttaaagga aaacacaaaa agaatatgct gtcaacaggg atgggaggaa gaccaccttt
121 actgctatac acatttgtag ctttttagatg ttgatcaata tgaatatatt atacacacag
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301 caccacaaa gtcactcagg catcctgaca agggtaagtg aggggagcct cttggaaaa

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## (2) INFORMATION FOR SEQ ID NO:2665:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2665

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181 caaagtgggt ccaacagaga aaggtctgtg ttcaccaggt ggccttgacc ctggagagtc  
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2281 ggcccgggtg gtactggtgg ccgtggacaa gggcgtgttc gtgctgaata agaagaacaa  
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5641 ggacctggt aagcagctct acaacgttga ggcacatcc tatgccctct tggccctact  
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5821 ataccaaaag gacgcccctg accaccagga actgaacctt gatgtgtccc tccaactgcc  
5881 cagccgcagc tccaagatca cccaccgtat ccactgggaa tctgccagcc tctcgcagtc  
5941 agaagag

## (2) INFORMATION FOR SEQ ID NO:2666:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2666

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121 ctggggagtc ccatgtactc tatcatcacc cccaacatct tgcggctgga gagcgaggag  
181 accatgggtc tggaggccca cgacgcgcaa ggggatgttc cagtcactgt tactgtccac  
241 gacttcccag gcaaaaaact agtgctgtcc agtgagaaga ctgtctgac ccctgccacc  
301 aaccacatgg gcaacgtcac cttcacgac ccagccaaca gggagtcaa gtcagaaaag  
361 gggcgcaaca agttcgtgac cgtgcaggcc accttcggga ccaagtggt ggagaagggt  
421 gtgctgggtc gcctgcagag cgggtacctc ttcattccaga cagacaagac catctacacc  
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541 cggacggtca tggtaacat tgagaacccg gaaggcatcc cggtaagca ggactccttg  
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661 atgggcccagt ggaagatccg agcctactat gaaaactcac cacagcaggt cttctccact  
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4081 acctgtgcgg tggtgacaat gtaccatgct aaggccaaag atcaactcac ctgtaataaa  
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4561 aagctgaaca agctctgccg tgatgaactg tgccgctgtg ctgaggagaa ttgcttcata

4621 caaaagtcgg atgacaaggt caccctggaa gaacggctgg acaaggcctg tgagccagga  
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4741 tacatcatgg ccattgagca gaccatcaag tcaggctcgg atgaggtgca ggttgagacag  
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4921 atcatcggga aggacacttg ggtggagcac tggcctgagg aggacgaatg ccaagacgaa  
4981 gagaaccaga aacaatgcca ggacctcggc gccttcaccg agagcatggt tgtctttggg  
5041 tgccccaact gaccacaccc ccattcc

## (2) INFORMATION FOR SEQ ID NO:2667:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2667

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61 ttttaaagga aaacacaaaa agaatatgct gtcaacaggg atgggaggaa gaccaccttt  
121 actgctatac acatttgtac ctttttagat ttgatcaata tgaatatatt atacacacag  
181 acacacacac agacacacac acacacacaa acaatacaat ttaatatcct aagaggatat  
241 tgacattaga caggtacaaa agctctagaa atgaggactt tcctcagtga tgactttttt  
301 caccacaaaa gtcactcagg catcctgaca agggtaagtg aggggagcct ccttgaaaaa  
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## (2) INFORMATION FOR SEQ ID NO:2668:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2668

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3781 tttttaaatg gatgctaaaa ttcctgaagt tcagctgcat acagtttgca cttatggact  
3841 cctgttggtt aagttcgttt tttgttttc ttctttttt aaacattcat agctggtcct  
3901 atttgtaaag ctactttac ttagaattag tggcacttgc ttttattaga gaattgatttc  
3961 aaatgctgta actttctgaa ataacatggc cttggagggc atgaagacag atactcctcc  
4021 aaggttattg gacaccgaa acaataaatt ggaacacctc ctcaaacctt cactcagga  
4081 atgtttgctg gggccgaaag aacagtccat tgaaaggag tattacaaaa acatggcctt  
4141 tgcttgaaag aaaataccaa ggaacaggaa actgatcatt aaagcctgag tttgctttc

## (2) INFORMATION FOR SEQ ID NO:2669:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (x) SEQUENCE DESCRIPTION: SEQ ID NO:2669

1 ctacctcaa ccatgggctt tttgggaata cttgttttt taatcttctt ggggaaaacc  
61 tggggacagg agcaaacata tgtcatttca gcacacaaaa tattcctgtt tggagcatct  
121 gaaaatattg tgattcaagt ttatggatac actgaagcat ttgatgcaac aatctctatt  
181 aaaagttatc ctgataaaaa atttagttac tctcaggcc atgttcattt atcctcagag  
241 aataaattcc aaaactctgc aatcttaaca atacaaccaa acaattgccc tggaggacaa  
301 aacccagttt cttatgtgta tttggaagtt gtatcaaagc atttttcaaa atcaaaaaga  
361 atgccaataa cctatgacaa tggatttctc ttcattcata cagacaaaac tgtttatact  
421 ccagaccagt cagtaaaagt tagagtttat tcgttgatg acgacttgaa gccagccaaa  
481 agagaaactg tcttaacctt catagatcct gaaggatcag aagttgacat ggtagaagaa  
541 attgatcata ttggaattat ctcttttctt gacttcaaga ttccgtctaa tctagatat  
601 ggtatgtgga cgatcaaggc taaatataaa gaggactttt caacaactgg aaccgcata  
661 tttgaagtta aagaatatgt cttgccacat ttttctgtc caatcgagcc agaataaat  
721 ttcattgggt acaagaactt taagaatttt gaaattacta taaaagcaag atatttttat  
781 aataaagtag tcaactgaggc tgacgtttat atcacatttg gaataagaga agacttaaaa  
841 gatgatcaaa aagaaatgat gcaaacagca atgcaaaaac caatgttgat aaatggaatt  
901 gctcaagtca catttgattc tgaaacagca gtcaaagaac tgtcatacta cagtttagaa  
961 gatttaaaaca acaagtacct ttatattgct gtaacagtca tagagtctac aggtggattt  
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1081 gttgctactc ctcttttctt gaagcctggg attccatata ccatcaaggt gcaggttaaa  
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1201 gtaaaccaag agacatctga cttggatcca agcaaaagtg taacacgtgt tgatgatgga  
1261 ttagcttctt ttgtgcttaa tctccatctt ggagtgcagg tgctggagtt taatgtcaaa  
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1381 tactcatctc tcagccaaaag ttacctttat attgattgga ctgataacca taaggctttg  
1441 ctagtgggag aacatctgaa tattattggt acccccaaaa gcccatatat tgacaaaata  
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1561 aaattttcag atgcatctta tcaaaagtata aacattccag taacacagaa catggttctt  
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1681 gattcagttc ggttaaatat tgaagaaaaa tgtggcaacc agctccaggt tcatctgtct  
1741 cctgatgcag atgcataatc tccaggccaa actgtgtctc ttaatatggc aactggaatg  
1801 gattcctggg tggcattagc agcagtggac agtctgtgt atggagtcca aagaggagcc  
1861 aaaaagccct tggaaagagt atttcaattc ttagagaaga gtgatctggg cgtggtggca  
1921 ggtggtggcc tcaacaatgc caatgtgttc cacctagctg gacttacctt cctactaat  
1981 gcaaatgcag atgactccca agaaaatgat gaaccttgta aagaaattct caggccaaga  
2041 agaacgctgc aaaagaagat agaagaaata gctgctaaat ataaacattc agtagtgaag  
2101 aatgttgtt acgatggagc ctgcgttaat aatgatgaaa cctgtgagca gcgagctgca  
2161 cggattagtt tagggccaag atgcatacaa gctttcactg aatgttgtgt cgtcgcaagc

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2221 cagctccgtg ctaatatetc tcataaagac atgcaattgg gaaggctaca catgaagacc
2281 ctgttaccag taagcaagcc agaaattcgg agttattttc cagaaagctg gttgtgggaa
2341 gttcatcttg ttcccagaag aaaacagttg cagtttgccc tacctgattc tctaaccacc
2401 tgggaaattc aaggcattgg catttcaaac actggtatat gtgtgtctga tactgtcaag
2461 gcaaaggtgt tcaaagatgt cttcctggaa atgaatatac catattctgt tgtacgagga
2521 gaacagatcc aattgaaagg aactgtttac aactatagga cttctgggat gcagtctctg
2581 gttaaaatgt ctgctgtgga gggaatctgc acttcggaaa gccagtcac tgatcatcag
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2701 acattcactg tgcttcctct ggaaattggc cttcacaca tcaatttttc actggagact
2761 tggtttgaaa aagaaatctt agtaaaaaca ttacgagtgg tgccagaagg tgtcaaaagg
2821 gaaagctatt ctggtgttac ttggatcct aggggtattt atggtaccat tagcagacga
2881 aaggagtctc catacaggat acccttagat ttggtcccca aaacagaaat caaaaggatt
2941 ttgagtgtaa aaggactgct tgtaggtgag atcttgtctg cagttctaag tcaggaaggc
3001 atcaatatcc taaccacact ccccaaaggg agtgcagagg cggagctgat gagcgttgtc
3061 ccagtattct atgtttttca ctacctggaa acaggaatc attggaacat ttttctattc
3121 gacccattaa ttgaaaagca gaaactgaag aaaaaattaa aagaagggat gttgagcatt
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3301 caaaattcaa tttgtaattc tttattgtgg ctagttaga attatcaatt agataatgga
3361 tctttcaagg aaaattcaca gtatcaacca ataaaattac aggttacctt gcctgttgaa
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3481 gatatatgcc ccctggtgaa aatcgacaca gctctaatta aagctgacaa ctttctgctt
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4261 tctggatcct ctcatgcggt gatggacatc tccttgcta ctggaatcag tgcaaatgaa
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4381 gatggacatg ttattctgca actgaattcg attccctcca gtgatttctt ttgtgtacga
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4561 cagaaagtct gtgaaggagc cgctgcaag tgtgtagaag ctgattgtgg gcaaatgcag
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4681 attgcatatg cttataaagt tagcatcaca tccatcactg tagaaaatgt ttttgcagg
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5281 cggaaacaat aaattggaac acctctcaa acctaccact caggaatgtt tgctggggcc
5341 gaaagaacag tccattgaaa gggagtatta caaaaacatg gcctttgctt gaaagaaaat
5401 accaaggaa caggaaactga tcattaaagc ctgagtttgc tttc

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## (2) INFORMATION FOR SEQ ID NO:2670:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2670

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1 ctacctccaa ccatgggcct tttgggaata ctttgttttt taatcttctt ggggaaaacc
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121 gaaaatattg tgattcaagt ttatggatac actgaagcat ttgatgcaac aatctctatt
181 aaaagttatc ctgataaaaa atttagttac tctcaggcc atgttcattt atcctcagag
241 aataaattcc aaaactctgc aatcttaaca atacaacca aacaattgcc tggaggacaa
301 aaccagttt cttatgtgta tttggaagtt gtatcaaagc atttttcaaa atcaaaaaga
361 atgccaataa cctatgacaa tggatttctc ttcattcata cagacaaacc tgtttatact

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421 ccagaccagt cagtaaaagt tagagtttat tcgttgaatg acgacttgaa gccagccaaa  
481 agagaaaactg tcttaacctt catagatcct gaaggatcag aagttgacat ggtagaagaa  
541 attgatcata ttggaattat ctcttttctt gacttcaaga ttccgctcaa tcctagatat  
601 ggtatgtgga cgatcaaggc taaatataaa gaggactttt caacaactgg aaccgcatat  
661 tttgaagtta aagaatatgt cttgccacat ttttctgtct caatcgagcc agaataaat  
721 ttcattgggtt acaagaactt taagaatttt gaaattacta taaaagcaag atatttttat  
781 aataaagtag tcaactgagge tgacgtttat atcacatttg gaataagaga agacttaaaa  
841 gatgatcaaa aagaaatgat gcaaacagca atgcaaaaca caatgttgat aaatggaatt  
901 gctcaagtca catttgattc tgaaacagca gtcaaaagac tgtcatacta cagtttagaa  
961 gattttaaaca acaagtacct ttatatgtct gtaacagtca tagagtctac aggtggattt  
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1501 actcactata attacttgat tttatccaag ggcaaaatta tccatttttg cagagggag  
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2221 cagctccgtg ctaatatctc tcataaagac atgcaattgg gaaggctaca catgaagacc  
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4501 gaataccaca gaccagataa acagtgtacc atgttttata gcacttccaa tatcaaaatt  
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4621 gaagaattgg atctgacaat ctctgcagag acaagaaaac aaacagcatg taaaccagag  
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5281 cggaacaat aaattggaac acctcctcaa acctaccact caggaatggt tgcgtgggccc  
5341 gaaagaacag tcattgaaa gggagtatta caaaaacatg gcctttgctt gaaagaaaat  
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## (2) INFORMATION FOR SEQ ID NO:2671:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2671

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61 gagtttaatg tcaaaactga tgctccagat cttccagaag aaaatcaggc caggggaaggt  
121 taccgagcaa tagcatactc atctctcagc caaagtacc tttatattga ttggactgat  
181 aaccataagg ctttgctagt gggagaacat ctgaatatta ttgttaccac caaaagccca  
241 tatattgaca aaataactca ctataattac ttgattttat ccaagggcaa aattatccac  
301 tttggcacga gggagaaatt ttcagatgca tcttatcaaa gtataaacat tccagtaaca  
361 cagaacatgg ttccttcac cgcacttctg gtctattata tcgtcacagg agaacagaca  
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481 caggttcacg tgtctcctga tgcagatgca tattctccag gccaaactgt gtctcttaat  
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1021 ctacacatga agaccctgtt accagtaagc aagccagaaa ttcggagtta tttccagaa  
1081 agctgtgtgt gggaaagtca tctgttccc agaagaaaac agttgcagtt tgcctacct  
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1201 gctgatactg tcaaggcaaa ggtgttcaaa gatgtcttcc tggaaatgaa tataccatat  
1261 tctgtgttac gaggagaaca gatccaattg aaaggaactg tttacaacta taggacttct  
1321 gggatgcagt tctgtgttaa aatgtctgct gtggagggaa tctgcacttc ggaaagccca  
1381 gtcattgatc atcagggcac aaagtctcc aaatgtgtgc gccagaaagt agagggctcc  
1441 tccagtcact tggtagactt cactgtgctt cctctggaaa ttggccttca caacatcaat  
1501 ttttctctgg agacttgggt tggaaaagaa atcttagtaa aaacattacg agtgggtgcca  
1561 gaaggtgtca aaagggaaag ctattctgggt gttactttgg atcctagggg tatttatgggt  
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## (2) INFORMATION FOR SEQ ID NO:2672:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2672

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(2) INFORMATION FOR SEQ ID NO:2673:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: \_ base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2673

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## (2) INFORMATION FOR SEQ ID NO:2674:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: \_ base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2674

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421 agcctgggca acatagtgaa aaaccatctc aaaaaagaaa aaattagcca ggcagtgtgg
481 catgcacctg tggtttcagc tacttaggag cagaggtggg aggatcgctt gattctggga
541 gttcaaggtt gcattgagct gtgatcgcg cagtgcactc tcgcttgggt gacagagcaa
601 gaccttgtct caaaaaattt aaacaaaac aaaaaaact ggttatttgg ctttttattg
661 ttgaattata agagttttta aaatatatt ctggaaacaa atcccttatt agagatatga
721 tttgcaataa tttctccaa tttttttt tttaaagaca aagtttcaact ttggtgcccc
781 ggctggtctt cattcctggc ttcaagagat gctcttacct ccacctctg aagcccaaaa
841 gggctggaat tacagccagt gagccactgc acccagcctc caattcttta gattttacat
901 tttagaacca aaatgggtta aatacactgt tctgtaatct gctcttttct ttaatagtag
961 ttcattgtaca tctttcaagg tccagagaaa gctctcactt tctccccgtt ttatttttcc
1021 ttcctctcatt ctttttcaact gctgcatagc attccattgt aattttgcca ctgtttatta
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1081 gaccagtcct ctgctgagct ttacagagcc cttagttggg atgttagtga gaaaccatga  
1141 cagcagtggg gactgtcctc tccctgacat gctgtcagct tttggatgat gtgaaaatgc  
1201 aagcaggcac aggaaatgtc tctctaactt gcttacactt cctccctgaa cctgctggtt  
1261 tcacaactcc tgcaaggcaca cctccctccc cgctgccag tgtcaccagc ctgttgcttc  
1321 tgtgagaaaag taccactgta agaggccaaa gggcatgac attttctctt ttcacctgtt  
1381 ctaggttgcc agcaaattccc acgggctcc tgacgctgcc cctggggcca caggctccctc  
1441 gagtgtctgga aggatgaagg attcctgcat cactgtgat gccatggcgc tgcgtctcgg  
1501 gttctttttc ttcggtaggc

## (2) INFORMATION FOR SEQ ID NO:2675:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: \_ base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2675

1 cagggcagac tggtagcaaa gccccacgc ccagccagga gcaccgcccgc ggactccagc  
61 acaccgaggg acatgctggg cctgcgcccc ccactgctcg ccctgggtggg gctgctctcc  
121 ctccgggtcgc tctctctca ggagtgcacg aagttcaagg tcagcagctg ccgggaatgc  
181 atcgagtcgg ggcccggctg cacttggtgc cagaagctga acttcacagg gccgggggat  
241 cctgactcca ttcgctgcca cccccggcca cagctgctca tgaggggctg tgcggctgac  
301 gacatcatgg accccacaag cctcgtgaa acccaggaa accacaatgg gggccagaag  
361 cagctgtccc cacaaaaagt gacgtttac ctgcgaccag gccaggcagc agcgttcaac  
421 gtgaccttcc ggccggccaa gggctacccc atcgacctgt actatctgat ggacctctcc  
481 tactccatgc ttgatgacct caggaatgtc aagaagctag gtggcgacct gctccgggcc  
541 ctcaacgaga tcaccgagtc cgcccgcat ggcttcgggt ccttcgtgga caagaccgtg  
601 ctgccgttcg tgaacacgca cctgataag ctgcgaaacc catgccccaa caaggagaaa  
661 gagtgccagc ccccgtttgc cttcaggcac gtgctgaagc tgaccaacaa ctccaaccag  
721 tttcagaccg aggtcgggaa gcagctgatt tccggaaacc tggatgcacc cgagggtggg  
781 ctggacgcca tgatgcaggt cgccgctgc ccggaggaaa tcggctggcg caacgtcacg  
841 cggtgctggt tgtttgccac tgatgacggc ttccatttcg cgggcgacgg aaagctgggc  
901 gccatcctga cccccaacga cgcccgctgt cactggagg acaacttga caagaggagc  
961 aacgaattcg actaccatc ggtggggccag ctggcgccaca agctggctga aaacaacatc  
1021 cagccccatc tcgcggtgac cagtaggatg gtgaagacct acgagaaact caccgagatc  
1081 atccccaagt cagccgtggg ggagctgtct gaggactcca gcaatgtggt ccatctcatt  
1141 aagaatgctt acaataaact ctcctccagg gtcttcctgg atcacaacgc cctccccgac  
1201 accctgaaag tcacctacga ctcctctgc agcaatggag tgacgcacag gaaccagccc  
1261 agaggtgact gtgatggcgt gcagatcaat gtcccgatca ccttcagggt gaaggtcacg  
1321 gccacagagt gcatccagga gcagtcgttt gtcattccgg cgctgggctt caccggacata  
1381 gtgaccgtgc aggttcttcc ccagtgtgag tgcgggtgcc gggaccagag cagagaccgc  
1441 agcctctgcc atggcaaggg cttcttgagg tgcggcatct gcaggtgtga cactggctac  
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1561 tgccggaagg acaacaactc catcatctgc tcagggtcgg gggactgtgt ctgcgggcag  
1621 tgcctgtgcc acaccagcga cgtccccggc aagctgatat acgggcagta ctgcagtggt  
1681 gacaccatca actgtgagcg ctacaacggc caggtctgcg gcggccccgg gagggggctc  
1741 tgcctctgcg ggaagtgcg ctgccacggc ggctttgagg gctcagcgtg ccagtgcgag  
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1861 cgctgcaacg tatgcgagtg ccattcaggc taccagctgc cttgtgcca ggagtgcctc  
1921 ggctgcccc caccctgtgg caagtacatc tctgcgccc agtgctgaa gttcgaaaag  
1981 ggccctttg ggaagaactg cagcgcgcg tgctccggcc tgcagctgtc gaacaacccc  
2041 gtgaagggca ggacctgcaa ggagagggac tcagagggct gctgggtggc ctacacgctg  
2101 gagcagcagg acgggatgga ccgctacctc atctatgtgg atgagagccg agagtgtgtg  
2161 gcaggcccca acatcgccgc catcgtcggg ggcaccgtgg caggcatcgt gctgatccgg  
2221 attctctgc tggatcatct gaaggtcttg atccacctga gcgacctcgg ggagtacagg  
2281 cgctttgaga aggagaagct caagtccag tggaaacaatg ataattccct tttcaagagc  
2341 gccaccacga cgtcatgaa cccaagttt gctgagagtt aggagcactt ggtgaagaca  
2401 aggcgctcag gacccacat gtctgcccc taccgcccgc gagacatggc ttggccacag  
2461 ctcttgagga tgtcaccaat taaccagaaa tccagttatt tccgcccctc aaaatgacag  
2521 ccatggccgg ccggtgcttc tgggggctcg tcggggggac agctccactc tgactggcac  
2581 agtctttgca tggagacttg aggaggctt gaggttggtg aggttaggtg cgtgtttcct  
2641 gtgcaagtca ggacatcagt ctgattaaag gtggtgcca tttatttaca tttaaacttg  
2701 tcagggtata aaatgacatc ccattaatta tattgttaat caatcacgtg tatagaaaaa  
2761 aaaataaaac ttcaat

## (2) INFORMATION FOR SEQ ID NO:2676:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: \_ base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2676

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1 ctgcctctgg tggggctgct ctccctcggg tgcgtcctct ctccaggagtg cacgaagttc
61 aaggtcagca gctgccggga atgcatcgag tccggggccc gctgcacctg gtgccagaag
121 ctgaacttca cagggccggg ggtacctgac tccattcgtc ggcacacctg gccacagctg
181 ctcatgaggg gctgtgcggc tgacgacatc atggacccca caagcctcgc tgaacccag
241 gaagaccaca atgggggcca gaagcagctg tccccacaaa aagtgcgctt ttacctgcga
301 ccaggccagg cagcagcgtt caacgtgacc ttccggcggg ccaagggcta ccccatcgac
361 ctgtactatc tgatggacct ctctactcc atgcttgatg acctcaggaa tgtcaagaag
421 ctagggtggc acctgctccg ggccctcaac gagatcaccc agtccggccg cattggcttc
481 gggctcctcg tggacaagac cgtgctgccg ttcgtgaaca cgcacctga taagctgcga
541 aacccatgcc ccaacaagga gaaagagtgc ccgcccccg ttgccttcag gcacgtgctg
601 aagctgacca acaactccaa ccagtttcag accgaggtcg ggaagcagct gatttcggga
661 aacctggatg caccggaggg tgggctggac gccatgatgc aggtcgccgc ctgcccggag
721 gaaatcggct ggcgcaacgt cagcgggtg ctggtgtttg cactgatga cggcttccat
781 ttgcggggcg acggaagct ggccgcatc ctgaccccca acgacggccg ctgtcacctg
841 gaggacaact tgtacaagag gagcaacgaa ttcgactacc catcggtggg ccagctggcg
901 cacaagctgg ctgaaaacaa catccagccc atcttcgagg tgaccagtag gatgtgaag
961 acctacgaga aactcaccga gatcatcccc aagtcagccg tgggggagct gtctgaggac
1021 tccagcaatg tgggtccatct cattaagaat gcttacaata aactctctc cagggtcttc
1081 ctggatcaca acgcccctcc cgacacctg aaagtcacct acgactcctt ctgcagcaat
1141 ggagtgacgc acaggaacca gccagaggt gactgtgatg gcgtgcagat caatgtcccg
1201 atcaccttcc aggtgaaggt cagggccaca gactgcatcc agggagcagtc gttgtcctc
1261 cgggcgctgg gcttcacgga catagtgacc gtgcaggctc ttcccagtg tgagtgcggg
1321 tgccgggacc agagcagaga ccgacgctc tgccatggca aggtctctt ggagtgcggc
1381 atctgcaggt gtgacactgg ctacattggg aaaaactgtg agtgccagac acagggccgg
1441 agcagccagg agctggaagg aagctgcccg aaggacaaca actccatcat ctgctcaggg
1501 ctgggggact gtgtctgcgg gcagtgcctg tgccacacca gcgacgtccc cggcaagctg
1561 atatacgggc agtactgcga gtgtgacacc atcaactgtg agcgctacaa cggccaggtc
1621 tgccggcgcc cggggagggg gctctgtctc tgccgggaag gccgctgcca cccgggcttt
1681 gagggtctcag cgtgccagtg cgagaggacc actgagggtc gcctgaaccc gcggcgtgtt
1741 gagtgtagtg gtcgtggccg gtgcccgtgc aacgtatgag agtgccattc aggtaccag
1801 ctgcctctgt gccaggagtg ccccggtgac ccctcacctc gtggcaagta catctcctg
1861 gccagatgcc tgaagtccga aaagggcccc tttgggaaga actgcagcgc ggcgtgtccg
1921 ggcctgcagc tgcgaacaa cccggtgaag ggcaggacct gcaaggagag ggactcagag
1981 ggctgctggg tggcctacac gctggagcag caggacggga tggaccgcta cctcatctat
2041 gtggatgaga gccgagagtg tgtggcaggc ccaacatcg ccgccatcgt cgggggcacc
2101 gtggcaggca tcgtgctgat cggcattctc ctgctgtgta tctggaaggc tctgatccac
2161 ctgagcgacc tccgggagta caggcgcttt gagaaggaga agctcaagtc ccagtggaac
2221 aatgataatc cccttttcaa gagegccacc acgacgggtc tgaaccccaa gtttgcgtag
2281 agttaggagc a
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(2) INFORMATION FOR SEQ ID NO:2677:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2677

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1 gagctcagaa attcaagacc agcctgggca aggtagagag acccccatgt ctacaaaaaa
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121 gaggtgggag aatgactcga gcccgtgagt tgaggctgca gtgagccgag atcacaccac
181 tccagcctag gcaagagtga gacctctctt caaaaaaaaa aaaaaaaaaa aaaaaaaaaa
241 aaccatcaaa atgttttgca cagcagtcac gccattttac atttctgcca gcaatgtgca
301 ccaggcttcc agtttcttca catcttcaat aactcttatt tcctttgctt taaactctaa
361 ccatcaaagt aggtgtaaag ggtatctcac tgtggtttga ttgcatcttc tctaagtact
421 aatagtgtta agtatcattt catgtgcagt ttggccattt atatgtcatt ggagaaatgt
481 ctactcaaac cgtttgctca tttagaaact taggtaggtt ggtctgagtg cagtgtgttt
541 taaaactaat ttttttttga gacaaagtct cactctgtcg cccaggctgg aatgcaatgg
601 tgagatcttg gctcactaca acctccatct cctgggttca agcaattctt ctgcctcagc
661 ctctcaagta gctgggatta caggcatgag ccaccacgac tggctaattt ttgtattttt
721 ggtagagacg ggggtttctc catgttgccc aggtggtct cgaactcttg acctcaggtg
781 atccacctgc ctgcgctcc acagggttag gattagaggt gtgagccacc gcaccaggcc
841 gtttaaaact aatggagcac aaccagttac caatatcttt gttccttctc cactccctct
901 gcttcaactt gactagccta aaataaataa atttaaaaaa ctgggacacag tggctcacac
961 ctgtaatccc agcactttgg gagggcagg caggaggatt acttgagcat aggagttcaa
1021 gatcagcctg ggcaactagt gaaaaacat ctcaaaaaag aaaaattagc caggcatggt
1081 ggcagtcacc tgtggtttca gctacttaga gcagaggtgg aggtatcgctt gattctggag
1141 ttcaagggtg cattgagctg tgatcgcgcc agtgcactct cgcttgggtg acagagtaag
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1201 accttgtctc aaaaaattta aaacaaaaca aaaaaaactg gttatttgtc tttttattgg  
1261 tgaattataa gaggttttaa aaatatattc tggaaacaaa tcccttatta gagatatgat  
1321 ttgcaaatat tttctccaat tttttttttt tttaaagaca aagtttcaact ttgtcgccca  
1381 ggctgggtctt gattcctggc ttcaagagat gctcttacct ccacctcctg aagcccaag  
1441 ggctgggaatt acagccagtg agcctgcacc cagcctccaa ttcttttagat ttacattttt  
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1621 cctcattctt tttcactgct gcatagcatt ccattgtaat ttggccactg tttattagac  
1681 cagtcctctg ctgagcttta cagagccctt agttggatgt tagtgagaac catgacagca  
1741 gtgagactgt catctccctg acatgctgtc agcttttggg tgatgtgaaa atgcaagcag  
1801 gcacaggaaa tgtctetaac ttgcttacac ttctcctctg aacctgctg tttcacaact  
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361 aatcccgaca ctttgggagg ccgaggcagg aggtattctt gagcatagga gttcaagatc  
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601 gaccttgtct caaaaaattt aaaaacaaaac aaaaaaact ggttatttgt cttttattg  
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961 ttcatgtaca tctttcaagg tccagagaaa gctctcactt tctccccgtt tttttttcc  
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 2581 agtctttgca tggagacttg aggagggtt gaggttggtg aggttaggtg cgtgttctc  
 2641 gtgcaagtca ggacatcagt ctgattaaag gtggtgcca tttatttaca tttaaacttg  
 2701 tcagggtata aaatgacatc ccattaatta tattgttaat caatcacgtg tatagaaaaa  
 2761 aaaataaaac ttcaat  
 1 ctcgccctgg tggggtgct ctcctcggg tgcgtcctct ctcaggagtg cacgaagttc  
 61 aaggctcagca gctgccggga atgcatcgag tcggggcccg gctgcacctg gtgccagaag  
 121 ctgaacttca cagggccggg ggatcctgac tccattcgct gcgacaccgg gccacagctg  
 181 ctcatgaggg gctgtgccc tgacgacatc atggacccca caagcctcgc tgaacccag  
 241 gaagaccaca atgggggcca gaagcagctg tccccacaaa aagtgcgctt ttacctgcga  
 301 ccaggccagg cagcagcgtt caacgtgacc ttcggcgggg ccaagggcta ccccatcgac  
 361 ctgtactatc tgatggacct ctctactcc atgcttgatg acctcaggaa tgtcaagaag  
 421 ctagggtggc acctgctcgg ggccctcaac gagatcaccc agtccggccc cattggcttc  
 481 gggctcctcg tggacaagac cgtgtcggc ttcgtgaaca cgcaccctga taagctgcga  
 541 aacccatgcc ccaacaagga gaaagagtgc ccgccccgt ttgcttcag gcacgtgctg  
 601 aagctgacca acaactcaa ccagtttcag accgaggtcg ggaagcagct gatttcgga  
 661 aacctggatg caccgaggg tgggctggac gccatgatgc aggtcgccgc ctgcccggag  
 721 gaaatcggct ggcgcaacgt cacgcggctg ctggtgtttg ccactgatga cggcttccat  
 781 ttcgcgggcg acggaagct gggcgccatc ctgaccccca acgacggccg ctgtcacctg  
 841 gaggacaact tgtacaagag gagcaacgaa ttcgactacc catcgggtgg ccagctggcg  
 901 cacaagctgg ctgaaaacaa catccagccc atcttcggcg tgaccagtag gatggtgaag  
 961 acctacgaga aactcaccga gatcatcccc aagtcagccg tggggagct gtctgaggac  
 1021 tccagcaatg tggatccatc cattaagaat gcttacaata aactctctc cagggtcttc  
 1081 ctggatcaca acgcccctcc cgacaccctg aaagtccact acgactcctt ctgcagcaat  
 1141 ggagtgcgc acaggaacca gccagaggt gactgtgatg gcgtgcagat caatgtcccg  
 1201 atcaccttcc aggtgaaggt cacggccaca gactgcaccc aggagcagtc gtttgtcatc  
 1261 cgggctgctg gcttcacgga catagtaccc gtgcaggtcc tccccagtg tgagtgcggg  
 1321 tgccgggacc agagcagaga ccgacgctc tgccatggca agggcttctt ggagtgcggc  
 1381 atctgcaggt gtgacactgg ctacattggg aaaaactgtg agtgccagac acagggccgg  
 1441 agcagccagg agctggaagg aagctgcccg aaggacaaca actccatcat ctgctcaggg  
 1501 ctgggggact gtgtctgcyg gcagtgccg tgccacacca gcgacgtccc cggcaagctg  
 1561 atatacggg agtactgcga gtgtgacacc atcaactgtg agcgtacaa cggccaggtc  
 1621 tgccggcgcc cggggagggg gctctgcttc tgcgggaagt gccgctgcca cccgggcttt  
 1681 gagggctcag cgtgccagtg cgagaggacc actgagggtc gcctgaaccc gcggcggtt  
 1741 gagtgtagtg gtcgtggccg gtgccgctgc aacgtatgcg agtgccatc aggtaccag  
 1801 ctgcctctgt gccaggagtg ccccggtgc cctcaccct gtggcaagta catctcctgc  
 1861 gccagtgcc tgaagttcga aaaggcccc tttgggaaga actgcagcg gcggtgtccg  
 1921 ggctgcagc tgtcgaacaa ccccgtaag ggcaggacct gcaaggagag ggactcagag  
 1981 ggctgctggg tggcctacac gctggagcag caggacggga tggaccgcta cctcatctat  
 2041 gtggatgaga gccgagagtg tgtggcaggc cccaacatcg ccgccatcgt cgggggcacc  
 2101 gtggcaggca tctgtctgat cggcattctc ctgctggtca tctggaaggc tctgatccac  
 2161 ctgagcgacc tccgggagta caggcgcttt gagaaggaga agctcaagtc ccagtggaa  
 2221 aatgataatc cccttttcaa gagcgccacc acgacggtca tgaaccccaa gtttgcgtgag  
 2281 agttaggagc a

## (2) INFORMATION FOR SEQ ID NO:2678:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2678

1 ggaattccgg gcccggtctt tcctcccgcc gccgcccggc tggctccggg gactggcctc  
 61 caggtccgac tgcgtccgagc tgaagcccag cagcactttg ctgccagccg cgggggcccgc  
 121 ggaggcgccc cggggccctc ccaggaggct ctctgggcca gagggccaga ttcggcacag  
 181 gcccccaagg gtccgtaagt aggagaggct gcccgagacc ggccggaccc ccattccccgc  
 241 ggccgcccgc gccgctggtc ccgcggtgc gaccgtggcg gctgccgctg gaaaatgtct  
 301 caggagaggc ccacgttcta ccggcaggag ctgaacaaga caatctggga ggtgcccgag  
 361 cgttaccaga acctgtctcc agtgggtctt ggccgctatg gctctgtgtg tgctgtttt  
 421 gacacaaaaa cggggttacg tgtggcagtg aagaagctct ccagaccatt tcagtccatc  
 481 attcatgcga aaagaacctc cagagaactg cggttactta aacatatgaa acatgaaaat  
 541 gtgattggtc tgttgagcgt ttttacacct gcaaggcttc tggaggaatt caatgatgtg  
 601 tatctgggtg cccatctcat gggggcagat ctgaacaaca ttgtgaaatg tcagaagctt  
 661 acagatgacc atgttcagtt ccttatctac caaattctcc gaggtctaaa gtatatatat  
 721 tcagctgaca taattcacag ggacctaaaa cctagtaatc tagctgtgaa tgaagactgt  
 781 gagctgaaga ttctggattt tggactggct cggcacacag atgatgaaat gacaggctac  
 841 gtggccacta ggtggtacag ggctcctgag atcatgctga actggatgca ttacaaccag  
 901 acagttgata ttgggtcagt gggatgcata atggccgagc tgttgactgg aagaacattg  
 961 ttctctggta cagaccatat tgatcagttg aagctcattt taagactcgt tggaaaccca  
 1021 ggggctgagc ttttgaagaa aatctcctca gactctgcaa gaaactatat tcagtctttg  
 1081 actcagatgc cgaagatgaa ctttgcgaa gtattttattg gtgccaatcc cctggctgtc  
 1141 gacttgctgg agaagatgct tgtattggac tcagataaga gaattacagc ggcccaagcc  
 1201 ctgacacatg cctactttgc tcagtaccac gatcctgatg atgaaccagt ggccgatcct  
 1261 tatgatcagt cctttgaaag cagggacctc cttatagatg agtggaaaag cctgacctat  
 1321 gatgaagtca tcagctttgt gccaccaccc cttgaccaag aagagatgga gtccctgagca  
 1381 cctggtttct gttctgttga tcccacttca ctgtgagggg aaggcctttt caccggaaact  
 1441 ctccaaatat tattcaagtg cctctgtgtg cagagatttc ctccatgggtg gaaggggggtg  
 1501 tgcgtgcgtg tgcgtgcgtg ttagtgtgtg tgcattgtg

## (2) INFORMATION FOR SEQ ID NO:2679:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2679

1 tggttaacgc cagggttttc ccagtcacga acgttgtaaa acgacggcca gtgccaaagt  
 61 aaaattaacc ttcactaaag ggaataagct tgcggccgct tcgggtttcc ggaggggccc  
 121 gagggcgggc gagggcgctc cgtgcgcgcc gcccgcgggc cgggttggtc cggggcgggg  
 181 gagggcgccg gcgcagcctg ggtcggggtc gggccggggt cggcacctgg gacatccctg  
 241 agggaggggc cgggagcggg agcgcccccag cggccggcgg cggggcgggc gagcgagcga  
 301 gcggcgcgga gccggcccga ggcgcgcgcc gagggagccc cgtccccggt cgtgggggca  
 361 ccgcccgcag gctctgcggg gtgggcagct cccgggacct ccattgagctc tccgcgcccc  
 421 gccgcagtg gcttttaccg ccaggagggt accaagacgg cctgggaggt gcgcgcgtg  
 481 taccgggacc tgcagcccgt gggctcgggc gcctacggcg cgggtgtgctc ggccgtggac  
 541 ggccgcaccg gcgctaaggt ggccatcaag aagctgtatc ggccctcca gtccgagctg  
 601 ttgcgcaagc gcgcctaccg cgagctgcgc ctgctcaagc acatgcgcca cgagaacgtg  
 661 atcgggctgc tggacgtatt cactcctgat gagaccctgg atgacttcaac ggacttttac  
 721 ctggtgatgc cgttcatggg caccgacctg ggcaagctca tgaacatga gaagctaggg  
 781 gaggaccgga tccagttcct cgtgtaccag atgctgaagg ggtgaggta tatccacgct  
 841 gccggcatca tccacagaga cctgaagccc ggcaacctgg ctgtgaacga agactgtgag  
 901 ctgaagatcc tggacttcgg cctggccagg caggcagaca gtgagatgac tgggtacgtg  
 961 gtgaccgggt ggtaccgggc tcccagagtc atcttgaatt ggatgcgcta cacgcagacg  
 1021 gtggacatct ggtccgtggg ctgcatcatg gcggagatga tcacaggcaa gacgtgttc  
 1081 aagggcagcg accacctgga ccagctgaag gagatcatga aggtgacggg gacgcctccg  
 1141 gctgagtttg tgcagcggtc gcagagcgat gagggcaaga acaacatgaa gggcctcccc  
 1201 gaattggaga agaaggattt tgctctatc ctgaccaatg caagcctct ggctgtgaac  
 1261 ctcttgagga agatgctggt gctggacgcg gagcagcggg tgacggcagg cgaggcgctg  
 1321 gccatccct acttcagatc cctgcacgac acggaagatg agccccaggt ccagaagtat  
 1381 gatgactcct ttgacgacgt tgaccgcaca ctggatgaat ggaagcgtgt tacttacaaa  
 1441 gaggtgctca gcttcaagcc tcccggcag ctgggggcca gggctccaa ggagacgcct  
 1501 ctgtgaagat ctctgggctc cggggtggca gtgaggacca ccttcacctt

## (2) INFORMATION FOR SEQ ID NO:2680:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2680

1 ggaattccgg gcccggtctt tctcccgc gcccgccggc tggccccgg gactggcctc  
61 cacgtccgac tgcgtccgagc tgaagcccag cagcactttg ctgccagccg cggggggcggc  
121 ggaggcgccc cggggccctc ccaggaggct ctctgggcca gaggccgaga ttcggcacag  
181 gcccccaagga gtccgtaagt aggagaggct gcccgagacc ggccggagccc ccattcccgc  
241 ggccgcccgc gccgtgggtc ccgcggtgc gaccgtggcg gctgccgctg gaaaatgtct  
301 caggagaggc ccacgttcta ccggcaggag ctgaacaaga caatctggga ggtgcccgag  
361 cgttaccaga acctgtctcc agtgggctct ggccctatg gctctgtgtg tgctgtttt  
421 gacacaaaaa cggggttacg tgtggcagtg aagaagctct ccagaccatt tcagtccatc  
481 attcatgcga aaagaacctc cagagaactg cggttactta aacatargaa acatgaaaat  
541 gtgattggctc tgttgacgt ttttacacct gcaagggtctc tggaggaatt caatgatgtg  
601 tatctggtga cccatctcat gggggcagat ctgaacaaca ttgtgaaatg tcagaagctt  
661 acagatgacc atgttcagtt ccttatctac caaattctcc gaggtctaaa gtatatcat  
721 tcagctgaca taattcacag ggaacctaaa cctagtaate tagctgtgaa tgaagactgt  
781 gagctgaaga ttctggattt tggactggct cggcacacag atgatgaaat gacaggctac  
841 gtggccacta ggtggtacag ggctcctgag atcatgctga actggatgca ttacaaccag  
901 acagttgata tttggtcagt gggatgcata atggccgagc tgttgactgg aagaacattg  
961 tttcctggta cagaccatat tgatcagttg aagctcattt taagactcgt tggaaaccca  
1021 ggggctgagc ttttgaagaa aatctcctca gactctgcaa gaaactatat tcagtctttg  
1081 actcagatgc cgaagatgaa ctttgcgaat gtatttattg gtgccaatcc cctggctgtc  
1141 gacttgctgg agaagatgct tgtattggac tcagataaga gaattacagc ggcccaagcc  
1201 cttgcacatg cctactttgc tcagtaccac gatcctgatg atgaaccagt ggcgatcct  
1261 tatgatcagt cctttgaaag cagggacctc cttatagatg agtggaaaag cctgacctat  
1321 gatgaagtca tcagctttgt gccaccaccc cttgaccaag aagagatgga gtcctgagca  
1381 cctggtttct gttctgttga tcccacttca ctgtgagggg aaggcctttt caccgggaact  
1441 ctccaaatat tattcaagt cctctgtgtg cagagatttc ctccatgggt gaaggggggtg  
1501 tgcgtgctg tgcgtgctg ttagtgtgtg tgcattgtg  
1 tggttaacgc cagggttttc ccagtcacga acgttgtaaa acgacggcca gtgccaaagt  
61 aaaattaacc ttcactaaag ggaataagct tgcggccgct tcgggtttcc ggagggggcg  
121 gagggcgggc gagggcgta cgtgcgcgcc gcccgccggc cgttggttcc ccggggcggg  
181 gagggcgccg gcgcagcctg ggtcgggggtc gggccggggt cggcacctgg gacatccctg  
241 aggggaaggc cgggagcggg agcgccccag cggccggcgg gcggggcggg gagcggacga  
301 gcggcgccga gccggcccga ggcgcgccgc gagggagccc cgtcccgggt cgtgggggca  
361 ccgcccagc gctctgcggg gtgggcagct cccgggcctg ccatgagctc tccgcgccc  
421 gcccgagtg gcttttaccg ccaggaggtg accaagacgg cctgggaggt gcgcgcccgtg  
481 taccgggacc tgcagcccgt gggctcgggc gcctacggcg cgggtgtgctc ggccgtggac  
541 ggccgcaccg gcgctaaggt ggccatcaag aagctgtatc ggcccttcca gtccgagctg  
601 ttcgccaagc gcgcctaccg cgagctgcgc ctgctcaagc acatgcgcca cgagaacgtg  
661 atcgggctgc tggacgtatt cactcctgat gagaccctgg atgacttcac ggacttttac  
721 ctggtgatgc cgttcatggg caccgacctg ggcaagctca tgaaacatga gaagctaggc  
781 gaggaccgga tccagttcct cgtgtaccag atgctgaagg ggctgaggtat tatccacgt  
841 gccggcatca tccacagaga cctgaagccc ggcaacctgg ctgtgaacga agactgtgag  
901 ctgaagatcc tggacttcgg cctggccagg caggcagaca gtgagatgac tgggtacgtg  
961 gtgaccgggt ggtaccgggc tcccaggtc atcttgtaatt ggatgcgcta caccgacag  
1021 gtggacatct ggtccgtggg ctgcatcatg cgggagatga tcacaggcaa gacgtgttc  
1081 aagggcagcg accacctgga ccagctgaag gagatcatga aggtgacggg gacgcctccg  
1141 gctgagtttg tgcagcggct gcagagcgat gaggccaaga acaacatgaa ggccctcccc  
1201 gaattggaga agaaggattt tgcctctatc ctgaccaatg caagccctct ggctgtgaac  
1261 ctccctggaga agatgctggt gctggacgag gagcagcggg tgacggcagg cgaggcgtg  
1321 gcccattcct acttcagatc cctgcacgac acggaagatg agccccaggt ccagaagtat  
1381 gatgactcct ttgacgacgt tgaccgcaca ctggatgaat ggaagcgtgt tacttataaa  
1441 gaggtgctca gcttcaagcc tcccggcag ctgggggcca gggctctcaa ggagacgcct  
1501 ctgtgaagat ctctgggctc cgggggtggca gtgaggacca cttcacctt

## (2) INFORMATION FOR SEQ ID NO:2681:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2681

1 ctcgatcaaa cctttttttt atggtacaca atagtcacag tactttttcca tataaaacag  
61 gtttagtggt ctttaattag tttggcacat ttaatacact cccatgacca gcatcccaaa  
121 tgtacctatc cgttttattt tattgtctca gaattgtcag ttatttaata aattatgtaa  
181 cttttttcct tatgtcaga tttgcacttc tttctaaaac tctgcccac cttaaagtcc  
241 cagattctcc ttgaactttt ttttttgact ttccaagtac atggaactct tcactctatc  
301 ctgctatata aggtgacaga atttccacta tgggatagat ggagttcaat tcctttgagt  
361 ttaaaataat ctaaatataa ttattcctta tgccctgttt ttccctcact tttgtatcca  
421 aatctctttt cagacaacag aacaattaat gtctgataag gaagacaatg atgatgatca  
481 cttcaaaatg aattcaggat tgtaatgtaa aattttagta ctctctcaca gtatggattc

541 taacatggct tctaaccctaa actaacatta gtagctctaa ctataaactt caaatctcag  
601 tagatgcaac ctactccctt aaaatgaaac agaagattga aattattaaa ttatcaaaaa  
661 gaaaatgatc cacgctctta gttgaaattt catgtaagat tccatgcaat aaataggagt  
721 gccataaatg gaatgatgaa atatgactag aggaggagaa aggtccttag atgagatggg  
781 attttaggca tccgtgtctc atgaggaaac agttgtgtca ctaggcaaaa cagtaaaaaa  
841 aaaaacctcc aagtgtgtct cttattttat tttttcttat aagacttcta caaattgagg  
901 tacctgggtg agttttttt caggttttat gctgtcattt tctgtaatg ctaaggactt  
961 aggacataac tgaattttct attttccact tcttttctgg tgtgtgtgta tatatatatg  
1021 tatataatac cacacacata tacatatata ttttttttag tatctcacc tcacatgctc  
1081 ctccctgagc actacccatg atagatgtta aacaaaagca aagatgaaat tccaactgtc  
1141 aaaatccccc ctccatctaa ttaatccctc acccaactat gttccaaaac gagaatagaa  
1201 aattagcccc aataagccca ggcaactgaa aagtaaagtc tatgtgttac tttgatccat  
1261 ggtcacaaact cataatcttg gaaaagtga cagaaaagac aaaagagtga actttaaaac  
1321 tcgaatttat tttaccagta tctcctatga agggctagta accaaaataa tccacgcatc  
1381 agggagagaa atgccttaag gcatacgttt tggacattta gcgtccctgc aaattctggc  
1441 catcgccgct tctttgttcc atcagaaggc aggaaacttt atattgtga cccgtggagc  
1501 tcacattaac tatttacagg gtaactgctt aggaccagta ttatgaggag aatttacctt  
1561 tcccgctctt ctttccaaga aacaaggagg ggggtgaagt acggagaaca gtatttcttc  
1621 tgttgaaagc aacttagcta caaagataaa ttacagctat gtacactgaa ggtagctatt  
1681 tcattccaca aaataagagt tttttaaaaa gctatgtatg tatgtgtgc atatagagca  
1741 gatatacagc ctattaagcg tcgtcactaa aacataaaac atgtcagcct tcttaacct  
1801 tactcgcccc agtctgtccc gacgtgactt cctcgacct ctaaagacgt acagaccaga  
1861 cacggcgagg gcggcgagg aggggattcc ctgcgcccc ggacctcagg gccgtcaga  
1921 ttcctggaga ggaagccaag tgccttctg cctcccccg gtatcccatc caaggcgatc  
1981 agtcacaaac tggctctcgg aagcactcgg gcaaagactg cgaagaagaa aagacatctg  
2041 gcggaaacct gtgcgcctgg ggcgggtgaa ctcgggagg agagggagg atcagacagg  
2101 agagtgggga ctacccctc tgctccc aaa ttggggcagc ttcctgggtt tccgatttcc  
2161 tcatttccgt gggtaaaaa cctgcccc accggcttac gcaattttt taaggggaga  
2221 ggagggaaaa atttggggg ggtacgaaaa ggcggaaaga aacagtcatt tcgtcacatg  
2281 ggcttggttt tcagtcttat aaaaaggaag gttctctcgg ttagcgacca attgtcatat  
2341 gacttgagc gacgtcagg agcacgtcca ggaactcctc agcagcgct ccttcagctc

## (2) INFORMATION FOR SEQ ID NO:2682:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2682

1 gtccaggaac tctcagcag cgcctccttc agctccacag ccagacgccc tcagacagca  
61 aagcctaccc ccgcgcgcgc cctgccccgc cgtgcgatg ctgccccgc cctgctgct  
121 gtgcgcggtc ctggcgctca gccatacagc aaatccttgc tgttcccc acc catgtcaaaa  
181 ccgaggtgta tgtatgagtg tgggatttga ccagtataag tgcgattgta cccggacagg  
241 attctatgga gaaaactgct caacaccgga atttttgaca agaataaaat tatttctgaa  
301 acccactcca aacacagtgc actacatact taccacttcc aagggtttt ggaacgttgt  
361 gaataacatt ccttctcttc gaaatgcaat tatgagttat gtgttgacat ccagatcaca  
421 tttgattgac agtccaccaa cttacaatgc tgactatggc taaaaaagct ggggaagcctt  
481 ctctaaccctc tcttattata cttagagcctt tctctctgtg cctgatgatt gcccgactcc  
541 cttgggtgtc aaaggtaaaa agcagcttcc tgattcaaat gagattgttg gaaaattgtc  
601 tctaagaaga aagttcatcc ctgatcccca gggctcaaac atgatgttg cattctttgc  
661 ccagcacttc acgcatcagt ttttcaagac agatcataag cgagggccag ctttccacaa  
721 cgggctgggc catgggggtg acttaaatca tatttacggt gaaactctgg ctgacagcg  
781 taaactgcgc cttttcaagg atggaaaaat gaaatatcag ataattgatg gagagatgta  
841 tcttcccaca gtcaaagata ctcaggcaga gatgatctac cctcctcaag tccctgagca  
901 tctacggttt gctgtggggc aggggtctt tgggtctgtg cctgggtctga tgatgtatgc  
961 cacaatctgg ctgaggggaa acaacagagt atgcgatgtg cttaaacagg agcatcctga  
1021 atgggggtgat gagcagttgt tccagacaag caggctaata ctgataggag agactattaa  
1081 gattgtgatt gaagattatg tgcaacactt gagtggctat cacttcaaac tgaaatttga  
1141 cccagaacta cttttcaaca acaatttcca gtacaaaaat cgtattgctg ctgaatttaa  
1201 caccctctat cactggcatc ccttctgccc tgacacctt caaattcatg accagaaata  
1261 caactatcaa cagtttatct acaacaactc tatattgtct gaacatggaa ttaccagtt  
1321 tgttgaatca ttcaccaggc aaattgtctg cagggttgct ggtggttaga atgttccacc  
1381 cgcagtacag aaagtatcac aggttccat tgaccagagc aggcagatga aataccagtc  
1441 ttttaattgag taccgcaaac gctttatgct gaagccctat gaatcattt aagaacttac  
1501 agggagaaaag gaaatgtctg cagagttgga agcactctat ggtgacatgc atgtgtgga  
1561 gctgtatcct gcccttctgg tagaaaagcc tcggccagat gccatctttg gtgaaacct  
1621 ggtagaagtt ggagcaccat tctccttgaa aggaacttat ggtaatgtta tatgttctcc  
1681 tgcctactgg aagccaagca cttttgggtg agaagtgggt tttcaaatca tcaacactgc  
1741 ctcaattcag tctctcatct gcaataacgt gaagggtgt ccttttactt cattcagtg

1801 tccagatcca gagctcatta aaacagtcac catcaatgca agttcttccc gctccggact  
1861 agatgataac aatcccacag tactactaaa agaacgttcg actgaactgt agaagtctaa  
1921 tgatcataatt tatttattta tatgaacctat gtctattaat ttaattattt aataatattt  
1981 atattaaact ccttatgtta cttaacatct tctgtaacag aagtcagtac tccgtgtgag  
2041 gagaaaggag tcatacttgt gaagactttt atgtcactac tctaaagatt ttgctgttgc  
2101 tgtaaagttt ggaaaacagt ttttattctg ttttataaac cagagagaaa tgagttttga  
2161 cgtcttttta cttgaatttc aacttatatt ataaggacga aagtaaagat gtttgaatac  
2221 ttaaacacta tcacaagatg ccaaaatgct gaaagttttt acactgtcga tgtttccaat  
2281 gcactcttcca tgatgcatta gaagtaacta atgtttgaaa ttttaaagta cttttgggta  
2341 tttttctgtc atcaaacaaa acaggatata gtgcattatt aaatgaatat ttaaattaga  
2401 cattaccagt aatttcattg ctacttttta aaatcagcaa tgaaacaata atttgaaatt  
2461 tctaaattca tagggtagaa tcacctgtaa aagcttggtt gatttcttaa agttattaaa  
2521 cttgtacata taccaaaaag aagctgtctt ggattttaat ctgtaaaatc agatgaaatt  
2581 ttactacaat tgcttgtaa aatattttat aagtgtgtt cctttttcac caagagtata  
2641 aaccttttta gtgtgactgt taaaacttcc ttttaaatac aaatgccaaa tttattaagg  
2701 tgggtggagcc actgcagtgt tatctcaaaa taagaatata ctgttgagat attccagaat  
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2881 ttaaaccttt tgaagcaaac ttttttttag ccttggtcac tgcagacctg gtactcagat  
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3061 ataaaatacc tcttcaaaat gcttaaatc atttcacaca ttaattttat ctgagtcttg  
3121 aagccaattc agtaggtgca ttggaatcaa gcctggctac ctgcatgctg ttccttttct  
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3241 ttttgtttta ctagttttaa gatcagagtt cactttcttt ggactctgcc tatattttct  
3301 tacctgaact tttgcaagtt ttcaggtaaa cctcagctca ggactgctat ttagtccctc  
3361 ttaagaagat taaaaaaaaa aaaaaag

## (2) INFORMATION FOR SEQ ID NO:2683:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2683

1 gagctcacat taactattta cagggttaact gcttaggacc agtattatga ggagaattta  
61 cctttcccg cctctctttcc aagaaacaag gaggggggga aggtacggag aacagtattt  
121 cttctgttga aagcaactta gctacaaaga taaattacag ctatgtacac tgaaggtagc  
181 tatttcattc cacaaaataa gagtttttta aaaagctatg tatgtatgtg ctgcatatag  
241 agcagatata cagcctatta agcgtcgtca ctaaaacata aaacatgtca gcctttctta  
301 accttactcg cccagctctg tcccagctg acttccctga cctctaaag acgtacagac  
361 cagacacggc ggcggcgccg ggagagggga ttccctgcgc cccggacct cagggccgct  
421 cagattcctg gagaggaagc caagtgtcct tctgcccctc cccggtatcc catccaaggc  
481 gatcagtcga gaactggctc tcgggaagcg tcgggcaaaag actgcgaaga agaaaagaca  
541 tctggcggaa acctgtgcgc ctggggcggt ggaactcggg gagagaggg agggatcaga  
601 caggagagtg gggactaccc cctctgctcc caaattgggg cagcttcctg ggtttccgat  
661 tttctcattt ccgtgggtta aaaaccctgc cccaccggg cttacgcaat ttttttaagg  
721 ggagaggagg gaaaaaattt gtgggggggt acgaaaaggc ggaaagaaac agtcattcac  
781 atgggcttgg ttttcagtct tataaaaagg aaggttctct cggttagcga ccaattgtca  
841 tacgacttgc agtgagcgtc aggagcacgt ccaggaactc ctcagcagcg cctccttcag  
901 ctccacagcc agacgcctc agacagcaaa gctaccccc gcgcgcgcgc ctgcccgcgc  
961 ctcggtatgt cgccgcgcgc ctgctgctgt gcgcggtcct ggcgctcagc catacaggtg  
1021 agtacctggc gccgcgcacc gggactccg gttccacgca cccgggcaga gtttccgctc  
1081 tgacctcctg ggtctatccc agtactccga cttctctccg aatagagaag ctacgtgact  
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1381 ctagtcaagt ctttctgctc cccaggaaaag cccggtattt gttttaagat aagcaaaatg  
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1621 ttatccttat ttagaataga aaattggat ttctacgttt tatccattct aaggcaggtt  
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1861 tatgagtgtg ggatttgacc agtataagtg cgattgtacc cggacaggat tctatggaga  
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1981 gttatcattg tatagatttg tgtcttataa tgagtcccat taatttctcc ctccctttct

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2101 cacagtgcac tacatactta cccactttcaa gggatttttg aacgttctga ataacattcc  
2161 ctctcttcga aatgcaatta tgagttatgt cttgacatgt aagtacaagt gtctttctaa  
2221 ggttttttagc ctctctcaaa aaaaatatgc tttataatac tgtaagccta atctaaaaaac  
2281 atattttccaa gcttatcaaa aagacttttaa gatagctttt aagtttgcct tccatcttaa  
2341 tcgccaaaaa tattgacatt tagtcccatc cagtttatac agtctgctca caactctgta  
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2461 ttgaatgccc atggggccaca gaattgttct gaacatgtag caccatttaa aataaatttg  
2521 gatttggatc agcaagaaaa taactttcca tgattctaaa gtgggtgcca tactcagcca  
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2641 gattataatg tgcagagtat atgtatttta ttaaagatgt atttcaagt gccattagac  
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2761 gtgccacttt ccacatttta caataaaaaa aatggttgat ttacttaaca aatgagaata  
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3121 ttatctatgg gtatttttta aagtatgagt ctatataaac tattatgtaa aagcaatga  
3181 gcgtcttggg ataagtcttt aatattttca aattatttct ttagaaatga aataattcta  
3241 attaaaatag aaaaaatcat tcagtaagaa gttgttcac catatcttag aactgttgtt  
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3661 agggctaaca ttaaaggaga tatacagata gatagatcca aataacctat ccactttttt  
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3781 gtaaaattat acacacacac agacatgcac acacatatat aaacattcac acacatacat  
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9121 ttgggaagag ggagaaaatg aaataaatat cattaaagat aactcaggag aatcttctt  
9181 acaattttac gtttagaatg ttttaaggta agaaagaaat agtcaatatg cttgtataaa  
9241 acaactgttc ctgttttttt taaaaaaaac acttgatttg ttattaacat tgatctgctg  
9301 acaaaacctg ggaatttggg ttgtgtatgc gaatgtttca gtgcctcaga caaatgtgta  
9361 ttaacttat gtaaaagata agtctggaaa taaatgtctg tttatttttg tactatttaa  
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## (2) INFORMATION FOR SEQ ID NO:2684:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2684

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121 tgtacctatc cgttttattt tattgtctca gaattgtcag ttatttaata aattatgtaa  
181 cttttttcct tatgctcaga ttgcaacttc tttctaaaac tctgcccac cttaaagtc  
241 cagattctcc ttgaactttt ttttttgact ttccaagtac atggaactct tcaactctac



301 ctgctatata aggtgacaga atttccacta tgggatagat ggagttcaat tcctttgagt  
361 ttaaaataat ctaaatataa ttattcccta tgcctgttt tccctcact tttgtatcca  
421 aatctctttt cagacaacag aacaattaat gtctgataag gaagacaatg atgatgatca  
481 cttcaaaaatg aattcaggat tgtaatgtaa aatttttagta ctctctcaca gtatggattc  
541 taacatggct tctaacccaa actaacatta gtagctctaa ctataaactt caaatttcag  
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1861 cacggcgggc gcggcgggag aggggattcc ctgcggcccc ggacctcagg gccgctcaga  
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## (2) INFORMATION FOR SEQ ID NO:2685:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2685

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181 gctccggcga cccgtcctct tctcctcct ccgggaacce gctcgtgtac ctggacgtgg  
241 acgccaacgg gaagccgctc ggccgctggt tgctggagct gaaggcagat gtcgtcccaa  
301 agacagctga gaacttcaga gccctgtgca ctggtgagaa gggcttcggc tacaaaggct  
361 ccaccttcca cagggtgatc cttccttca tgtgccaggc gggcgacttc accaaccaca  
421 atggcacagg cgggaagtcc atctacggaa gccgctttcc tgacgagaac tttactatga  
481 agcagctggg gccaggtgct ctgtccatgg ctaatgctgg tctaacacc aacggtcccc  
541 agttcttcat ctgcaccata aagacagact ggttgatgg caagcatggt gtgttcggtc  
601 acgtcaaaga gggcatggac gtcgtgaaga aaatagaatc tttcggctct aagagtggga  
661 ggacatccaa gaagattgtc atcacagact gtggccagtt gagctaact gtggccaggg  
721 tgctggcatg gtggcagctg caaatgtcca tgcacccagg tggccgctt gggctgtcag  
781 ccaagtgccc tgaacgata cgtgtgccc ctccactgtc acagtgtgcc tgaggaggc

841 tgctagggat gttagacgga attcc

(2) INFORMATION FOR SEQ ID NO:2686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2686

1 ttttgcagac gccaccgccg aggaaaaccg tgtactatta gccatggtc

(2) INFORMATION FOR SEQ ID NO:2687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2687

1 cggaacgca acatgaaggt gctccttgcc gccgccctca tcgcggggtc cgtcttcttc  
61 ctgctgctgc cggaaccttc tgcggccgat gagaagaaga aggggcccaa agtcaccgctc  
121 aaggtgtatt ttgacctacg aattggagat gaagatgtag gccgggtgat ctttggcttc  
181 ttcggaaga ctgttccaaa aacagtggat aattttgtgg ccttagctac aggagagaaa  
241 ggatttggct acaaaaacag caaattccat cgtgtaatca aggacttcat gatccagggc  
301 ggagacttca ccaggggaga tggcacagga ggaaagagca tctacggtga gcgcttcccc  
361 gatgagaact tcaaactgaa gactacggg cctggctggg tcagcatggc caacgcagggc  
421 aaagacacca acggctccca gttcttcac acgacagtca agacagcctg gctagatggc  
481 aagcatgtgg tgtttggcaa agttctagag ggcattggag tggcgcgaa ggtggagagc  
541 accaagacag acagccggga taaaccctg aaggatgtga tcatcgaga ctgcccgaag  
601 atcgaggtgg agaagccctt tgccatcgcc aaggagttag gcacagggac atctttcttt  
661 gagtgaccgt ctgtgcaggg cctgtagtcc gccacagggc tctgagctgc actggccccg  
721 gtgctggcat ctggtggagc ggacccactc cctcacatt ccacagggcc atggactcac  
781 ttttgaaca aactcctacc aacttgacc aataaaaaaa aatgtgggtt tttttttttt  
841 ttaataaaaa a

(2) INFORMATION FOR SEQ ID NO:2688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2688

1 gaaggtgctc ctgcccgcg ccctcatcgc ggggtccgctc ttcttctctg tgctgccggg  
61 accttctgcg gccgatgaga agaagaagg gcccgaagtc accgtcaagg tgtattttga  
121 cctacgaatt ggagatgaag atgtaggccg ggtgatcttt ggtctctttg gaaagactgt  
181 tccaaaaaca gtggataatt ttgtggcctt agctacagga gagaaaggat ttggctacaa  
241 aaacagcaaa ttccatcgtg taatcaagga cttcatgatc cagggcggag acttcaccag  
301 gggagatggc acaggaggaa agagcatcta cggtgagcgc tccccgatg agaacttcaa  
361 actgaagcac tacgggcctg gctgggtgag catggccaac gcaggcaagg acaccaacgg  
421 ctcccagttc ttcattcacga cagtcaagac agcctggcta gatggcaagc atgtgggtgt  
481 tggcaaagtt ctagagggca tggaggtggt gcggaagggt gagagacca agacagacag  
541 ccgggataaa cccctgaagg atgtgatcat cgcagactgc ggcaagatcg aggtggagaa  
601 gccctttgcc atcgccaagg agtagggcac agggacatct ttctttgagt gaccgtctgt  
661 gcaggccctg tagtccgcca caggcctctg agctgcactg gccccggtgc tggcatctgg  
721 tggagcggac cactccctc cacttccac agggccatgg actcactttt gtaacaaact  
781 cctaccaaca ctgaccaata aaaaaaatg tgggtttttt ttttaataa aag

(2) INFORMATION FOR SEQ ID NO:2689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2689

1 gaattccctt gtaagggttt ctaacaaaa caccagtcac ataagtgcatt tttattttat  
61 atttttgttt atttatttga gacggagtct cttgtctctc aggtctggag gcagtggcgc  
121 catctctgct cgctgcaacc tccacctcct ggggtccagc gattctcctg cctcagcctc  
181 ccgagggggg agctgggact acaggtgcgc accaccatgc ccagctaatt ttgtattttt  
241 cgtagagatg gggtttcacc atgttgctca ggctggtctt gaactcctga cctcaggtga  
301 tcttcccgcg tcggcctccc aaagtgcctg aattacaggc gtgatccacc gcacccggcc  
361 tattttttga gagagggtca cactctgtcg tcccggctgg aatgcagtga tgcgatcacc

421 gccactaca gcctcgacct ccggggtcaa gcaatcctcc ccgcccagcc tcttgagtag  
481 cgagcgccctc gacgcccagc taatttttat ttttatttat tttttttag agacggcgctc  
541 tctctaagat gccagggctg gtggccgggtg tcgaactcct aagatgaagc gatcctcccc  
601 ggcttgggcc tccgcgcctc ctaaagcgcc aggtatgagc caccgcgcct ggccataaag  
661 tgcattttaa ttaaagtatt attaatgtct ttgcctgaag aaattcgctt ttaaattgtg  
721 acttatcttt cacccaaaaa tcaaagcaca attcagcccc gagggggggg cggtagggagc  
781 tggggggggg gggggcaggg aaagaccagg agcagagatt caaaaagagt aagagggcaa  
841 aatgtgcata atgcatcttc acaggtaaga gcctggccag gctcctgttt taatggcttc  
901 ctcctgaaga agattcaagc agagtgtatg atattttcgg aaagtagagc attttgaag  
961 catttcataa tctctcaaaa ccggagactg ctctgtctcc acctcgtag agaaaaagc  
1021 gatgctcaaa ggcaacctcc ttcctgacat tgcttgtag gacgcgacgt ggtgtttgccc  
1081 cgcgcggaat gcggacgcaa ggctgctcct aggtctcggg gacgcgcat cccattttcc  
1141 gctcgcgag gcgtagggtc cgggcgcggg accccagtcg acctgactg gcggcgcgac  
1201 cttgaggcct gcgttcgcct cagttgcccc ctctgtgcaa tggggagagc cgcctcagc  
1261 cttgacaacg gccgaagagc cgccgcgctt ccgtctcccc cgtgcgcgcg ccatgctgcc  
1321 caccgccgtt ccgcaactgac cctcccccg gccccgcgtc ccgtactgcc gccccgccc  
1381 gagtcccatg ccgcagccac ccgcagggag ccgcagggc ggaacctgcc tccgcgcgtt  
1441 agcgcgacg cgccgctcat gtgtcgtccc catcagcgcc ggcttccgct tataggccag  
1501 atgcaactgtc actctggcga agtcgcagac ccgattggcc gggacggagg gcgagaccg  
1561 ggttgcgggc gggggccgaac gtggtataaa acggggcgga ggccaggctc gtgccgtttt  
1621 gcagacgcca ccgcccaggga aaaccgtgta ctattagcca tggtaaccc caccgtgttc  
1681 ttcgacattg ccgtcgacgg cgagcccttg ggccgctct ccttgaggt cggggggggc  
1741 gcggcggtgc ggaatggggc ccagaaagtg ggccggggc ggggtgggtg gtacgcccc  
1801 aaaggccccg gcgcggggcg accctgcttg agggcgagc gcggcgggc tgcggcgcca  
1861 tttcctgacg agggggcatt ttgggaagtc ccgagtcgc gggaggaggc cgggacggc  
1921 cggacaaagg caggcggggc ggctgcgagg ccgttggggg agggggccc cgtccgccc  
1981 cccgcctcat gtggccgcgc cctgtcctgt ccgacgcagc tgctcggcg ccgcgtcag  
2041 gtccgcgcct tgagagtcgt tgtccgccc agcttggcct gggcgccgca gaccggagcc  
2101 agaagcacgc tcgcgggggc ttgcgaccgc cttcctggga agctgtcccc tggcaggcat  
2161 ggggtgctta catcctgagc tgggaagctg tttgcttag ggtttttctc aaggatcgag  
2221 gcgcggtgtg agcccgccca tgctcggtcc ttagatccc gggaggccat gttataaaag  
2281 gagacttgct gggatgtgac gggttggcac ttgaaatc ttcatttgg ataaagttag  
2341 aatatttata catgtgcccc aaacgtccct ccgtgtcccc caccccaag cggaaatgtg  
2401 aaaatgggccc ttgcctttgc tgggtcccaa ggaccgcctt ccactgcagt gacggcgctg  
2461 gcggggggagg cgctcttgag cccctcccga ttgtccctct gcctagcaag caagtgcga  
2521 ctggccacaa ggcaggcctc ttccgaccaa ggtggattac cagtattac ctaattagtt  
2581 ttgagagcgt taaatgagtt cttaaagatc agttgtaatt atagcatagt atctaaactt  
2641 ggcgcgtgtc ttcaaagtta aatattgagt acgattccgt tccagttaac atggatagac  
2701 cttaggaggat agcgaatatg gatgttagtg gttttattcc tttaaatcac atctcaaaag  
2761 gccaccaatg gctagtttgg atcttattcc gaaaatagat tgatcctcat gcagtcttcg  
2821 tgaggacaga gcgatttccct tgttgccctac cctgtccata gtgcctggca cataggcact  
2881 gaaacactgc atgttaatcc acaccccacc ccacctatga gtgtagtcaa agctggtaag  
2941 tgacaagggc tttcgtggaa acttgccctg acctaatgtt gggcatcagg ttaccacaaag  
3001 agcttcaggg aatgagaaa ggacttcgag gtcttgatga gaatggagg gtaactgcca  
3061 atgagggctt tggctttagc gaaagtctga aagggaagcc ataggaaactt aaacgtaccg  
3121 actataaagc tctgagaaaa gctgatgttt tagaaagacc atacattcta ggtacaaata  
3181 cctaaaaact aaaaaataag tacgttggcc aggcggggcg atcacgaagt caggagattg  
3241 agaccatcct gggcccctgg tgaaacccca cctctattaa aaatacaaaa attagctggg  
3301 cgtggtggcg cttgcctgta atctcagcta ctctagaggc tgaggcagga gatcgcttga  
3361 accccggagg cggaggctgc agtgagccga gatcgtgcca ctgactcca gcctggtgac  
3421 agcgagactc ttgtctcaaa aaaaaaaaag tacattgcta taagagaagt gcacacggat  
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3601 cgtattatac attcaagaaa ggttcaaaac cagatatact agaaaccaat ctttattttt  
3661 taccacctac ctaggtaagg gcctggatac caagaagtga ctgctcatct aatccataaa  
3721 gctatgttaa cagattggag gtagtagcat tttcattaca agtgactaaa agaacagctg  
3781 tttacccctg atcgtgcagc agtgcttgc gttccttaga attttgcctt gtaagtctta  
3841 gctcaagttg ggggggtgtg atagacattt aagaagccat atatcttttc agaagttagt  
3901 gtgatgtact aaaagtgtga gacactttct agaagtctca ctatttaagt tatgactagt  
3961 attggatttt tggcatgtct ttgggtttca tgtttcttaa cccaactgcc tgcaggccct  
4021 tatggctgtc agggagcagtt cttgggaatt aaagtaatta ctgaagaagt attctagtga  
4081 gaaaatgaat ttatgactca gaagccccta aagacatggg tactaagcaa caaaataagc  
4141 agatgttaat taactgtaat tttctcttac agctgtttgc agacaaggta ccaaagacag  
4201 cagggttggtc cattttctaa gttaacaaa gatgttccaa ttgtgacagt ttgtgtgtg  
4261 gtgtgtatat atatattttt atgtatgtat atatgtgttt aatttttttt taaacagaaa  
4321 atttcgtgc tctgagcact ggagagaaaag gatttgggta taagggttcc tgccttcaca  
4381 gaattattcc aggggtttatg tgcagggtac gaaatttact gaattttatt ttatttgggt  
4441 tgctcccttc atttgggatt gagccagaat atttcaggat acacatatct gaactgttac

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4501 tctaccattt cggttctatt taacccttct attcagtttg aacttggggt taaagtttga
4561 accttgcaga ttgtggcacac ttcattggtta tgttgtcaga agtgacattt ttcctatafg
4621 ttgacagggt ggtgacttca cagccataa tggcactggt ggcaagtcca tctatgggga
4681 gaaatttgaa gatgagaact tcatcctaaa gcatacgggt cctggcatct tgtccatggc
4741 aaatgctgga cccaacacaa atggttccca gtttttcatc tgcactgcca agactgagtg
4801 gtaagggtac aacatggcac actaaccacc tgactaaatg aaaagtggcc ctggggggaa
4861 cgggaacaaac actacttttc ttcaaccttt gtttccacag actttttcat ccctaagata
4921 ctagaagaag agcatacata aatgacaaat atagccaatg tgatacagaa tgtcagatac
4981 tatgatagaa acttggccct tagctgggtg gttgaattag gtgctacttt tttgagatgg
5041 agttttgctc tgttgccagg ttggagtgcg gtggcacaat ctgggctcac tgcaacctct
5101 gcctcctggg ttcaagcgat tctcctgcct tggcctcctg agtagctgag aatacagatg
5161 tgtgccagca tgcctggcta attttttgta tttttgtgga gacgggggtt catcatgttg
5221 gccaaagctgg tcttgaactc gtgacttaag gtgaaccacc tgccttggcc ccccaaagtg
5281 ctgggatttc aggcattgag cactgcgccc aaccaattaa gtgctttttt tttttttttt
5341 cttttctcag actggatctc gctcttatct ccagggttgg agtgcaagtg tgccatctca
5401 gctcactgca acctcctccc gggttcaagc aattcttctg cctcagcttc tcaagtagct
5461 ggaactacag gcatgcacca ccaactccag ctaaattgtg tattattagt agagcgggat
5521 ttaccatgtt gtccaggctg gtctcgaact cctgggctca agtgatctgc ctgccttgac
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5641 tttatgttac tattaataac atgcgggttg ttgggtttt tgtttctttg gggtttttgt
5701 tttgttttgt ttgtttttgg gggagggggg cgcaattcat tctatatgtg taactctttt
5761 ttgagatgga gtttcgctct gtgcgccagg ctggagtgcg gtggcgcgat ctgcgctcac
5821 tgcaagctcc gcctcccagg ttcacgccat tctcctgcct cagcctccc agtagctggg
5881 actataggca catgccacca tgcccggcta attttttcta ttttttagtag agcagggtt
5941 tcaccgtgtt agccaggatg gtctcgatct cctgacctcg tgatccgccc gccttggcct
6001 cccaaagtgc tgggattaca ggcgtgagcc accgcaccg gcctatatgt gtaactctt
6061 aatggttaatt ggagaatcat gtttaatgac atttagtaca aaaggcttca gttaaaaaaa
6121 aaaaaaaa gctacctttc tcgtcttggt tcatgacaca tggaggctgc ttgtttgtgg
6181 ttgccagtca taatgattgt tcttctttt caaggttggg tggcaagcat gtgggtgttg
6241 gcaaagtga aagaagcatg aatattgtgg aggccatgga gcgctttggg tccagggaatg
6301 gcaagaccag caagaagatc accattgtcg actgtggaca actcgaataa gtttgacttg
6361 tgttttatct taaccaccag atcattcctt ctgtagctca ggagagcacc cctccacccc
6421 atttgctcgc agtatcctag aatctttgtg ctctcgctgc agttccctt gggttccatg
6481 ttttcttgt tccctcccat gcctagctgg attgcagagt taagtttatg attatgaaat
6541 aaaaactaaa taacaattgt cctcgtttga gtttaagtgt gatgtaggct ttattttaag
6601 cagtaatggg ttacttctga aacatcactt gtttgcttaa ttctacacag tacttagatt
6661 ttttttactt tccagtcaca ggaagtgtca atgtttgtt agtgaatat t

```

## (2) INFORMATION FOR SEQ ID NO:2690:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2690

```

1 gtgtactatt agccatggtc aaccccaccg tgttcttcga cattgccgtc gacggcgagc
61 ccttgggccc cgtctccttt gagctgtttg cagacaaggt cccaaagaca gcagaaaatt
121 ttcgtgctct gagcactgga gagaagatg ttggttataa gggttcctgc tttcacagaa
181 ttattccagg gtttatgtgt cagggtgggt acttcacacg ccataatggc actggtggca
241 agtccatcta tggggagaaa ttggaagatg agaacttcat cctaaagcat acgggtcctg
301 gcatcttgct catggcaaat gctggacca acacaaatgg ttcccagttt ttcattctgca
361 ctgccaaagc tgagtgtgtg gatggcaagc atgtggtgtt tggcaaaagt aaagaaggca
421 tgaatattgt ggaggccatg gagcgctttg ggtccaggaa tggcaagacc agcaagaaga
481 tcaccattgc tgactgtgga caactcgaat aagtttgact tgtgttttat ctttaaccacc
541 agatcatctc tctgttagct caggagagca cccctccacc ccatttgctc gcagtatcct
601 agaattcttg tgcctcctgc gcagtccct ttgggttcca tgttttctt gttccctccc
661 atgcctagct ggattgcaga gttaagttaa tgattatgaa ataaaaacta aataacaatt
721 gtc

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## (2) INFORMATION FOR SEQ ID NO:2691:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2691

```

1 gaattccgga gttccgggcg cgcgcgacgt cagtttgagt tctgtgttct ccccgcccgt
61 gtcccgcgcc acccgcgccc gcgatgctgg cgtgcgctg cggtcccgcc tggtctggcc
121 tgcctcctcg cccgcgctcc gtgcgctgc gcctcccgcc ggcccgcgcc tgcagcaagg

```

181 gctccggcga cccgtcctct tctcctcct cccggaaccc gctcgtgtac ctggacgtgg  
241 acgccaacgg gaagccgctc ggccgcgtgg tgctggagct gaagcgagat gtcgtcccaa  
301 agacagctga gaacttcaga gccctgtgca ctggtgagaa gggcttcggc tacaaaggct  
361 ccaccttcca cagggtgatc ccttccttca tgtgccaggc gggcgacttc accaaccaca  
421 atggcacagg cgggaagtcc atctacggaa gccgctttcc tgacgagaac tttaactga  
481 agcacgtggg gccaggtgtc ctgtccatgg ctaatgctgg tcctaacacc aacggctccc  
541 agttcttcat ctgcaccata aagacagact ggttggatgg caagcatgtt gtgttcggtc  
601 acgtcaaaga gggcatggac gtcgtgaaga aaatagaatc tttcggctct aagagtggga  
661 ggacatccaa gaagattgtc atcacagact gtggccagtt gagctaactc gtggccaggg  
721 tgctggcatg gtggcagctg caaatgtcca tgcacccagg tggccgctt gggctgtcag  
781 ccaagggtgcc tgaacgata cgtgtgccc ctcactgtc acagtgtgcc tgaggaaagg  
841 tgctagggat gttagacgga attcc  
1 ttttgcagac gccaccgccc aggaaaaccg tgtactatta gccatggtc  
1 cgggaacgca acatgaagg gtccttgcc gccgcccctca tcgcggggtc cgtcttcttc  
61 ctgctgtctc cgggaccttc tgcggccgat gagaagaaga aggggcccaa agtcaccgtc  
121 aaggtgtatt ttgacctag aattggagat gaagatgtag gccgggtgat ctttggcttc  
181 ttcggaaga ctgttccaaa aacagtggat aattttgtgg ccttagctac aggagagaaa  
241 ggtattggct acaaaaacag caaattccat cgtgtaatca aggacttcat gatccagggc  
301 ggagacttca ccaggggaga tggcacagga ggaagagca tctacgtga gcgcttcccc  
361 gatgagaact tcaaactgaa gcactacggg cctggctggg tcagcatggc caacgcaggc  
421 aaagacacca acggctccca gttcttcac acgacagtca agacagctg gctagatggc  
481 aagcatgtgg tgtttggcaa agttctagag ggcattggagg tggcgaggaa ggtggagagc  
541 accaagacag acagccggga taaacccctg aaggatgtga tcatcgaga ctgcggcaag  
601 atcgaggtgg agaagccctt tgccatcgcc aaggagtagg gcacagggac atcttctctt  
661 gagtgaacct ctgtgcaggc cctgtagtcc gccacagggc tctgagctgc actggccccc  
721 gtgctggcat ctggtggagc ggaccactc cctcacatt ccacaggccc atggactcac  
781 ttttgaataa aactcctacc aacactgacc aataaaaaaa aatgtgggtt ttttttttt  
841 ttaataaaaa a  
1 gaaggtgtct cttgcccgcg ccctcatcgc ggggtccgtc ttcttctctg tctgcccggg  
61 accttctgcg gccgatgaga agaagaagg gcccaaagtc accgtcaagg tgtattttga  
121 cctacgaatt ggagatgaag atgtaggccg ggtgatcttt ggtctctttg gaaagactgt  
181 tccaaaaaca gtggataatt ttgtggcctt agctacagga gagaaaggat ttggctacaa  
241 aaacagcaaa ttccatcgtg taatcaagga cttcatgac cagggcgagg acttcaccag  
301 gggagatggc acaggaggaa agagcatcta cgtgtagcgc tccccgatg agaacttcaa  
361 actgaagcac tacgggctgt gctgggtgag catggccaac gcaggcaaa acaccaacgg  
421 ctcccagttc ttcatcacga cagtcaagac agcctggcta gatggcaagc atgtgggtgt  
481 tggcaaaagt ctagagggca tggaggtggt gcggaagggt gagagacca agacagacag  
541 ccgggataaa cccctgaagg atgtgatcat cgcagactgc ggcaagatcg aggtggagaa  
601 gccctttgcc atcgccaagg agtagggcac agggacatct ttctttgagt gaccgtctgt  
661 gcaggccctg tagtccgcca cagggtctct agctgactg gcccgggtgc tggcatctgg  
721 tggagcggac ccactccct cacttccac aggccatgg actcacttt gtaacaaact  
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## (2) INFORMATION FOR SEQ ID NO:2692:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2692

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## (2) INFORMATION FOR SEQ ID NO:2693:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2693

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## (2) INFORMATION FOR SEQ ID NO:2694:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2694

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134161	aaaagtgtgg	attcacaaag	ggcagtcatt	gtggccattt	ttataaataa	tctaccacag
134221	actagtaaaa	agccttgcat	gaataccatg	gatatttaatt	tgaattcttc	tttttagatt
134281	tttctttcct	tagcaatttg	ttttgtcatt	ttggattaga	attatatctg	tagaatattt
134341	cagttataat	aggttacaac	ttttattcca	ctgaacatct	ttagttttat	ttaggtcatc
134401	tggtaggtat	aaacttcaga	agttaatat	caatatttat	aaaaaccatt	aacaagtgtg
134461	acactttaa	agtttaaaat	attcttttga	cacaactggt	tccaagtgtg	gttacgtatt
134521	ttaattcaat	caaatgttga	aattgttcag	tagatagttt	taattatagg	agaaactcac
134581	ccccatgaca	tttggatgtc	ttaaaagttc	tgttatcttt	ctttgcagtt	attcattctt
134641	tattggatat	ctgctctgtt	atttccagta	tggaccatgc	atttcatgcc	aatacttgga
134701	agtttataat	taagtaagtt	tgtttgttat	tttttacttt	ttagaaaatg	ttttccatat
134761	tccccaatct	taattattca	tgattcttta	gattgcattt	aaaacatttt	gtgtgaattt
134821	aatgttcact	gacactgctg	tctgataatc	cagatattct	acatgtagct	ctcaagccaa
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135001	tggtgtttta	ccagctatca	agtattcctat	ttctaggatt	agataaattg	ataactataa
135061	ttaaaactga	atataactct	ttcattagg	acttttaagt	tgttcacact	taattccatt
135121	tgtacagtaa	ttttaacttt	ctgaaactga	agcattttta	agggtcacca	gggatagttc
135181	ctgtagcatt	catcagattc	ttagggttga	gaggagatgt	gggtgagatg	taaaaaaggt
135241	taagaatatc	tactttatac	acatacataa	aacattaaag	gtcagtggtat	tttcaggtct
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135421	cttgggctat	ttgggttaatt	tctctgaacg	ttagtttgct	catctgaaaa	tggaaataat
135481	aatagcaact	tcttgacagg	gttatagtga	gaattgagtt	catcactgtg	aaatgcttag
135541	aaatgtgcatt	gacacatagt	taatactcaa	ggaattagcc	acatcactat	catcatcact
135601	gattatcttc	cactcttacc	ctcttccagt	tcattttctg	cccagcagaa	tgatctttta
135661	aaaagtaaat	cagatcatgt	tactctattg	cttgaagtct	atcccatttg	attaagaata
135721	acaacctaat	cctctgtgga	tgtgtccctc	ttcaccagcc	tgtctcatgc	tgtctccctt
135781	actcttagtt	cctcaaacat	accaaactct	cctgtccag	agtccttttcg	tgggttttcc
135841	atctgcctag	gatgtctctc	tctctattt	tgtgtacctt	gctaactcct	gcttactgtc

135901 tttcagttct cagcttaaga gttatatctt catgataaca ttctttgata tccttaccct  
135961 aagattaagt tagattgata tccttaccct aagaataagt tagattaggt ctctctattg  
136021 tagcacctta gactctgtca ttggacaaat cacagcccta attaatattt cttaaaattt  
136081 ttttaacattc tctctcatgc tagaccacaa gtttcatgca ggtaaggcgg agattgtgtc  
136141 catttggttg acccctttgt ctccagggcc tggtagaatg cctcatatcat agtaagaatt  
136201 caattaatat tttaacacaga gaaaaaatta gcaacttatt taaacaataa taactgcttc  
136261 agaggtaaac tgggcacatc ttagttatat tatgtgatat atgatgcttt ttgattgttt  
136321 ttttaaattgt tctacaaggt agatattgtt agaggctcta agttacttga tgtgttactt  
136381 gtggtgattg tattcttttc tttttattca tttaggcaga gccttaagca ccagttccata  
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136501 tccttccatt ctgttttaca gtttagctgag cagatgacac agtcagatgc acaggtaaaa  
136561 tttgggctaa tagcatttta aacagcaact ctatttttct ttggcagtta gtaaatctca  
136621 ttggaatgct tgggtcagtc tatttaagag gattttaatt tatttctattt ggggtgtttt  
136681 ttttgatctg tgggattatt tatatcccat aattactttt caccagagc attgtattag  
136741 attcctaact gctgtcattg cctctggggt ctgctggtc cctcttttg ttggttaactg  
136801 gttggtcaca gcattcttct cagaatcctt tcattctttt ctgcatgaga acaaaaattc  
136861 ttttgttcat atttgtataa gatctgatat agctgcaatc aatcttgcat tttttcttca  
136921 ccaacgcatt gcgaccttta gggatacaag tatgtttgtg catgtatatg tatgtatcag  
136981 tcttttaaat ttgatatagt catacatttg tttttatttt gaaaagttag agtgttgaat  
137041 tggatccca tttatgaaac attatattct aaaaatttgt agtacgatta ttgggaatta  
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137401 tttagtagag acgggggttc gccatgttgg ccaggctggt ctgcaactcc tgacctcagg  
137461 tgggtccacc gccttggcct cccaaagtcg tgggattaca ggtgtgagcc accgcgccca  
137521 tcttatatgt aataatttta atgggacct gaattgaata tttcttctt gaatagcaat  
137581 gacatagccc cttctattgt acatctgcaa gctgatacag ggaattcctt tgtacctgcg  
137641 ctcttccctg ccagtcagct atgggggtga aagtgtaggg gttcatcaa gtcctaaaac  
137701 tggtagcaac tcctagggca gggctgattc ggaaggacag accctagggg aggggtggaac  
137761 tttaaaaaga agttctgaag gtagtaagaa ggaatgagg agtagtgtta ggaagggtc  
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137881 tccttttttc ctttctttt ttgtcctcac ttcattcgtg catccttctt gattcctctt  
137941 accttgctaa aaggagaagt ttgtttgggt atcctatatc aatggcagga aggttgtttt  
138001 ctcttttacc tttatcctat agattcatat tctcaacacc aacctctcc ttttcagtt  
138061 tccttcttgc ttctcttgac accacagagt ttgcagctag tacttgaga ggaataat  
138121 acagagatac ttggaccaag agtaagatga agaaagtcta aacaacagta tagtctatag  
138181 tggcaagaga gtagtatggg gctgcttagc cagggtgggt gtacataaag tatatcttca  
138241 gtttatataa actgcttata gatggaaatc agaaaattta aattctctta actgtccaag  
138301 aaaattctca ttttttcaaa ttggggactg ataaaatgta ccagttctgc ttactgtcca  
138361 ttgcttgaaa tggagctttg aggtggactg tataatttct tcaatcttaa ctccaaattc  
138421 tgatcagcga cgccctctgc tgttactat taatatttat ttaccaatca aagtaaagta  
138481 ttgaagtttt cctggcagtt ttcactttgt gttttagtc atttaggctg ctataacaaa  
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138781 atcacttccc caaaggcccc acctcttaat agtatcacat tgggtgttag gtgtctggga  
138841 ggacaccaat cttaagcca tatcatctca cttggaaaaa agtcaaaaata aaaccagtag  
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139021 ctctcacatt tctagaggca gaagtccaca gtgtgtcaat agggccatgt tctctggaag  
139081 gcttttaggg agaatatatt tcatatcttt ctcttagctt ctcggtgtca ctggcaatcc  
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139201 tgattaaggg cataccttac tttaatatga cctcatctta actaattatg tcttcaataa  
139261 ccctatttcc aaataaggcc acattctgaa gtattgggag ttagaactta aagctttttg  
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139441 atagttcttt agccccaat tttttttttt tttttttttt tttttttttt tttttgagac  
139501 ggagtctcgc tctgtcgcct aggcggact ggcgactgca gtggcgcaat ctcggtcac  
139561 tgcaagctcc gcttcccggg ttcacgccat tcccctgcct cagcctcccg agtagctggg  
139621 actacaggcg cctgccaccg cgcccgcta atttttttgt attttttagt gagacggggg  
139681 ttcaccttg tagccaggat ggtctcgatc tctgacctc atgatccacc gcctcgcc  
139741 tcccaaagtg ctgggattac aggcgtgagc caccgcgcc ggcctgcccc caattattta  
139801 gtttttctat aaacaggga atttatttgt gtggccctta gaactaattt aatttccact  
139861 ctaattccta ctatgttta tataatgctt ttagaaattt gtattattca gaaaataaac  
139921 atatactatt gtatctgttg cctacactta gattttattg cctgctatat ttaaatttta  
139981 tttagatttt aattgtttta ttaaagaaag aatgtgcctg taatctcagc acttttgaga  
140041 ggccaaggca gaaggattgc ttgagcccag gagtttgaga ccagactgag caacacaggg  
140101 agaccccat ctctacaaaa aataaaaaaa ttctccaggc ctcatggcac atacctgtag  
140161 ttctagttac ttgggagact ggggtgggag gatgcattga gccaggaga ttgaggtgc  
140221 agtgagccat gatcaggcca ctgactcca gcttggacaa cagagtgaga gcttgtctag  
140281 atagatagat agatagataa tctaataaga taatagacag attatctaaa tagataatag  
140341 acagattatc taaatagata atagacagat tatctaaata gataatagac agattatcta

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140401 aatagataat agacagatta tctaaataga taatagacag attatctatc taaatagata
140461 atagattatc taaatagata atagatagat agattagata gatagataga tagatagagc
140521 ttggacaaca gagtgagagc ctgtctagat agatagaaac aaagaaagaa agaaagaatg
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140641 ttgttggcat taagatgcaa actttgtttt aaacagtga gtaaatcaaa gatgggactg
140701 ttaagttatt tgtgttattt acctgctttt tgaaaatgta aaaataaaac tctaggttta
140761 attagtagta tgctatttag taatgaagta aagctagagg ctctgaacaa atcttgtgta
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140941 aggtgccctc aacaacttag agtctagcct gagacacaag taagtaggta attattatag
141001 aatgggtatga tctttggagg actgggtatt ggctggctca tgggagtaca agataggtac
141061 ccagtgatga agtcaggaaa ggtttcttat ggtgatatga tgacgtctat gctgattata
141121 aggtcagtgat agaataaact ttgtgctttt aaatttgcat agcactgtat tagagagttc
141181 atcttcaaaa taatcgaaaa ggctgagtggt ggtgacccat ggctgtaatc ccagcaactt
141241 gggaggccga ggtgggcaga ttgcttgagc taggagttcg agaccaggct ggccaacatg
141301 gtgaaacccc gtcttacta aaaatacaaa aattagccag gagtatggt gcgcacctgt
141361 aatgccagct acttgggagg ctgaggcagg aggatcactt gaaccaggga ggtggaggtt
141421 gaagtaagcc gaggtcatgc cactgcactc cagcctgggc aacagagtga gactccatct
141481 caaaaaaaaa aaaaatgac aaagaaaggt gaattttcat ctacctatt tctgtgagg
141541 aaaatggact attttcaaat atttttaata aggtcaaaa tgagggatc

```

## (2) INFORMATION FOR SEQ ID NO:2695:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2695

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1 cctctctcgg cttagcagagc ttcccaact ggtaaccctt ccacacccca atcttcatgg
61 accagagatc ttggatgttc cttccacagt tcaaaagacc cctttcgtca ccaccctgg
121 gtatgacact ggaaatggta ttcagcttcc tggcacttct ggtcagcaac ccagtgttgg
181 gcaacaaatg atctttgagg aacatggttt taggcggacc acaccgcca caacggccac
241 ccccataagg cataggccaa gaccataccc gccgaatgta ggtgaggaaa tccaaattgg
301 tcacattccc agggaaagatg tagactatca cctgtacca cacggtccgg gactcaatcc
361 aaatgcctct acaggacaag aagctctctc tcagacaacc atctcatggg ccccatcca
421 ggacacttct gagtacatca tttcatgtca tcctgttggc actgatgaag aacctttaca
481 ggtaattaat tgttctcttc acttctcatg gggcagcaca gaaaggaata agttaggtaa
541 ctgaagtgc cagccctcga ataaaaagt gcttcatggc cgggtgtgat ggctcacgcc
601 tgtaatccca gcactttggg aggccgaggc aggtggatca tttgaggtaa ggagttcaag
661 accagcctgg ccaacatggt gaaacctcgt ctcttgaaaa aaaaaaaaaa aaagtggctc
721 caccttttag aacctcttag aagatggcac atttaagccc tgcttttttt tttttttaa
781 tcccaatatg gctctacttt ggaggacata ccagagagtc actagccttt tatttccata
841 gagaaaatga aactatttct cttattctca cacatttgag gttccttttt gagtaagata
901 gatggttcta gaaaagaaag aaagatatcc tacctgaatt tccatttggg tgcagaagtc
961 taaaacacta cttttacgat ttgtccttga agaaccaccc tatctacaac atatctaaag
1021 aaaaaaaaaa acagcgaagc tgtgcatagc ag

```

## (2) INFORMATION FOR SEQ ID NO:2696:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2696

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1 atcaaacaga aatgactatt gaaggcttgc agcccacagt ggagtatgtg gttagtgtct
61 atgtctcagaa tccaagcggg gagagtcagc ctctggttca gactgcagta accagtagct
121 aacctactgt tggtttccat tttcaaagtc aaattttgtt cttgggtgtc tgaatgccca
181 cgacatgtct tttgcaatta cacataggga aagtgaactt gttggttagt ttatgtcttg
241 agctgagccc tttacgaaca tcttttttcc ttctcagtgc caagcgagga atttacagag
301 aaagaagttg tgaaaccacc atagttagtt gctgtgcttt gaatttcttt ttgctcaaat
361 ggccctcagc aaatcttatt tgccatagc aaatctacaa aaaattttcc tagaccgtct
421 tttctacaac tggatggtaa agttgattga agtgtgcctc atgtagcttt atgtttgggg
481 catttgaagg gctatggctg gaccagagtg taatataaat gcttaataga gaggggaaaa
541 gaagagtgtg agaaccatta tagggctggg ctcacgcctg taatcccagc attttgggag
601 gctgaggcgg atcacgaggt caggagtctg agaccagcct gaccaacatg gtgaaacccc
661 atctctacta aaaatacaaa aattagccag tcgcggtggc acgtgcctgt aatcccagct
721 actcacggag gctgaggcag aagaatcact tggacccagg aggcagaagt tgcagtgagc
781 caagatcatg cctctgcacc ccagcctagg tgatagagtg agactccatc tcaaaaaaaaa
841 acaaaacaaa acaattataa caatttgaat ctgaaccata tgcaaatcag ctttaccact
901 tccaaggtat aagaaaatcc aggtctatga gactaacatc acattgtaaa aatcaaatcg
961 tggtagaata cctttaaatt aatataaata catccccatt gtggggagacat tttgcagggt

```

```

1021 atctgcttat ctcacataca ccatgtttta ataagtgatg caacattgca tattttctaa
1081 accaagaaaa attaagcaag tgtttaagtg atttttcctt tgatagtggg ttaattggac
1141 ttcacaaag aaaaaggat ctgcaaaact gctttgcatg ttataaaact gcttatttca
1201 caacttgctt tcacataacc tcttaccatt aatttgctta acagacattg atcgccctaa
1261 aggactggca ttcactgatg tggatgtcga ttccatcaaa attgcttggg aaagcccaca
1321 ggggcaagtt tccaggtaca ggggtgacct ctcgagccct gaggatggaa tccatgagct
1381 attccctgca cctgatggtg aagaagacac tgcagagctg caaggcctca gaccgggttc
1441 tgagtacaca gtcagtgtgg ttgccttgca cgatgatatg gagagccagc ccctgattgg
1501 aaccagctcc acaggtatat ggttaattgc acacaggtgc catgggagca gcggctttat
1561 gcctactgaa tgaattatgc ttcactgggc tattgattcc cgtgtaaggg tgaaaaagaa
1621 ttattaggaa agatcctctt taaagaggaa tggtaagaaa caataaaact taggtgatat
1681 ttaaggaaac aagtctgatt aaaagaaatt ttggagtatc ctggcttata cacaagacca
1741 taaagcaaga catttgaaga ggatactaaa gttgtggatt atttcctaag ctctgactcc
1801 ctgtgattac cctcactatg tataaagaaa agaagtttgg cattacagag cttacttata
1861 aaaaggaacc caaactcggg catttcatag cagcatgatt ctgagcacac gtgggtaaga
1921 cctttcttct ctggttagat atcatatgct ggtgtataat tagcttaa at gattgtgatt
1981 tagacaccta ggaaataatc aatagggcaa ttgctttcca taatacttta tcttcttggtg
2041 ctttatttct gaagcagagt agaattgctaa agatgtatcc tagtgacagc ataaacccta
2101 gaggtgacag tctgtattat tgcttttcgc ttctcttttc tgcttctgtt gggagccagt
2161 tttcttctta cgccgcatta cagagagaac gtcaaattta gcaagccata tctgccatag
2221 gtccaaataa agagacaata aaaattattc tctctttttt ggatggaata ctgctgaaa
2281 tggttatcca tacaagata ctttatgtag aatagaaaaa ggaggccggg tgcagtggct
2341 cacacatgta atcctagtgc tttgggaggc taagccggga gcaactgatt aggccaggag
2401 ttcattgatca gcctgggcaa tgaagtgaga ccccgctctc acaaaaaaat atgaaaaaat
2461 tagcgagggtg tggtgacaca tgcctgtagt cccagctact caagaggctg aggtagagga
2521 tcacttgagc ctacgagttc aaggctgcag tgagctatga taactccact gcactgtgc
2581 ctggatgaca cagagagacc gtttctaaat taattaatta acaattttaa gaaagaaaaa
2641 gggccattgc ttatttttcc atacaaaagt aaaataaatc ataattggcca ataagccaat
2701 gtaacttttt tttttaaggg aaagcaaaac ttgtaaaacc taaaatctct tagagttttg
2761 gcatttacct aaatgttttc agtgattctg agaattgggt gatataaaac acatttctca
2821 gaaacactt tcttcatttt gcacccctta ctgtactttc ttgtactgaa tctttgcttg
2881 accaggaac ccacctagcc caacaagaac aatccattct acttcttgga actacgttta
2941 ttttcttttt cccctatttc ctataagata acctctaacc aatgacaact tcgacagcta
3001 ttcttgcacc aactgacctg aagttcactc aggtcacacc cacaagcctg agcgcccaat
3061 ggacaccacc caatgttcag ctcaactggat atcgagtgcg ggtgaccccc aaggagaaga
3121 ccggaccaat gaaagaagtc aaccttgctc ctgacagctc atccgtggtt gtatcaggac
3181 ttatc

```

## (2) INFORMATION FOR SEQ ID NO:2697:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2697

```

1 ctgcactttt gataacctga gtcccgccct ggagtacaat gtcagtgttt acactgtcaa
61 ggatgacaag gaaagtgtcc ctatctctga taccatcatc ccaggtaata gaaaataagc
121 tgctatcctg agagtgcacat tccaataaga gtggggatta gcatctta at cccagatgc
181 ttaaggggtg caactatatt tgggatttaa ttccgatctc ccagctgcac tttccaaaac
241 caagaagtca aagcagcgat ttggacaaaa tgcttgctgt taactactgt ttactgtctg
301 tgcttctact ggatgtctgt tgttgcagcg agtatgta at ggagtggcag ccatggcttt
361 aactctgtat tgtctgtc caatggaagta tgactaaaac actgtcacgt gctctgactc
421 agtactgata ggctcaaaagt aatatggtaa atgcatccca tcagtacatt tctgcccgat
481 tttacaatcc atatcaattt ccaacagctg cctatttcat cttgcagttt caaatccttc
541 tttttgaaaa ttggatttta aaaaaaagtt aagtaaaagt cacaccttca gggttgttct
601 ttcttgtggc cttgaaagac aacattgcaa aggcctgtcc taaggatagg cttgtttgtc
661 cattgggtta taacataatg aaagcattgg acagatcgtg tcccccttg gactcttcag
721 tagaatgctt ttactaacgc taattacatg ttttgattat gaatgaacct aaaatagttg
781 caatggcctt aacctaggcc tgccttctct cagcctgaat gtgcttttga atggcacatt
841 tcacaccata cattcataat gcattagcgt tatggccatg atgttgctat gaggtttcta
901 tgggagaaaa aaaatcaatt tatcacccat ttattatttt ttccggttgt tcatgcaagc
961 ttatttttcta ctaaaacagt tttggaatta ttaaaagcat tgctgatact tacttcagat
1021 attatgtcta ggctctaaga atggtttcga catcctaaac agccatatga tttttaggaa
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## (2) INFORMATION FOR SEQ ID NO:2698:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2698

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## (2) INFORMATION FOR SEQ ID NO:2699:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2699

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## (2) INFORMATION FOR SEQ ID NO:2700:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2700

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2401 aggaaactta agatgaatac atgcgtgtac ctacttttac ataagaaatg tattcctgaa
2461 aagctgcatt taaatcaagt cccaaattca ttgacttagg ggagttcagt atttaatgaa
2521 accctatgga gaatttatcc ctttacaatg tgaatagtca tctcctaatt tgtttcttct
2581 gtctttatgt ttttctataa cctggatttt ttaaatcata ttaaaattac agatgtgaaa
2641 ataaagcaga agcaaccttt ttccctcttc ccagaaaacc agtctgtgtt tacagacaga
2701 agagaaggaa gccatagtgt cacttcacaa caattattta ttcatgtct ttactggacc
2761 tgaattttaa actgcaatgc cagtcctgca ggagtgtgg cattaccctc tgcagaacag
2821 tgaagggtat tgcactacat tatggaatca tgcaaaaaaa a

```

## (2) INFORMATION FOR SEQ ID NO:2701:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2701

1 acgcgtggcg agcggaggca gcgctgcctg ttcgcgccat gggggcaccg tggggctcgc  
61 cgacggcggc ggcgggcggg cggcgcgggt ggcgccgagg ccgggggctg ccatggaccg  
121 tctgtgtgct ggcggccgcc ggcttgacgt gtacggcgct gatcacctac gcttgctggg  
181 ggcagctgcc gccgctgcc tgggcgtcgc caaccccgtc gcgaccggtg ggcgtgtgc  
241 tgtggtggga gcccttcggg gggcgcgata gcgcccag gcgcccct gactgcccgc  
301 tgcgcttcaa catcagcggc tgccgcctgc tcaccgaccg cgcgtcctac ggagaggctc  
361 aggcctgtct tttccaccac cgcgacctcg tgaaggggccc ccccgactgg ccccgccct  
421 ggggcatcca ggcgcacact gccgaggagg tggatctgcg cgtgttgac tacgaggagg  
481 cagcggcggc ggcagaagcc ctggcgacct ccagccccag gcccccggc cagcgtggg  
541 tttggatgaa cttcgagtcg ccctcgact ccccggggct gcgaagcctg gcaagtaacc  
601 tcttcaactg gacgtctctc taccggcggt actcggacgt ctttgtgct tatggtacc  
661 ttacccccag aagccacccc ggcgaccgc cctcaggcct ggcccccca cgtgccagga  
721 aacaggggct ggtggcatgg gtgtgagcc actgggacga gcgccaggcc cgggtccgct  
781 actaccacca actgagccaa catgtgaccg tggacgtgtt cggccggggc gggccggggc  
841 agccggtgcc cgaattggg ctctgcaca cagtggccc ctacaagtc tacctggctt  
901 tcgagaactc gcagcacctg gattatatca ccgagaagct ctggcgcaac gcgttgctc  
961 ctggggcggt gccggtgtg ctgggccag accgtgcaa ctacgagcg tttgtgccc  
1021 ggcgcgctt catccacgtg gacgacttc caagtgcctc ctccctggcc tcgtacctg  
1081 ttttcctcga ccgaacccc gcggtctatc gccgtactt ccactggcg cggagctacg  
1141 ctgtccacat cactccttc tgggacgagc cttggtgccg ggtgtgccag gctgtacaga  
1201 gggctgggga ccggcccaag agcatacgga acttgccag ctggttcgag cggtag

## (2) INFORMATION FOR SEQ ID NO:2702:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2702

1 cagatactct gacccatgga tcccctgggc ccggccaagc cacagtggtc gtggcgctgc  
61 tgtctgacca cgctgtgtt tcagctgctg atggctgtgt gtttcttctc ctatctgct  
121 gtgtctcaag acgatccac tgtgtacct aatgggtccc gcttcccaga cagcacagg  
181 acccccgccc actccatccc cctgatcctg ctgtggacgt ggccttttaa caaacccata  
241 gctctgcccc gctgctcaga gatggtcct ggacggctg actgcaacat cactgcccac  
301 cgcaaggtgt atccacaggc agacgcggtc atcgtgcacc accgagaggt catgtacaac  
361 cccagtgcgc agtccacag ctcccagag cggcaggggc agcgatggt ctggttcagc  
421 atggagtccc caagccactg ctggcagctg aaagccatgg acggatactt caatctcacc  
481 atgtcctacc gcagcgactc cgacatcttc acgcccacg gctggctgga gccgtggtc  
541 ggccaagcctg cccaccacc gctcaacctc tcggccaaga ccgagctggt ggctgggca  
601 gtgtccaact gggggccaaa ctccgccagg gtgcgtact accagagcct gcaggcccat  
661 ctcaaggtgg acgtgtacg acgtcccac aagcccctgc ccagggaac catgatggag  
721 acgctgtccc ggtacaagtt ctatctggcc ttcgagaact ccttgacccc cgactacatc  
781 accgagaagc tgtggaggaa cgccctggag gcctgggccc tgcccgtggt gctgggccc  
841 agcagaagca actacgagag gttcctgccc ccgacgcct tcacccacgt ggacgacttc  
901 cagagcccca aggacctggc ccggtacctg caggagctgg acaaggacca gcgccgtac  
961 ctgagctact ttcgtggcg ggagacgtg cggcctcgt ccttcagctg ggactcgt  
1021 ttctgcaagg cctgctgga actgcaggag gaatccaggt accagacacg cggcatagcg  
1081 gcttggttca cctgagaggc ccggcatggg gcctgggctg ccaggg

## (2) INFORMATION FOR SEQ ID NO:2703:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2703

1 aaggagcaca gttccaggcg gggctgagct agggcgtagc tgtgatttca ggggcacctc  
61 tggcggtcgc cgtgatttga gaatctcggg tctcttggt gactgatcct gggagactgt  
121 ggatgaataa tgctgggcac ggccccaccc ggaggctgcg aggcttggg gtcctggccg  
181 ggggtggtct gctcgtgcc ctctggctcc tgtggctgct ggggtcagcc cctcgggta  
241 ccccggcacc ccagcccacg atcaccatcc ttgtctggca ctggcccttc actgaccagc  
301 cccagagct gccagcgac acctgcaccc gctacggcat cggccgtgc cacctgagt  
361 ccaaccgaag cctgctggcc agcgcgacg ccgtggtctt ccaccacgc gagctgcaga  
421 ccggcggtc ccacctgccc ctggcccagc ggccgcgagg gcagccctg gtgtgggct  
481 ccatggagtc tcctagccac accacggcc tcagccacct ccgaggcatc ttcaactggg  
541 tgctgagcta ccggcgcgac tcggacatct ttgtgcccta tggccgctg gagccctact  
601 gggggccctc gccaccgctg ccagccaaga gcagggtggc cgctgggtg gtcagcaact  
661 tccaggagcg gcagctgcgt gccaggctgt accggcagct ggcgcctcat ctgcgggtg



721 atgtcttgg ccgtgccaat ggacggccac tgtgcgccag ctgcctggtg cccaccgtgg  
781 cccagtaccg cttctacctg tcctttgaga actctcagca ccgcgactac attacggaga  
841 aattctggcg caacgcactg gtggctggca ctgtgccagt ggtgctgggg ccccccaggg  
901 ccacctatga ggcttcgtg ccggctgacg ccttcgtgca tgtggatgac tttggctcag  
961 cccgagagct ggcggttttc ctactggca tgaatgagag ccgataccaa cgcttctttg  
1021 cctggcggtga caggctccgc gtgcgactgt tcaccgactg gcgggaacgt ttctgtgcca  
1081 tctgtgaccg ctacccacac ctaccccgca gccaaagtcta tgaggacctt gagggttggg  
1141 ttcaggcctg agatccgctg gccgggggag gtgggtgtgg gtggaaggcg tgggtgtcga  
1201 aatcaaacca ccaggcatcc ggcccttacc ggcaagcagc gggctaaccg gaggctgggc  
1261 acagaggtca ggaagcaggg gtgggggggtg cagggtggga ctggagcatg cagaggaggt  
1321 gagagtggga gggaggtaac ggggtgcctgc tgcggcagac gggaggggaa aggtgtccga  
1381 ggacctctcc caccctgaac aaatcttggg tgggtgaagg cctggctgga agagggtgaa  
1441 aggcaggggc cttggggctg gggggcacc cagcctgaag tttgtggggg ccaaacctgg  
1501 gaccccgagc ttcctcggta gcagaggccc tgtgtgtccc gagacacagg caggggtccc  
1561 tgccacgtcc atagtctga ggtccctgtg tgtaggctgg ggccggggccc aggagaccac  
1621 ggggagcaaa ccagcttggg ctgggctcag ggaggggagg cgggtggacaa taaacgtctg  
1681 agcagtga aa aaaaaaaaa a

## (2) INFORMATION FOR SEQ ID NO:2704:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2704

1 ctgctctgc gcggcagctg ctttagaagg tctcgagcct cctgtacctt cccagggatg  
61 aaccgggccc tccctctgga aggcgagggt tcgggccaca gtgagcgagg gccaggggcg  
121 tgggcgcgag cagagggaaa ccggatcagt tgagagagaa tcaagatgag cggatgaggc  
181 gcttgtgggg cgcgcccgga aagccctcgg gcgcgggctg ggagaaggag tgggcggagg  
241 cgccgcagga ggctcccgga gcctggtcgg gccggctggg ccccgggcgc agtgaagaa  
301 agggacgggc ggtgcccggg tgggcgtcct ggccagctca ccttgccctg gcggtcggc  
361 ccgcccggca cttgggagga gcagggcagg gcccgcgccc tttgcattct gggaccggcc  
421 ccttccattc ccggggcagg gcgagcgagg agcgagcggg ggagccgcag ctacagcatg  
481 agagccgggt ccgctcctcc acgctgcgg acgctggcg agcgaggca cgcgtgcctg  
541 ttcgcgccat gggggcaccg tggggctcgc cgacggcggc ggccggcggg cggctgggt  
601 ggcgccgagg ccgggggctg ccatggaccg tctgtgtgct ggccggcgcc ggcttgacgt  
661 gtacggcgct gatcacctac gcttgcctgg ggcagctgcc gccgtgccc tgggcgtcgc  
721 caaccccgtc gcgaccggtg ggcgtgctgc tgtgtggga gcccttcggg gggcgcgata  
781 gcgccccgag gccgcccctt gactgccggc tgcgttcaa catcagcggc tgccgctgc  
841 tcaccgagcg cgcgtcctac ggagaggctc agcccgctgt tttccaccac cgcgacctcg  
901 tgaaggggcc ccccgactgg ccccgccctt ggggcaccca ggccgacact gccgaggagg  
961 tggatctgcg cgtgttgga ctagaggagg cagcgcgggc ggccagaagc cctgcgacct  
1021 ccagccccag gcccccgggc cagcgctggg tttggatgaa cttcgagtcg ccttcgact  
1081 ccccggggct gcgaagcctg gcaagtaacc tcttcaactg gacgctctcc taccggcggg  
1141 actcgagcgt cttgtgcct tatggctacc tctacccag aagccacccc ggcgacccgc  
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1261 actgggacga gcgccaggcc cgggtccgct actaccacca actgagcaa catgtgaccg  
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1381 cagtgcccg ctacaagttc tacctggctt tcgagaactc gcagcagctg gattatata  
1441 ccgagaagct ctggcgcaac gcgttgctcg ctggggcggt gccggtgtg ctgggcccag  
1501 accgtgcaa ctacgagcgc tttgtgcccc gggcgccctt catccacgtg gacgacttcc  
1561 caagtgcctc ctccctggcc tcgtacctgc ttttctcga ccgcaacccc gcggtctatc  
1621 gccgtactt cactggcgcc cggagctacg ctgtccacat cactccttc tgggacgagc  
1681 cttggtgccc ggtgtgccag gctgtacaga gggctgggga ccggcccaag agcatagcga  
1741 acttgccag ctggttcgag cgtggaagcc gcgctccctt ggaagcgacc caggggaggc  
1801 caagttgtca gctttttgat cctctactgt gcatctcctt gactgcgca tcatggaggt  
1861 aagttcttca aacacccatt tttgtctat gggaaaaaaa cgatttacca attaatatta  
1921 ctacgacag agatgggggc ccggtttcca tttttttgc acagctagca attgggctcc  
1981 ctttgcgtct gatgggcac attgtttagg ggtgaaggag ggggttcttc ctaccttgt  
2041 aaccagtga gaaatgaaat agcttagcgg caagaagccg ttgaggcggt ttctgaatt  
2101 tccccatctg ccacaggcca ttttgtggc ccgtgcagct tccaaatctc atacacaact  
2161 gttcccagat cacgtttttc tggaccaagg tgaagcaaat ttgtggttgt agaaggagcc  
2221 ttgttggtgg agagtgaag gactgtggct gcagggtgga ctttgttgtt tggattcttc  
2281 acagccttgg ctctgagaa aggtgaggag ggcagtcaca gaggggcgcc tgacttctt  
2341 cacaagtact atctgttccc ctgtcctgtg aatggaagca aagtgctgga ttgtcttgg  
2401 aggaaactta agatgaatac atgcgtgtac ctactttac ataagaaatg ttttctgaa  
2461 aagctgcatt taaatcaagt cccaaattca ttgacttagg ggagttcagt atttaatgaa  
2521 accctatgga gaatttatcc ctttacaatg tgaatagtc tctcctaatt tgtttctct  
2581 gtctttatgt ttttctataa cctggatttt ttaaatcata taaaattac agatgtgaaa



2641 ataaagcaga agcaaccttt ttccctcttc ccagaaaacc agtctgtgtt tacagacaga  
2701 agagaaggaa gccatagtgt cacttccaca caattattta tttcatgtct ttactggacc  
2761 tgaaatttaa actgcaatgc cagtcctgca ggagtgtgtg cattaccctc tgcagaacag  
2821 tgaaagggtat tgcactacat tatggaatca tgcaaaaaaa a  
1 acgcgtggcg agcggaggca gcgtgcctg ttcgcgcat gggggcaccg tggggctcgc  
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181 ggcagctgcc gccgctgccc tgggcgtcgc caaccccgtc gcgaccggtg ggcgtgtctg  
241 tgtgtgtgga gcccttcggg gggcgcgata gcgccccgag gccgccccct gactgccccg  
301 tgcgtttcaa catcagcggc tgcgcctgc tcaccgaccg cgctcctac ggagaggctc  
361 aggcgtgtgt tttccaccac cgcgacctg tgaaggggccc ccccgactgg ccccgccct  
421 ggggcatcca gccgcacact gccgaggagg tggatctgcg cgtgttggac tacgaggagg  
481 cagcggcgcg ggcaagaacc ctggcgacct ccagccccag gccccgggc cagcgtggg  
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661 tctaccacag aagccacccc ggccgaccgc cctcaggcct ggccccgcca ctgtccagga  
721 aacaggggct ggtggcatgg gtggtgagcc actgggacga gcgccaaggcc cgggtccgct  
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841 agccggtgcc cgaaattggg ctcctgcaca cagtggcccc ctacaagttc tacctggctt  
901 tcgagaactc gcagcacctg gattatatca ccgagaagct ctggcgcaac gcgttgcctg  
961 ctggggcggt gccggtggtg ctgggcccag accgtgccc aactcagcgc tttgtgcccc  
1021 gcggcgccct catccacgtg gacgaactcc caagtgcctc ctccctggcc tcgtacctgc  
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1141 ctgtccacat cactccttc tgggacgagc cttggtgccg ggtgtgccag gctgtacaga  
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1 cagatactct gaccatgga tcccctgggc ccggccaagc cacagtggct gtggcgctgc  
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121 gtgtctcaag acgatccac tgtgtaccct aatgggtccc gcttcccaga cagcacaggg  
181 accccgccc actccatccc cctgacctg ctgtggacgt ggccttttaa caaacccata  
241 gctctgcccc gctgctcaga gatgtgctt ggcacggctg actgcaacat cactgcccac  
301 cgcaagggtg atccacaggc agacgggtc atcgtgcacc accgagaggt catgtacaac  
361 cccagtgcgc agctcccacg ctcccagag cggcaggggc agcgatggat ctggttcagc  
421 atggagtccc caagccactg ctggcagctg aaagccatgg acggatactt caatctcacc  
481 atgtcctacc gcagcgactc cgacatcttc acgcccacg gctggctgga gccgtggctc  
541 ggccagcctg cccaccacac gctcaacctc tcggccaaga ccgagctggt ggcctgggca  
601 gtgtccaact gggggccaac ctccgcccag gtgcgctact accagagcct gcaggcccat  
661 ctcaagggtg acgtgtacgg acgtccccc aagcccctgc cccagggaac catgatggag  
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781 accgagaagc tgtggaggaa cgccctggag gcctggggcg tggccgtggt gctgggcccc  
841 agcagaagca actacgagag gttcctgccc cccgacgctc tcacccacgt ggacgacttc  
901 cagagcccca aggacctggc ccggtacctg caggagctgg acaaggacca cgcccgtac  
961 ctgagctact ttcgctggcg ggagacgctg cggcctcgct cctcagctg ggcactcgct  
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1 aaggagcaca gttccaggcg gggctgagct agggcgtagc tgtgatttca ggggcacctc  
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121 ggtgataaa tgcgtggcac ggccccaccc ggaggctgcg aggcctgggg gtcctggccg  
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361 ccaaccgaag cctgctggcc agcgccgacg ccgtggtctt ccaccacgc gagctgcaga  
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481 ccatggagtc tcctagccac acccagggc tcagccacct ccgagggcat tcaactggg  
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661 tccaggagcg gcagctgcgt gccaggctgt accggcagct ggccgctcat ctgcgggtg  
721 atgtctttgg ccgtgccaat ggacggccac tgtgcgccag ctgcctgggt cccaccgtg  
781 cccagtaccg ctctacctg tcttttga actctcagca ccgcgactac attacggaga  
841 aattctggcg caacgcactg gtggctggca ctgtgccagt ggtgtgggg ccccccaggg  
901 ccacctatga ggccttcgtg ccggctgacg ccttcgtgca tgtggatgac tttggtcag  
961 cccgagagct ggcggctttc ctactggca tgaatgagag ccgataccaa cgcttctttg  
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1141 ttcaggcctg agatccgctg gccgggggag ggccttacc ggcaagcagc ggctaaccg gaggtggg  
1201 aatcaaacca ccaggcatcc ggccttacc ggcaagcagc ggctaaccg gaggtggg  
1261 acagaggtca ggaagcagg gtgggggggt cagggtggga ctggagcatg cagaggaggt  
1321 gagagtggga gggaggtaac ggggtgctgc tgcggcagac gggaggggaa aggctgccga  
1381 ggacctccc caccctgaac aaatcttggg tgggtgaagg cctggctgga agagggtgaa

1441 aggcaggggcc cttggggctg gggggcacc cagcctgaag ttggggggg ccaaacctgg  
 1501 gaccccgagc ttctcggta gcagaggccc tgggtcccc gagacacagg cagggtccc  
 1561 tgccacgtcc atagttctga ggtccctgtg tgtaggctgg ggcggggccc aggagaccac  
 1621 ggggagcaaa ccagcttgtt ctgggctcag ggaggaggg cgggtggaaa taaactctg  
 1681 agcagtga aa aaaaaaaaaa a

## (2) INFORMATION FOR SEQ ID NO:2705:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2705

1 cccccctcca agataatttt taaaaaacct tctcctttgc tcacctttgc ttcccagcct  
 61 tcccatcccc ccaccgaaag caaatcattc aacgacccc gacctccga cggcaggagc  
 121 cccccgacct ccaggcgga ccgcccctccc tccccggggg tccgggcccgc gcgagagggc  
 181 gcgagcacag ccgaggccat ggaggtagc gcggaccagc cgcgctgggt gagccaccac  
 241 caccgcgcg tgcacacgg gcagcaccgc gacacgcacc acccgggcct cagccactcc  
 301 tacatggacg cggcgagta cccgctgcgc gaggagggtg atgtgctttt taacatcgac  
 361 ggtcaaggca accacgtccc gccctactac ggaaactcgg tcaggggccac ggtgcagagg  
 421 taccctccga cccaccacgg gagccagggtg tgcgcgccgc ctctgcttca tggatcccta  
 481 ccctggctgg acggcggcaa agccctgggc agccaccaca cgcctcccc ctggaatctc  
 541 agccctttct ccaagacgtc catccaccac ggctccccgg ggcctctctc cgtctacccc  
 601 ccggcctcgt cctcctcctt gtcggggggc cagccagacc cgcacctctt cacttcccg  
 661 cccacccgcg cgaaggacgt ctccccggac ccatcgctgt ccacccagg ctcggccggc  
 721 tcggcccggc aggacgagaa agagtgcctc aagtaccagg tgccctggc cgacagatg  
 781 aagctggagt cgtccactc ccgtggcagc atgaccgccc tgggtggagc ctctcgtcg  
 841 acccaccacc ccatcaccac ctaccgccc tacgtgccc agtacagctc cggactcttc  
 901 cccccagca gcctgctggg cggctcccc accggcttcg gatgcaagtc caggcccaag  
 961 gcccggtcca gcacagaagg caggagtggt gtgaactgtg gggcaacctc gacccactg  
 1021 tggcggcgag atggcacggg aactacctg tgcaacgcct gcgggctcta tcacaaatg  
 1081 aacggacaga accggcccct cattaagccc aagcgaagge tgtctgcagc caggagagca  
 1141 gggagctcct gtgcgaactg tcagaccacc acaaccacac tctggaggag gaatgccaat  
 1201 ggggacctg tctgcaatgc ctgtgggctc tactacaagc ttcacaatat taacagaccc  
 1261 ctgactatga agaaggaagg catccagacc agaaccgaa aaatgtctag caaatccaaa  
 1321 aagtgaataa aagtgcata ctactggag gacttcccca agaacagctc gtttaacccg  
 1381 gccgccctct ccagacacat gtcctcctg agccacatct cgccttcag ccactccagc  
 1441 cacatgctga ccacgcccac gccgatgcac ccgccatcca gcctgtcctt tggaccacac  
 1501 caccctcca gcattgtcac cgccatgggt tagagccctg ctcgatgtc acagggcccc  
 1561 cagcgagagt cctgcagtc ccttcgact tgcattttt caggagcagt atcatgaagc  
 1621 ctaaacgcga tggatatatg tttttgaagg cagaaagcaa aattatgtt gccactttgc  
 1681 aaaggagctc actgtggtgt ctgtgttcca accactgaat ctggacccca tctgtgaata  
 1741 agccattctg actcatatcc cctatttaac aggtctctta gtgctgtgaa aaaaaaatg  
 1801 ctgaacattg catataactt atattgtaag aaatactgta caatgacttt attgcatctg  
 1861 ggtagctgta aggcataag gatgccaaag agtttaagga atatgggaga aatgggtgtg  
 1921 aaattaagaa gaaactaggt ctgatattca aatggacaaa ctgccagttt tgtttcctt  
 1981 cactggccac agttgtttga tgcattaaaa gaaataaaaa aaaag

## (2) INFORMATION FOR SEQ ID NO:2706:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2706

1 acacagagag aaaggctaaa gttctctgga ggatgtggct gcagagcctg ctgctcttgg  
 61 gcactgtggc ctgcagcatc tctgacccc cccgctcgcc cagccccagc acgcagccct  
 121 gggagcatgt gaatgccatc caggaggccc ggcgtctcct gaacctgagt agagacactg  
 181 ctgtgagat gaatgaaca gtagaagta tctcagaat gtttgacct caggagccga  
 241 cctgcctaca gaccgcctg gactgtaca agcaggccct gcggggcagc ctcaccaagc  
 301 tcaaggcccc cttgaccatg atggccagcc actacaagca gcaactgcc ccaaccccg  
 361 aaacttctg tgcaaccagc attatcacct ttgaaagtt caaagagaac ctgaaggact  
 421 ttctgcttgt catcccttt gactgctggg agccagtcca ggagtgcagc cggccagatg  
 481 aggtctggca agccggggg ctgctctctc atgaaacaag agctagaaac tcaggatggg  
 541 catcttgagg ggaccaagg gtgggccaca gccatgggtg gaggggcctg gacctgcct  
 601 gggcacactg accctgatac aggcattggc gaagaatggg aatattttat actgacagaa  
 661 atcagtaata ttatatatt tatattttta aaattttat ttattttat atttaagttc  
 721 atattccata ttattcaag atgttttacc gtaataatta ttattaaaaa tagcttctaa  
 781 aaaaaaaaa

## (2) INFORMATION FOR SEQ ID NO:2707:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2707

1 ttctctctga ccagcaccat gcttctcctg gtgacaagcc ttctgctctg tgagttacca  
61 caccagcat tcctcctgat cccagagaaa tcggatctgc gaacagtggc accagcctct  
121 agtctcaatg tgaggtttga ctccaggacg atgaatttaa gctgggactg ccaagaaaac  
181 acaaccttca gcaagtgttt cttactgac aagaagaaca gagtctgga acccaggctc  
241 agtaacaacg aatgttcgtg cacatttcgt gaaatttgc tgcataagg agtcacattt  
301 gaggttcacg tgaatactag tcaaagagga ttccaacaga aactgcttta tccaaattca  
361 ggaagggagg gtaccgctgc tcagaatttc tctgtttca tctacaatgc ggatttaatg  
421 aactgtacct gggcgagggg tccgacggcc ccccgtagc tccagtattt ttgtacata  
481 cgaactcaa agagaaggag ggagatccgg tgtccttatt acatacaaga ctcaggaacc  
541 catgtgggat gtcacctgga taacctgtca ggattaacgt ctgcaatta ctttctggtt  
601 aacggaacca gccgagaaat tggcatccaa ttctttgatt cacttttga cacaagaaa  
661 atagaacgat tcaacctcc cagcaatgac accgtacgtt gcaacacgac gcactgcctc  
721 gtacggtgga aacagcccag gacctatcag aagctgtcgt acctggactt tcagtaccag  
781 ctggacgtcc acagaaaaga taccagcct ggacggaaa acctactgat taatgtttct  
841 ggtgatttgg aaaatagata caactttcca agctctgagc ccagagcaaa acacagtgtg  
901 aagatcagag ctgcagacgt ccgcatcttg aattggagct cctggagtga agccattgaa  
961 tttggttctc taggatacag cggctgttcc cgccagttcc acagatcaaa gacaaactga  
1021 atgataacca tgaggtggaa gacgagatca tctgggagga attcacccca gaggaagggg  
1081 aaggctaccg cgaagaggtc ttgaccgtga aggaaattac ctgagacca gaggggtgtg  
1141 gaatggcatg gacatctccg cctccgcgac acgggggaac tgttttctg atgatgctgt  
1201 gaacctttat atcattttct atgtttttat taaaaacat gacatttggg gccaggcgcg  
1261 gtggtcacg cctgtaatcc cag

## (2) INFORMATION FOR SEQ ID NO:2708:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2708

1 ttctcagagt ggctgcagtc tcgtgctgg atgtgcacat ggtggtcatt ccctctgctc  
61 acaggggcag ggtccccc ttactggact gaggttgccc cctgctccag gtctgggtg  
121 ggagcccatg tgaactgtca gtggggcagg tctgtgagag ctccctcac actcaagtct  
181 ctctcacagt ggccagagaa gaggaaggct ggagtcagaa tgaggacca gggcgggcat  
241 agcctgccca aaggccctg ggattacagg caggatgggg agccctatct aagtgtctcc  
301 cagcctccac cccagccatt ccaggccagg aagtccaaac tgtgccctc agagggaggg  
361 gcagcctca ggccattca gactgccag ggagggctgg agagccctca ggaaggcggg  
421 tgggtgggct gtcggttctt ggaagggttc attaatgaaa accccaagc ctgaccacct  
481 agggaaaagg ctcaccgttc ccatgtgtgg ctgataagg ccaggagatt ccacagtcca  
541 gtagttccc ccgctccct ggcattttgt ggtcaccatt aatcatttcc tctgtgtatt  
601 taagagctct tttgccagt gacccagcta cacagagaga aaggctaaag ttctctggag  
661 gatgtggctg cagagcctgc tgccttggg cactgtggcc tgcagcatct ctgacccgc  
721 ccgctcgcgc agcccagca cgcagccctg ggagcatgtg aatgccatcc aggagggccg  
781 gcgtctcctg aacctgagta gagacactgc tgcagagatg gtaagtgaaga gaatgtggg  
841 ctgtgctagg caccagtggc cctgactggc cagcctgtc agcttgataa catgacattt  
901 tccttttcta cagaatgaaa cagtagaagt catctcagaa atgtttgacc tccaggtaag  
961 atgcttctct ctgacatagc ttccagaag cccctgccct ggggtggagg tggggactcc  
1021 attttagatg gcaccacaca gggtgttcca ctttctctcc agtcagctgg ctgcaggagg  
1081 agggggtagc aactgggtgc tcaagaggct gctggccgtg cccctatggc agtcacatga  
1141 gtccttttat cagctgagcg gccatgggca gacctagcat tcaatggcca ggagtcacca  
1201 ggggacaggt ggtaaagtgg gggtcacttc atgagacagg agctgtgggt ttggggcgct  
1261 cactgtgccc cgagaccaag tcctgttgag acagtgtgta ctacagagag gcacagaggg  
1321 gtttcaggaa caaccttgc ccaccagca ggtccagggt agggccacc cccctctccc  
1381 tgaatgatgg ggtgagagtc acctccttcc ctaaggctgg gctcctctcc aggtggcgct  
1441 gaggggtggc tgggcggggc agtgagaagg gcagggtcgt gcctgccatg gacaggggcag  
1501 ggtctatgac tggaccagc ctgtgcccct cccaagccct actcctgggg gctgggggca  
1561 gcagcaaaaa ggagtgggtg agagtcttg taccactgtg ggcacttggc cactgctcac  
1621 cgacgaacga cattttccac aggagccgac ctgcctacag acccgcttgg agctgtacaa  
1681 gcagggcctg cggggcagcc tcaccaagct caagggccct ttgacctga tggccagcca  
1741 ctacaagcag cactgccctc caaccccggt gagtgcctac ggcagggcct ccagcaggaa  
1801 tgccttaatc taggggggtg ggtcgacatg gggagagatc tatggctgtg gctgttcagg

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1861 acccgggg gtttctgtgc caacagttat gtaatgatta ggtccaga gaggaggcag
1921 acagcccatt tcatcccaag gagtcagagc cacagagcgc tgaagccac agtgctcccc
1981 agcaggagct gctcctatcc tggtcattat tgtcattacg gttaatgagg tcagagggtga
2041 gggcaaaccc aaggaaactt ggggcctgcc caaggcccag aggaagtgcc caggcccacag
2101 tgccaccttc tggcaggact ttcctctggc cccacatggg gtgcttgaat tgcagaggat
2161 caaggaaggg aggctacttg gaatggacaa ggacctcagg cactccttcc tgcgggaagg
2221 gagcaaatgt tgtggccttg actccactcc ttctgggtgc ccagagacga cctcagccca
2281 gctgccctgc tctgccctgg gaccaaaaag gcaggcgttt gactgcccag aaggccaacc
2341 tcaggctggc acttaagtca ggcccttgac tctggctgcc actggcagag ctatgcactc
2401 cttggggaac acgtgggtgg cagcagcgtc acctgaccga ggtcagtggt tgtgtcctgg
2461 agtgggcctc ctggcctctg agttctaaga ggcagtagag aaacatgctg gtgcttcctt
2521 cccccacgtt acccacttgc ctggactcaa gtgtttttta ttttctttt tttaaaggaa
2581 acttctctgt caaccagat tatcaccttt gaaagtttca aagagaacct gaaggacttt
2641 ctgtctgtca tcccctttga ctgctgggag ccagtccagg agtgagaccg gccagatgag
2701 gctggccaag ccggggagct gctctctcat gaaacaagag ctagaaactc aggatggtca
2761 tcttgagggg accaaggggt gggccacagc catgggtgga gtggcctgga cctgccctgg
2821 gcacactgac cctgatacag gcattggcaga agaattggaa tattttatc tgacagaaat
2881 cagtaatat tttatattta tttttttaaa atattttatt attttttat ttaagttcat
2941 attccatatt tattcaagat gttttaccgt aataattatt attaaaaata tgcttctact
3001 tgctcagtg tctagtttgt ttttaacctat gagcaaatgc cat

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(2) INFORMATION FOR SEQ ID NO:2709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2709

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1 acacagagag aaaggctaaa gttctctgga ggatgtggct gcagagcctg ctgctcttgg
61 gcaactgtgc ctgcagcatc tctgcacccg cccgctcggc cagccccagc acgcagccct
121 gggagcatgt gaatgccatc caggaggccc ggcgtctcct gaacctgagt agagacactg
181 ctgctgagat gaatgaaaca gtagaagtca tctcagaaat gtttgacctc caggagccga
241 cctgcctaca gaccccgctg gagctgtaca agcagggcct gcggggcagc ctcaccaagc
301 tcaagggccc cttgaccatg atggccagcc actacaagca gcaactgcct ccaaccccg
361 aaacttctct tgcaaccagc attatcacct ttgaaagttt caaagagaac ctgaaggact
421 tctgtcttgt catccccttt gactgctggg agccagtcga ggagtggagc cggccagatg
481 aggtgtggca agccggggag ctgctctctc atgaaacaag agctagaaac tcaggatggt
541 catcttgtag ggaccaaggg gtgggccaca gccatggtgg gagtggcctg gacctgccct
601 gggcacactg accctgatac aggcattggc gaagaatggg aatattttat actgacagaa
661 atcagtaata tttatatatt tatattttta aaatatttat ttattttatt atttaagttc
721 atattccata tttattcaag atgttttacc gtaataatta ttattaaaaa tagcttctaa
781 aaaaaaaaaa
1 ttctctctga ccagcaccat gcttctctctg gtgacaagcc ttctgctctg tgagttacca
61 caccagcatc tctcctgat cccagagaaa tcggatctgc gaacagtggc accagcctct
121 agtctcaatg tgaggtttga ctccaggagc atgaatttaa gctgggactg ccaagaaaac
181 acaaccttca gcaagtgttt cttaactgac aagaagaaca gactcgtgga acccaggctc
241 agtaacaacg aatgttctgt cacatttctg gaaatttctg tgcatgaagg agtcacattt
301 gaggttcacg tgaatactag tcaaagagga tttcaacaga aactgcttta tccaaattca
361 ggaagggagg gtaccgctgc tcagaatttc tctgtttca tctacaatgc ggatttaatg
421 aactgtacct gggcgagggg tccgacggcc ccccgtagc tccagtattt tttgtacata
481 cgaactcaa agagaaggag ggagatccgg tgccttatt acatacaaga ctcaggaacc
541 catgtgggat gtcacctgga taacctgtca ggattaacgt ctgcgaatta ctttctggtt
601 aacggaacca gccgagaaat tggcatccaa ttctttgatt cacttttgga cacaagaaa
661 atagaacgat tcaaccctcc cagcaatgtc accgtacgtt gcaacacgac gcaactgctc
721 gtacggtgga aacagcccag gacctatcag aagctgtcgt acctggactt tcagtaccag
781 ctggacgtcc acagaaagaa taccagcct ggcacggaaa acctactgat taatgtttct
841 ggtgatttgg aaaatagata caactttcca agctctgagc ccagagcaaa acacagtgtg
901 aagatcagag ctgcagacgt ccgcatcttg aattggagct cctggagtga agccattgaa
961 tttggttctt taggatacag cggctgttcc cgccagttcc acagatcaaa gacaaactga
1021 atgataacca tgaggtggaa gacgagatca tctgggagga attcacccca gaggaaggga
1081 aaggctaccg cgaagaggct ttgaccgtga aggaatttac ctgagacca gaggggtgag
1141 gaatggcatg gacatctccg cctccgcgac acgggggaac tgtttcttg atgatgctgt
1201 gaacctttat atcattttct atgtttttat ttaaaaacat gacatttggg gccaggcgcg
1261 gtggctcacg cctgtaatcc cag
1 ttctcagagt ggctgcagtc tcgctgctgg atgtgcacat ggtggctcatt ccctctgctc
61 acaggggagc ggggtccccc ttactggact gaggttgccc cctgctccag gtctctgggtg
121 ggagcccatt tgaactgtca gtggggcagg tctgtgagag ctccccctac actcaagtct
181 ctctcacagt ggccagagaa gaggaaggct ggagtcagaa tgaggacca gggcgggcat
241 agcctgccc aaggcccctg ggattacagg caggatgggg agccctatct aagtgtctcc

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301 cagcggccac ccagccatt ccaggccagg aagtccaaac tgtgcccctc agagggaggg  
361 ggcagcctca ggccattca gactgcccag ggagggtg agagccctca ggaaggcg  
421 tgggtgggct gtcggttctt ggaaagggtt attaatgaaa accccaagc ctgaccacct  
481 agggaaaagg ctcaccgttc ccatgtgtg ctgataagg ccaggagatt ccacagttca  
541 ggtagttccc cgcctccctt ggcattttgt ggtcaccatt aatcatttcc tctgtgtatt  
601 taagagctct tttgccagt agcccagta cacagagaga aaggctaaag ttctctggag  
661 gatgtggctg cagagcctgc tgccttggg cactgtggcc tgcagcatct ctgacccgc  
721 ccgctcggcc agcccagca cgcagccctg ggagcatgtg aatgccatcc aggaggcccg  
781 gcgtctctg aacctgagta gagacactgc tgcgtgagatg gtaagtgaga gaattgtggc  
841 ctgtgctagg caccagtggc cctgactggc cagcctgtc agcttgataa catgacattt  
901 tccttttcta cagaatgaaa cagtagaagt catctcagaa atgtttgacc tccaggtaag  
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1021 attttagatg gcaccacaca ggggtgtcca ctttctctcc agtcagctgg ctgaggagg  
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1141 gctcctttat cagctgagcg gccatgggca gacctagcat tcaatggcca ggagtcacca  
1201 ggggacaggt ggtaaagtgg ggtcacttc atgagacagg agctgtgggt ttggggcgct  
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1321 gtttcaggaa caaccttgc ccaccagca ggtccagggt agggccacc cccctctccc  
1381 tgaatgatgg ggtgagagtc acctccttcc ctaaggctgg gctcctctcc aggtgccgt  
1441 gaggggtggc tgggcggggc agtgagaagg gcaggttcgt gcctgccatg gacagggcag  
1501 ggtctatgac tggaccagc ctgtgcccct cccaagccct actcctgggg gctgggggca  
1561 gcagcaaaaa ggagtgggtg agagtcttg taccactgtg ggcacttggc cactgctcac  
1621 cgacgaacga cattttccac aggagccgac ctgcctacag acccgctgg agctgtacaa  
1681 gcagggcctg cggggcagcc tcaccaagct caaggccccc ttgaccatga tggccagcca  
1741 ctacaagcag cactgcccct caaccccggt gactgcctac ggcagggcct ccagcaggaa  
1801 tgtcttaatc taggggggtg ggtcgacatg gggagagatc tatggctgtg gctgttcagg  
1861 acccagggg gttctgtgc caacagttat gtaatgatta gccctccaga gaggaggcag  
1921 acagccatt tcatcccaag gactcagagc cacagagcgc tgaagccac agtgcctccc  
1981 agcaggagct gctcctatcc tggctattat tgtcattacg gttaatgagg tcagagggtga  
2041 gggcaaaccc aaggaaactt ggggcctgcc caaggccag aggaagtgcc caggcccaag  
2101 tgccaccttc tggcaggact ttctctggc cccacatggg gtgcttgaat tgcagaggat  
2161 caaggaaggg aggctacttg gaatggacaa ggacctcagg cactccttcc tgcgggaagg  
2221 gagcaaatgt tgtggccttg actccactcc ttctgggtgc ccagagacga cctcagccca  
2281 gctgcccctg tctgcccctg gaccaaaaa gtaggcgttt gactgcccag aaggccaacc  
2341 tcaggctggc acttaagtca ggcccttgac tctggtgcc actggcagag ctatgcactc  
2401 cttggggaac acgtgggtg cagcagcgtc acctgaccca ggtcagtggt tgtgtcctgg  
2461 agtgggccc ctggcctctg agttctaaga ggcagtagag aaacatgctg gtgcttctt  
2521 cccccacgtt acccacttgc ctggactcaa gtgtttttta ttttctttt tttaaaggaa  
2581 acttcctgtg caaccagat tatcacctt gaaagtttca aagagaacct gaaggacttt  
2641 ctgcttgta tccccttga ctgctgggag ccagtccagg agtgagaccg gccagatgag  
2701 gctggccaag cggggagct gctctctcat gaaacaagag ctagaaactc aggatgtca  
2761 tcttgagggg accaagggtt gggccacagc catggtggga gtggcctgga cctgcccctg  
2821 gcacactgac cctgatacag gcatggcaga agaattggaa tattttatac tgacagaaat  
2881 cagtaatat tatatatata ttttttaaa atatttattt atttatttat ttaagttcat  
2941 attccatatt tattcaagat gttttaccgt aataattatt attaaaaata tgcttctact  
3001 tgtccagtgt tctagttgt ttttaaccat gagcaaatgc cat

## (2) INFORMATION FOR SEQ ID NO:2710:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2710

1 atcctggctg atatggtgaa accccatctc tactaaaaat acaaaaatta gctgggcgtg  
61 gtgggtggcg catgtaatcc cagctactca ggaggctgag gcaggagaat tacttgaaac  
121 tgggaggcag aggttgagat gaaccgagat cgcgccattg cactccagtc tggcgacaga  
181 gcgagactcc gtctctaaat aaataaataa ataaatttag ccttctactc aagaacttat  
241 ctggctttgt cttaatgtaa aaataatttc ttttgcataa attattgaga gaaatttact  
301 attatttagt gtttatcagt tttctttaaa ctcaccactt ttgatgaat atgaaatct  
361 aaaaacttgg ccgggcgcag tggctcacac ctgtaatctc agcactttgg gaggccaagg  
421 tgggaggatc atctgaggtc aggagttcaa gatcagcctg accaaccatg tgaaaccctt  
481 tctctactaa aaatacaaaa attagctggg cgtgggtggg ggtgcctgta attgtagcta  
541 cttgggaggc tgaggcatga gaatcacttg aaccagaaaa gcagagggtg cagtgcctg  
601 agatgggtgc actgcactcc agcctgggtg acagagttag actctgtcct aaaaaaaaaa  
661 aaaaaaaaaa tggctgggag tgggtgcctta tgcctgtaat cccagcactt tgggagttca  
721 gcgtgggtgg atcacctgag gtcaggagtt caagtccagc ctgaccaaca tgggaaacc  
781 ccgtctctac taaaaaagta caaaaaaat agccgggtgt ggtggcacac tctgtaac  
841 ccagctactc aggaggctga ggcaggagaa tcacttgaat ttgggagctg gagattgtag

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201 tcagccaaga tgggtgccatt gcactccagt ctgggtgaca gagtgagact ccatctcaaa
961 aaaaaaaaaa aaatcttaaa aactccttcc agaagattta atacttactt tcaccaaac
1021 acccgacttg agtatcacca ataacagagg atacagtccg ttttcagtag agccttagta
1081 gcaaaaggggt ttcatTTTTtA tttttcagat acaggatcct gccctgtcac ccaagctgga
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1201 tataggacaa tttttaaaaa atttcattgt aaagacagga ttccactgtg ttgccaggc
1261 tgcaagtctt ggctcaagt gatcattcca ctttaactc ttgccctcaa gcagtcctcc
1321 cactcagac tcccaaaatg ctgggattat ggggtgagc caccatttcc agcctactag
1381 caaggtctt gttacatatt acttggcatg atttatgtaa tttaaaaaaa ttgtttgtt
1441 ttcaaataga aaagtaaaat aacgaatatg cttttccaat aacataatcc ctttctcact
1501 tgagaatttt cctctaaaaa gatatgctag atttatttca tgctttatgt gcctctggtg
1561 tgtccccctta taacctcctc catatcattt agggatggtc tcagctgcaa gtaagaactg
1621 ccacaacagg tgatgtaagc ccaaaaaaaa aaaaaaaaaa aaagcaaagc caagcaaac
1681 aaagcccat taattatttc ccataataat aagtctggga gaaagaagat tccagagttg
1741 gctcagcagc ttagtgacag caaggcccta ggctggcatt ttcttggcct tcccgatggt
1801 cccaagatga ctctcatggc ctcaaacatc acttcctcac atcctgtcag ggagaaagag
1861 gcaagtgagc aacaacaatt tgtggtgttt ggatcatttg tcagagagga agaacttcc
1921 taaaaactcc gcctctgtg tttgacatcc tcctcctatt ccttggccat ggtggtatct
1981 catggtcact cctctatctg ccactgtaaa gaggaactgg attgctatat tctgcttaga
2041 cacatgagga tgcagcccac cttcccagaa catgtgcgga attagatttc tacaacaca
2101 tttgtcttgc ttctgcccac ctctctcact agaatgcaca ttccataggg gcaaacattt
2161 ttgtctattt tgttcacagc tatattctca acacctagaa gagtgcaga aattcaataa
2221 atagttgtta agtgagcaaa tgaatgcatg aataaggaaa aggtacatg gctattgagt
2281 aggtaaccag cagtgttgat ccccccaac agcatacaac tccagtctga tgaacatcat
2341 gctactaagt ggccactcat ccccaagtc tctgacctta ctttttctct cttttctccc
2401 agggagttag ccataactgg cggctgctct tgcgccaatg

```

## (2) INFORMATION FOR SEQ ID NO:2711:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2711

```

1 ccaatgagcc tccccaatc ctctgcctc ttagaagaca agatgtgtga gggcaacaag
61 accactatgg ccagcccaca gctgatgcc ctggtgggtg tcttgagcac tatctgctt
121 gtcacagtag ggctcaacct gctggtgctg tatgccgtac ggagtgcgc gaagctccac
181 actgtgggga acctgtacat cgtcagcctc tcggtggcgg acttgatcgt gggcgccgtc
241 gtcatgccta tgaacatcct ctacctgtc atgtccaagt ggctcactgg ccgtcctctc
301 tgctctttt ggctttccat ggactatgtg gccagcacag cgtccatttt cagtgtcttc
361 atcctgtgca ttgatcgcta ccgctctgtc cagcagcccc tcaggtacct taagtatcgt
421 accaagaccc gagcctcggc caccattctg ggggcctggt ttctctctt tctgtgggtt
481 attcccattc taggctggaa tcacttcatg cagcagacct cgggtgcgcg agaggacaag
541 tgtgagacag acttctatga tgtcacctgg ttcaaggcca tgactgccat catcaacttc
601 tacctgcccc ccttgctcat gctctggttc tatgccaaga tctacaaggc cgtacgacaa
661 cactgccagc accgggagct catcaatagg tccctccctt ccttctcaga aattaagctg
721 aggccagaga accccaaggg ggatgccaa aaaccaggga aggagtctcc ctgggaggtt
781 ctgaaaagga agccaaaaga tgtggtggt ggatctgtct tgaagtcacc atcccaaac
841 cccaaggaga tgaatcccc agttgtcttc agccaagagg atgatagaga agtagacaaa
901 ctctactgct ttccacttga tattgtgcac atgcaggctg cggcagaggg gtagtagcag
961 gactatgtag ccgtcaaccg gagccatggc cagctcaaga cagatgagca gggcctgaac
1021 acacatgggg ccagcgagat atcagaggat cagatgttag gtgatagcca atccttctct
1081 cgaacggact cagataccac cacagagaca gcaccaggca aaggcaaat gaggagtggg
1141 tctaacacag gcctggatta catcaagttt acttgaaga ggctccgctc gcattcaaga
1201 cagtatgtat ctgggttgca catgaaccgc gaaaggaagg ccgccaaca gttgggtttt
1261 atcatggcag ccttcactct ctgtggatc cttatttca tcttctcat ggtcattgcc
1321 ttctgcaaga actgttgcaa tgaacatttg cacatgttca ccatctggct gggctacatc
1381 aactccacac tgaacccct catctacccc ttgtgcaatg agaacttcaa gaagacattc
1441 aagagaattc tgcataattc ctctaaagg aggtctgtag gggatgcaac aaaatgatcc
1501 ttatgatgtc caacaaggaa atagaggacg aaggcctgtg tgttgccagg caggcacctg
1561 ggctttcttg aatccaaacc acagtcttag gggcttggtg gtttgaaaag ttcttaggca
1621 ccatagaaga acagcagatg gcggtgatca gcag

```

## (2) INFORMATION FOR SEQ ID NO:2712:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2712

```
1 atgagcctcc ccaattctct ctgctcttta gaagacaaga tgtgtgaggg caacaagacc
61 actatggcca gccccagct gatgcccttg gtggtggtcc tgagcactat ctgcttggtc
121 acagtagggc tcaacctgct ggtgctgtat gccgtacgga gtgagcgga gctccacact
181 gtggggaacc tgtacatcgt cagcctctcg gtggcgagct tgatcgtggg tgccgtcgtc
241 atgcctatga acatcctcta cctgctcatg tccaagtggg cactgggccc tctctctgc
301 ctcttttggc tttccatgga ctatgtggcc agcacagcgt ccattttcag tgtcttcac
361 ctgtgcattg atcgctaccg ctctgtccag cagcccctca ggtaccttaa gtatcgtacc
421 aagacccgag cctcgccac cattctgggg gcctggtttc tctctttct gtgggttatt
481 cccattctag gctggaatca cttcatgcag cagacctcgg tgcgcccaga ggacaagtgt
541 gagacagact tctatgatgt cacctggttc aaggctatga ctgccatcat caacttctac
601 ctgcccacct tgctcatgct ctggttctat gccaaagtct acaaggccgt acgacaacac
661 tgccagcacc gggagctcat caataggtcc ctcccttctc tctcagaaat taagctgagg
721 ccagagaacc ccaaggggga tgccaagaaa ccagggaagg agtctccttg ggaggttctg
781 aaaagggaagc caaagatgc tgggtgtgga tctgtcttga agtcaccatc ccaaaccctc
841 aaggagatga aatccccagt tgtcttcagc caagaggatg atagagaagt agacaaactc
901 tactgctttc cacttgatat tgtgcacatg caggctgcgg cagaggggag tagcagggac
961 tatgtagccg tcaaccggag ccatggccag ctcaagacag atgagcaggg cctgaacaca
1021 catggggcca gcgagatata agaggatcag atgttaggtg atagccaatc cttctctcga
1081 acggactcag ataccaccac agagacagca ccaggcaagg gcaaatgag gagtgggtct
1141 aacacaggcc tggattacat caagtttact tggaaaggcc tccgctcgca ttcaagacag
1201 tatgtatctg ggttgacat gaaccgcgaa aggaaggccg ccaaacagt gggtttatc
1261 atggcagcct tcactctctg ctggatccct tatttcatct tcttcatggt catgtcttc
1321 tgcaagaact gttgcaatga acatttgcac atgttcacca tctggctggg ctacatcaac
1381 tccacactga accccctcat ctacccttgg tgcaatgaga acttcaagaa gacattcaag
1441 agaattctgc atattcgctc ctaaggaggg ctctgagggg atgcaacaaa atgatcctta
1501 tgatgtccaa caaggaaata gaggacgaag gcctgtgtgt tgccaggcag gcacctgggc
1561 tttctggaat ccaaacaca gtcttagggg cttggtagtt tggaaagttc ttaggcacca
1621 tagaagaaca gcagatggcg gtgatcagca gagagattga actttgagga ggaagcagaa
1681 tctttgcaag aaagtcagac ctgttctctg taactgggtt caaaaagaaa aaaaaaaaaa
1741 aa
```

## (2) INFORMATION FOR SEQ ID NO:2713:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2713

```
1 atcctggctg atatggtgaa acccatctc tactaaaaat aaaaaaatta gctgggcgtg
61 gtggtggcgg catgtaatcc cagctactca ggaggctgag gcaggagaat tacttgaacc
121 tgggaggcag aggttgcatg gaaccgagat cgcgccattg cactccagtc tggcgacaga
181 gcgagactcc gtctctaaat aaataaataa ataaatttag ccttctactc aagaacttat
241 ctggctttgt cttaatgtaa aaataatttc tttttgctaa attattgaga gaaatttact
301 atttattagt gtttatcagt tttctttaa ctcaccactt tttgatgaat atgaaaatct
361 aaaaacttgg cggggcgagc tggctcacac ctgtaatctc agcactttgg gaggccaagg
421 tgggcgagtc atctgaggtc aggagttcaa gatcagcctg accaacatga tgaaaccctc
481 tctctactaa aaatacaaaa attagctggg cgtggtgggt ggtgcctgta attgtagcta
541 cttgggagggc tgaggcatga gaatcacttg aaccagaaa gcagaggttg cagtgaagctg
601 agatggtgcc actgcactcc agcctgggtg acagagttag actctgtcct aaaaaaaaaa
661 aaaaaaaaaa tggctgggcg tgggtgcctc tgcctgtaat ccagcactt tgggagcca
721 gcgtgggtgg atcacctgag gtcaggagtt caagtccagc ctgaccaaca tgggtgaacc
781 ccgtctctac taaaaaagta caaaaaaat agccgggtgt ggtggcacac tcctgtaatc
841 ccagctactc aggaggctga ggcaggagaa tcacttgaat ttgggagctg gagattgtag
901 tcagccaaga tgggtgccatt gcactcagc ctgggtgaca gagtgaactg ccatctcaaa
961 aaaaaaaaaa aaatctttaa aactccttcc agaagattta atacttactt tcaccaacc
1021 acccgacttg agtatcacca ataacagagg atacagtccg ttttcagtag agccttagta
1081 gcaaagggtt ttcattttta ttttccagat acaggatctt gccctgtcac ccaagctgga
1141 gtgcagtgat gtgatcatag ctgactgcag cctcctgagt agctaggact ataggtgtat
1201 tataggacaa ttttataaaa atttcattgt aaagacagga ttccactgtg ttgcccaggc
1261 tgcaagtctt ggcctcaagt gatcattcca cttttaactc ttgcccctca gcagtcctcc
1321 caactcagac tcccaaatg ctgggattat ggggtgtgag caccatttcc agcctactag
1381 caagggtctt gttacatatt acttggcatg atttatgtaa tttaaaaaaa ttggttgttt
1441 ttcaaataga aaagtaaaat aacgaatatg cttttccaat aacataatcc cttctcact
1501 tgagaatttt cctctaaaaa gatatgctag atttatttca tgccttatgt gcctctggtg
1561 tgtcccctta taacctctc catatcattt agggatggtc tcagctgcaa gtaagaactg
1621 ccacaacagg tgatgtaagc ccaaaaaaaaa aaaaaaaaaa aaagcaaac caagcaaac
1681 aaagccatt taattatttc ccataataat aagcttggga gaaagaagat tccagagttg
1741 gctcagcagc ttagtgacag caaggcccta ggctggcatt ttcttggcct tcccgatggt
```

1801 cccaagatga ctctcatggc ctcaaacatc acttcctcac atcctgtcag ggagaaagag  
1861 gcaagtgagc aacaacaatt tgtggtgttt ggatcatttg tcagagagga agaactgttc  
1921 taaaaactcc gcctctgctg tttagacatc tcacccattt ccttgccat ggtggtatct  
1981 catggtcact cctctatctg ccactgtaaa gaggaactgg attgctatat tctgcttaga  
2041 cacatgagga tgcagccca cttcccagaa catgtgcgga attagatttc tacaaacaca  
2101 tttgtcttgc ttctgcccac ctctctcact agaatgcaca ttccataggg gcaaacattt  
2161 ttgtctatct ttttcacagc tatattctca acacctagaa gagtgacaga aattcaataa  
2221 atagttgtta agtgagcaaa tgaatgcacg aataaggaaa aggtgacatg gctattgagt  
2281 aggttaaccag cagtgttgat caccccaac agcatacaac tccagtctga tgaacatcat  
2341 gctactaagt ggccactcat caccgaagt tctgacctta ctttttctct cttttctccc  
2401 agggagttag ccataactgg cggctgctct tgcgccaatg  
1 ccaatgagcc tcccgaattc ctctgctctc ttagaagaca agatgtgtga gggcaacaag  
61 accactatgg ccagccccc gctgatgccc ctggtggtgg tctgagcac tatctgcttg  
121 gtcacagtag ggctcaacct gctggtgctg tatgccgtac ggagttagcg gaagctccac  
181 actgtgggga acctgtacat cgtcagcctc tcggtggcgg acttgatcgt ggtgcccgc  
241 gtcacgcta tgaacatcct ctacctgctc atgtccaagt ggtcactggg ccgtcctctc  
301 tgcctctttt ggctttccat ggactatgtg gccagcacag cgtccatttt cagtgtcttc  
361 atcctgtgca ttgatcgcta ccgctctgct cagcagcccc tcaggtacct taagtatcgt  
421 accaagacc gagcctcggc caccattctg ggggctgggt ttctctcttt tctgtgggtt  
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601 tacctgccc ccttgctcat gctctggttc tatgccaaga tctacaaggc cgtacgacaa  
661 cactgccagc accgggagct catcaatagg tccctccctt ccttctcaga aattaagctg  
721 aggccagaga accccaagg ggatgccaag aaaccaggga aggagtctcc ctgggaggtt  
781 ctgaaaagga agccaaaaga tgctggtggt ggatctgtct tgaagtcacc atcccaaac  
841 ccaagaggga tgaattcccc agttgtcttc agccaagagg atgatagaga agtagacaaa  
901 ctctactgct ttccacttga tattgtgcac atgcaggctg cggcagaggg gagttagagg  
961 gactatgtag ccgtcaaccg gagccatggc cagctcaaga cagatgagca gggcctgaac  
1021 acacatgggg ccagcgagat atcagaggat cagatgttag gtgatagcca atccttctct  
1081 cgaacggact cagataccac cacagagaca gcaccaggca aaggcaaatt gaggagtggg  
1141 tctaacacag gcctggatta catcaagttt acttggaaga ggctccgctc gcattcaaga  
1201 cagtatgtat ctgggttgca catgaaccgc gaaaggaagg ccgccaacaa gttgggtttt  
1261 atcatggcag ccttcacctc ctgctggatc ccttatttca tcttcttcat ggtcattgcc  
1321 ttctgcaaga actgttgcaa tgaacatttg cacatgttca ccatctggct gggctacatc  
1381 aactccacac tgaacccct catctacccc ttgtgcaatg agaacttcaa gaagacattc  
1441 aagagaattc tgcatattcg ctctaaggg aggtctctgag gggatgcaac aaaatgatcc  
1501 ttatgatgtc caacaaggaa atagaggacg aaggcctgtg tgttgccagg caggcacctg  
1561 ggtcttctg aatccaaacc acagtcttag gggcttggtg gtttggaag ttcttaggca  
1621 ccataagaaga acagcagatg gcggtgatca gcag  
1 atgagcctcc ccaattcctc ctgctcttta gaagacaaga tgtgtgaggg caacaagacc  
61 actatggcca gcccagct gatgccctg gtggtgtgct tgagcactat ctgcttggtc  
121 acagtagggc tcaacctgct ggtgctgtat gccgtacgga gtgagcgaa gctccacact  
181 gtggggaacc tgtacatcgt cagcctctcg gtggcgact tgatcgtggg tgccgtcgtc  
241 atgcctatga acatcctcta cctgctcatg tccaagtggg cactgggccc tctctctg  
301 ctcttttggc ttccatgga ctatgtggcc agcacagcgt ccattttcag tgtcttcac  
361 ctgtgcattg atcgctaccg ctctgtccag cagccctca ggtaccttaa gtatcgatcc  
421 aagaccgag cctcgccac cattctgggg gcctggttct tctcttttct gtgggttatt  
481 cccattctag gctggaatca ctctatgag cagacctcgg tgcgcccaga ggacaagtgt  
541 gagacagact tctatgatgt cacctggttc aaggctcatg ctgccatcat caacttctac  
601 ctgcccacct tgctcatgct ctggttctat gccaagatct acaaggccgt acgacaacac  
661 tgccagcacc gggagctcat caataggctc ctcccttct tctcagaaat taagctgagg  
721 ccagagaacc ccaaggggga tgccaagaaa ccagggaagg agtctccctg ggaggttctg  
781 aaaaggaagc caaagatgc tgggtgtgga tctgtcttga agtcaccatc ccaaaccccc  
841 aaggagatga aatccccagt tgtcttcagc caagaggatg atagagaagt agacaaactc  
901 tactgtcttc cacttgatat tgtgcacatg caggctgcgg cagaggggag tagcaggac  
961 tatgtagccg tcaaccggag ccatggccag ctcaagacag atgagcagg cctgaacaca  
1021 catggggcca gcgagatc agaggatcag atgttaggtg atagccaatc cttctctcga  
1081 acggactcag ataccaccac agagacagca ccaggcaagg gcaaatgag gagtgggtct  
1141 aacacaggcc tggattacat caagtttact tggagaggc tccgctcgca ttcaagacag  
1201 tatgtatctg ggttgacat gaaccgcaa aggaaggccg ccaaacagtt ggtttttatc  
1261 atggcagcct tcatcctctg ctggatccct tatttcatct tctcatggt cattgccttc  
1321 tgcaagaact gttgcaatga acatttgac atgttcacca tctggctggg ctacatcaac  
1381 tccacactga acccctcat ctacccttg tgcaatgaga acttcaagaa gacattcaag  
1441 agaattctgc atattcgctc ctaaggagg ctctgaggg atgcaacaaa atgactctta  
1501 tgatgtccaa caaggaaata gagagcaag gcctgtgtgt tgccaggcag gcacctgggc  
1561 tttctggaat ccaaacaca gtcttaggg cttggtagtt tggaaagttc ttaggcacca  
1621 tagaagaaca gcagatggcg gtgatcagca gagagattga actttgagga ggaagcagaa  
1681 tctttgcaag aaagtcagac ctgtttcttg taactgggtt caaaaagaaa aaaaaaaaaa



1741 aa

## (2) INFORMATION FOR SEQ ID NO:2714:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2714

```
1  cacgcgtccg cgagaaggag gactcgcaag cctcggcggc ccggaaccgg cctcggactg
61  tcgacggaac ctgaggccgc ttgccctccc gccccatgga ggggcccccg gggctgcggc
121 cgggcgcggg cgggccctgg gagatgcggg agcggctggg caccggcggc ttcgggaacg
181 tctgtctgta ccagcatcgg gaacttgatc tcaaaatagc aattaagctc tgtcgccatg
241 agctaagtac caaaaacaga gaacgatggt gccatgaaat ccagattatg aagaagttga
301 accatgccaa tgttgtaaag gcctgtgatg ttcctgaaga attgaatatt ttgattcatg
361 atgtgcctct tctagcaatg gaatactgtt ctggaggaga tctccgaaag ctgtcaaca
421 aaccagaaaa ttgttggtga cttaaagaaa gccagatact ttctttacta agtgatatag
481 ggtctgggat tcgatatatt catgaaaaca aaattataca tcgagatcta aaacctgaaa
541 acatagtctt tcaggatggt ggtggaaaga taatacataa aataattgat cgtggatattg
601 ccaaagatgt tgatcaagga agtctgtgta catcttttgt gggaacactg cagtactctg
661 cccagagctt ctttgagaat aagccttaca cagccactgt tgattattgg agctttggga
721 ccatggtatt tgaatgtatt gctggatata ggcctttttt gcatcatctg cagccattta
781 cctggcatga gaagattaag aagaaggatc caaagtgtat atttgcatgt gaagagatgt
841 caggagaaat tcggttttagt agccattttac ctcaacccaa tagcctttgt agtttaatatg
901 tagaacccat ggaaaactgg ctacagtgtg tgttgaattg ggaccctcag cagagaggag
961 gacctgttga ccttactttg aagcagccaa gatgttttgt attaattgat cacattttga
1021 atttgaagat agtacacatc ctaaattatg cttctgcaa gataatttct tttctgttac
1081 cacctgatga aagtcttcat tcactacagt ctcgtattga gcgtgaaact ggaataaata
1141 ctggtttctc agaacttctt tcagagacag gaattttctt ggatcctcgg aaaccagcct
1201 ctcaatgtgt tctagatgga gttagaggct gtgatagcta tatggtttat ttgtttgata
1261 aaagtaaaac tgtatatgaa gggccatttg cttccagaag tttatctgat tgtgtaaatt
1321 atattgtaca ggacagcaaa atacagcttc caattataca gctgcgtaaa gtgtgggctg
1381 aagcagtgca ctatgtgtct ggactaaaaa aagactatag caggctcttt cagggacaaa
1441 gggcagcaat gttaaagtct cttagatata atgctaactt aacaaaaatg aagaacactt
1501 tggatctcagc atcacacaac ctgaaagcta aattggagtt ttttcacaaa agcattcagc
1561 ttgacttgga gagatacagc gagcagatga cgtatgggat atcttcagaa aaaaatgctaa
1621 aagcatggaa agaaatggaa gaaaaggcca tccactatgc tgaggttggg gtcattggat
1681 acctggagga tcagattatg tctttgcatg ctgaaatcat ggagctacag aagagccctt
1741 atggaagacg tcagggagac ttgatggaat ccttggaaca gcgtgccatt gatctatata
1801 agcagttaaa acacagacct tcagatcact cctacagtga cagcacagag atggtgaaaa
1861 tcattgtgca cactgtgcag agtcaggacc gtgtgctcaa ggagctggtt ggtcatttga
1921 gcaagtgtgt gggctgtaag cagaagatta ttgatctact ccctaagggt gaagtggccc
1981 tcagtaatat caaagaagct gacaatactg tcattgttcat gcagggaaaa aggcagaaag
2041 aaatatggca tctccttaaa attgcctgta cacagagttc tgcccgggcc cttgtaggat
2101 ccagtctaga aggtgcagta acccctcaga catcagcatg gctgcccccg acttcagcag
2161 aacatgatca ttctctgtca tgtgtggtaa ctccccaaga tggggagact tcagcacaaa
2221 tgatagaaga aaatttgaa tcgcttggcc atttaagcac tattattcat gaggcaaatg
2281 aggaacaggg caatagtatg atgaactctg attggagttg gttaacagaa tgagttgtca
2341 cttgttctact gtccccaac ctatgggaat tgttgctata catgttgtaa atgtgtttt
2401 ccccatgaa accattcttc agacatcagt caatggaaga aatggctatg aacagaaact
2461 acatttctac tatgatcaga agaacatgat tttacaagta taacagtttt gagtaattca
2521 agcctctaaa cagacaggaa tttagaaaaa gtcaatgtac ttgtttgaat atttgtttta
2581 ataccacagc tatttagaag catcatcagc acacatttgc cttcagctctt ggtaaaacat
2641 tacttattta actgattaaa aataccttct atgtattagt gtcaactttt aacttttggg
2701 cgtaaagaaa agtgtagtgt tgtatacaga gaagaaaacc tcaagtaata ggcattttaa
2761 gtaaaagtct acctgtgttt ttttctaaaa aggctgctca caagttctat ttcttgaaga
2821 ataaattcta cctccttggt ttgactgaa caggttctct tcctggcctc ataaggagtt
2881 ggtgtaatca ttttaaatc cactgaaaat ttaacagtat ccccttctca tcgaagggat
2941 tgtgtatctg tgcttctaata attagttggc tttcataaat catgttggtg tgtgtatatg
3001 tatttaagat gtacatttaa taatatcaaa gagaagatgc ctgttaattt ataattgatt
3061 tgaattttac atgttttttc atttgtaaaa atgagtcatt tgttttaaca atctttcatg
3121 tcttgtcata caaatttata aaggctctga ctcttttctc tgaattgta attccaaaat
3181 ccaaaaagct ctgaaaacaa ggtttccata agcttgggtg caaaattcat ttgcttgcaa
3241 tctaattcga actgaccttg aatcttttta tcccatttag tgtgaatatt cctttatttt
3301 gctgcttgat gatgagaggg agggctgctg ccacagactg tggtaggggc tggttaatgt
3361 agtatggtat atgcacaaaa ctacttttct aaaatctaaa atttcataat tctgaaacaa
3421 cttgccccaa gggtttcaga gaaaggactg tggacctcta tcactgtcta agtaatttag
3481 aagatattat ttgtcttaaa aaatgtgaaa tgcttttata ttctaattag ttttactttt
3541 gtgtattaaa tggtttttaa attaaaaaaa aaaaaaaa
```

## (2) INFORMATION FOR SEQ ID NO:2715:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2715

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1 gcccgcgtta agattcccgc attttaatgt tttcaggggg gtgtcatagc cccgggtttg
61 gccgccccag cccgccttc cccgccccgg ggagcccgcc cccttccccg cgtccctgcc
121 gacagagtta gcacgacatc agtatgagct ggtcaccttc cctgacaacg cagacatgtg
181 gggcctggga aatgaaagag cgcttgaggc cagggggatt tggaaatgtc atccgatggc
241 acaatcagga aacaggtgag cagattgcca tcaagcagtg ccggcaggag ctcagccccc
301 ggaaccgaga gcggtgggtc ctggagatcc agatcatgag aaggctgacc caccccaatg
361 tgggtggctgc ccgagatgtc cctgagggga tgcagaactt ggcgcccatt gacctgcccc
421 tgctggccat ggagtactgc caaggaggag atctccggaa gtacctgaac cagtttgaga
481 actgctgtgg tctgcgggaa ggtgccatcc tcacctgtct gactgacatt gcctctgcgc
541 ttagatacct tcatgaaaac agaatacacc atcgggatct aaagccagaa aacatcgtcc
601 tgcagcaagg agaacagagg ttaatacaca aaattattga cctaggatat gccaaaggagc
661 tggatcaggg cagtctttgc acatcattcg tggggaccct gcagtacctg gccccagagc
721 tactggagca gcagaagtac acagtgaccg tcgactactg gagcttcggc accctggcct
781 ttgagtgcac caggggcttc cgcccttcc tcccaactg gcagcccggt cagtggcatt
841 caaaagtgcg gcagaagagt gagggtggaca ttgttgttag cgaagacttg aatggaacgg
901 tgaagtttc aagctcttta ccctacccca ataacttta cagtgtcctg gctgagcgac
961 tggagaagtg gctgcaactg atgctgatgt ggcacccccg acagaggggc acggatccca
1021 cgtatgggcc caatggctgc ttcaaggccc tggatgacat cttaaactta aagctggttc
1081 atatcttgaa catggtcacg ggcaccatcc acacctacc tgtgacagag gatgagagtc
1141 tgcagagctt gaaggccaga atccaaagg acacgggcat cccagaggag gaccaggagc
1201 tgctgcagga agcgggcctg gcgttgatcc ccgataagcc tgccactcag tgtatttcag
1261 acggcaagtt aatgagggc cacacattgg acatggatct tgtttttctc ttgacaaca
1321 gtaaaatcac ctatgagact cagatctccc cacggcccca acctgaaagt gtcagctgta
1381 tccttcaaga gcccaaggag aatctgcctc tcttcagct gaggaagggt tggggccagg
1441 tctggcacag catccagacc ctgaaggaa attgcaaccg gctgcagcag ggacagcgag
1501 ccgccatgat gaatctctc cgaaacaaca gctgcctctc caaaatgaag aattccatgg
1561 cttccatgtc tcagcagctc aaggccaagt tggatttctt caaaaccagc atccagattg
1621 acctggagaa gtacagcgag caaacggagt ttgggatcac atcagataaa ctgctgtctg
1681 cctggaggga aatggagcag gctgtggagc tctgtggcgg ggagaacgaa gtgaaactcc
1741 tggtagaacg gatgatggct ctgcagaccg acattgtgga cttacagagg agccccatgg
1801 gccggaagca ggggggaacg ctggacgacc tagaggagca agcaaggag ctgtacagga
1861 gactaaggga aaaacctcga gaccagcgaa ctgagggtag cagtcaggaa atggtacggc
1921 tgctgcttca ggcaattcag agcttcgaga agaaagtgcg agtgatctat acgcagctca
1981 gtaaaactgt ggtttgcaag cagaaggcgc tggaaactgt gcccaagggt gaagagggtg
2041 tgagcttaat gaatgaggat gagaagactg ttgtccggct gcaggagaag cggcagaagg
2101 agctctggaa tctcctgaag attgcttgta gcaaggctcg tggctctgtc agtggaagcc
2161 cggatagcat gaatgcctct cgacttagcc agcctgggca gctgatgtct cagccctcca
2221 cggcctccaa cagcttacct gagccagcca agaagagtga agaactggtg gctgaagcac
2281 ataacctctg caccctgcta gaaaatgcca tacaggacac tgtgagggaa caagaccaga
2341 gtttcacggc cctagactgg agctggttac agacggaaga agaagagcac agctgcctgg
2401 agcaggcctc atgatgtggg gggaactcgac cccctgacat ggggcagccc atagcaggcc
2461 ttgtgcagtg gggggactcg acccctgac atggggctgc ctggagcagg ccgcgtgacg
2521 tggggctgcc tggccgcggc tctcacatgg tggttcctgc tgactgatg gcccaggggt
2581 ctctggtatc cagatggagc tctcgcttcc tcagcagctg tgactttcac ccaggacca
2641 ggacgcagcc ctccgtgggc actgccggcg ccttgtctgc aactggagg tcctccatta
2701 cagaggccca gcgcacatcg ctggccccc aaacgttcag gggtagagcc atggcagctc
2761 cttcctctgc cgtgagaaaa gtgcttgagg tacggtttgc cacacacgtg actggacagt
2821 gtccaattca aatctttcag ggcaagatcc gagcagcgtt tggtagacagc ctgtcctctc
2881 ctgctctcca aaggccctgc tcctgtcct ctctcacttt acagcttgtg tttcttctg
2941 attcagcttc tcctaaacag acagtttaat tatagttgcg gcctggcccc atcctcactt
3001 cctcttttta tttcactgct gctaaaattg tgtttttacc tacaaaaaaa aaaaaaaa
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## (2) INFORMATION FOR SEQ ID NO:2716:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2716

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1 ggcacgagca tggcccttgt gatccagggt gggaaactaa ggcccagaga agtgaggacc
61 ccgcagacta tcaatcccag tctcttcccc tcaactcctg tgaagctctc cagcatcatc
```

121 gaggtcccat cagcccttgc cctgttgat gaataggcac ctctggaaga gccaaactgtg  
181 tgagatggtg cagcccagtg gtggcccgcc agcagatcag gacgtactgg gcgaagagtc  
241 tctctggtg aagccagcca tgctgcacct gccttcagaa cagggcgctc ctgagaccct  
301 ccagcgctgc ctggaggaga atcaagagct ccgagatgcc atccggcaga gcaaccagat  
361 tctgctggag cgctgcgagg agcttctgca tttccaagcc agccagaggg aggagaagga  
421 gttcctcatg tgcaagttcc aggaggccag gaaactgggtg gagagactcg gcctggagaa  
481 gctcgatctg aagaggcaga aggagcagcg tctgctggag gtggagcacc tgaagagatg  
541 ccagcagcag atggctgagg acaaggcctc tgtgaaagcc caggtgacgt ccttgctcgg  
601 ggagctgcag gagagccaga gtcgcttga ggctgccact aaggaatgcc aggtctctgga  
661 gggctgggcc cgggcccga gcgagcagcg gcggcagctg gagagtgaag gcgagcgct  
721 gcagcagcag cacagcgtgc aggtggacca gctgcgcatg cagggccaga gcgtggaggc  
781 cgcgctccgc atggagcgcc aggcgcctc ggaggagaag aggaagctgg cccagtgtca  
841 ggtggcctat caccagctct tccaagaata cgacaaccac atcaagagca gcgtggtggg  
901 cagtgaagcg aagcgaggaa tgcagctgga agatctcaaa cagcagctcc agcaggccga  
961 ggagccctg gtggccaaac aggagtgat cgataagctg aaggaggagg ccgagcagca  
1021 caagattgtg atggagaccg ttccggtgct gaaggccag gcggatatct acaaggcgga  
1081 cttccagctg gagaggcagg cccgggagaa gctggccgag aagaaggagc tctgcagga  
1141 gcagctggag cagctgcaga gggagtacag caaactgaag gccagctgtc aggagtcggc  
1201 caggatcgag gacatgagga agcggcatgt cgaggtctcc cagggccctc tgcccccg  
1261 ccctgcctac ctctcctctc ccctggccct gccagccag aggaggagcc cccccagga  
1321 gccacctgac ttctgctgtc ccaagtcca gtatcaggcc cctgatattg acacctgca  
1381 gatacatgtc atggagtga ttgagtggc cggccagtg caaggccact gcctgccga  
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1561 accttacgct tcagctgttg atccgctggt cccctctttt ggggtagatg cggccccgat  
1621 caggcctgac tcgctgctct tttgttccc ttctgtctgc tcgaaccact tgctctgggc  
1681 taatccctcc ctctcctcc acccggcact ggggaagtca agaattgggc ctggggctct  
1741 cagggagaac tgcttcccct ggcagagtgt ggtggcagct ctctctcca cggacaccg  
1801 accgcccgc cgtgtgccc tgggagtgt gccctcttac catgcacac ggtgctctcc  
1861 ttttggctg catgctatc cattttgca ccagaccgat gtgtattta ccagctacta  
1921 ttgatggaca tttgggtgt ttcccatctt tttgttacca taaataatgg catagtaaaa  
1981 aaaaaaaaaa aaaa

## (2) INFORMATION FOR SEQ ID NO:2717:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2717

1 cacgcgtccg cgagaaggag gactcgcaag cctcggcgcc ccggaaccgg cctcggactg  
61 tcgacggaac ctgaggccgc ttgccctccc gccccatgga gcggcccccg gggctgcggc  
121 cgggcccggg cgggccctgg gagatgcggg agcggctggg caccggcgcc ttcgggaacg  
181 tctgtctgta ccagcatcgg gaacttgatc tcaaaatagc aattaagtct tgcgcctag  
241 agctaagtac caaaaacaga gaacgatggt gccatgaaat ccagattatg aagaagttga  
301 accatgccaa tgttgtaaag gcctgtgatg ttcctgaaga attgaattt ttgattcatg  
361 atgtgcctct tctagcaatg gaatactgtt ctggaggaga tctccgaaag ctgctcaaca  
421 aaccagaaaa ttgttgtgga cttaaagaaa gccagatact ttctttacta agtgatatag  
481 ggtctgggat tcgatatatt catgaaaaca aaattataca tcgagatcta aaacctgaaa  
541 acatagtctc tcaggatggt ggtggaaaaga taatacataa aataattgat ctgggatatg  
601 ccaaagatgt tgatcaagga agtctgtgta catcttttgt gggaacactg cagtatctgg  
661 cccagagct ctttgagaat aagccttaca cagccactgt tgattattgg agctttggga  
721 ccatggtatt tgaatgtatt gctggatata ggcctttttt gcatcatctg cagccattta  
781 cctggcatga gaagattaaag aagaaggatc caaagtgtat atttgcatgt gaagagatgt  
841 caggagaagt tcggtttagt agccatttac ctcaaccaa tagcctttgt agtttaatag  
901 tagaaccat. ggaaaactgg ctacagttga tgttgaattg ggaccctcag cagagaggag  
961 gacctgttga cttactttg aagcagccaa gatgtttgt attaatggat cacattttga  
1021 atttgaagat agtacacatc cttaaataatga cttctgcaaa gataatttct tttctgttac  
1081 cacctgatga aagtcttcat tcaactacag ctctgtattga gcgtgaaact ggaataaata  
1141 ctggttctca agaacttctt tcagagacag gaatttctct ggatcctcgg aaaccagcct  
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1381 aagcagtga ctatgtgtct ggactaaaag aagactatag caggctcttt cagggacaaa  
1441 gggcagcaat gttaagtctt cttagatata atgctaactt aacaaaaatg agaacactt  
1501 tgatctcagc atcacaacaa ctgaaagcta aattggagtt ttttcacaaa agcattcagc  
1561 ttgacttga gagatacagc gagcagatga cgtatgggat atcttcagaa aaaatgctaa  
1621 aagcatggaa agaaatggaa gaaaaggcca tccactatgc tgaggttggt gtcattggat

1681 acctggagga tcagattatg tctttgcatg ctgaaatcat ggagctacag aagagccctt  
1741 atggaagacg tcagggagac ttgatggaat ctctggaaca gcgtgccatt gatctatata  
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1981 tcagtaatat caaagaagct gacaatactg tcatgttcat gcagggaaaa aggcagaaag  
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2101 ccagtctaga aggtgcagta acccctcaga catcagcatg gctgcccccg acttcagcag  
2161 aacatgatca ttctctgtca tgtgtggtaa ctctcaaga tggggagact tcagcacaaa  
2221 tgatagaaga aaatttgaac tgccttggcc atttaagcac tattattcat gaggcaaatg  
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2341 cttgttctact gtcccaaac ctatggaagt tgttgctata catgttgaa atgtgtttt  
2401 ccccatgaa accattcttc agacatcagt caatggaaga aatggctatg aacagaaact  
2461 acatttctac tatgatcaga agaacatgat tttaacaagta taacagtttt gagtaattca  
2521 agcctctaaa cagacaggaa tttagaaaaa gtcaatgtac ttgtttgaat atttgtttta  
2581 ataccacagc tatttagaag catcatcacg acacatttgc cttcagtcctt ggtaaaacat  
2641 tacttattta actgattaaa aataccttct atgtattagt gtcaactttt aacttttggg  
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2761 gtaaaagtct acctgtgttt ttttctaaaa aggctgctca caagttctat ttcttgaaga  
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3121 tcttgtcata caaatttata aaggctctga ctctttatc tgtaatttga attccaaaat  
3181 ccaaaaagct ctgaaaacaa ggtttccata agcttggtga caaaattcat ttgcttgcaa  
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3421 cttgccccaa gggtttcaga gaaaggactg tggacctcta tcatctgcta agtaatttag  
3481 aagatattat ttgtcttaaa aaatgtgaaa tgcttttata ttctaattag ttttcacttt  
3541 gtgtattaaa tggtttttaa attaaaaaaa aaaaaaaa  
1 gccgcggtta agattccccg attttaattgt tttcaggggg gtgtcatagc cccgggtttg  
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121 gacagagtta gcacgacatc agtatgagct ggtcaccttc cctgacaacg cagacatgtg  
181 gggcctggga aatgaaagag cgccttggga cagggggatt tggaaatgac atccgatggc  
241 acaatcagga aacagggtgag cagattgcca tcaagcagtg ccggcaggag ctcagcccc  
301 ggaaccgaga gcggtggtgc ctggagatcc agatcatgag aaggctgacc caccacaatg  
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421 tgctggccat ggagtactgc caaggaggag atctccggaa gtacctgaac ccttctgaga  
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541 ttagatacct tcatgaaaac agaatacatc atcgggatct aaagccagaa aacatcgtcc  
601 tgcagcaagg agaacagagg ttaatacaca aaattattga cctaggatat gccaggagc  
661 tggatcaggg cagtctttgc acatcattcg tggggacctt gcagtacctg gcccagagc  
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841 caaaagtgcg gcagaagagt gaggtggaca ttgttgttag cgaagacttg aatggaacgg  
901 tgaaagtttc aagctcttta cctaccacca ataactttaa cagtgtcctg gctgagcgac  
961 tggagaagtg gctgcaactg atgctgatgt ggcacccccg acagaggggc acggatccca  
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1081 atatcttgaa catggtcacg ggcaccatcc acacctacco tgtgacagag gatgagagtc  
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1441 tctggcacag catccagacc ctgaaggaa attgcaaccg gctgcagcag ggacagcgag  
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1561 cttccatgtc tcagcagctc aaggccaagt tggatttctt caaaaccagc atccagattg  
1621 acctggagaa gtacagcgag caaacaggat ttgggatcac atcagataaa ctgctgctgg  
1681 cctggaggga aatggagcag gctgtggagc tctgtggggc ggagaacgaa gtgaaactcc  
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1861 gactaaggga aaaacctcga gaccagcgaa ctgagggtga cagtacggaa atggtacggc  
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1981 gtaaaactgt ggtttgcaag cagaaggcgc tggaaactgt gcccaagggt gaagaggtgg  
2041 tgagcttaat gaatgaggat gagaagactg ttgtccggct gcaggagaag cggcagaagg  
2101 agctctggaa tctcctgaag attgcttga gcaaggctcg tggctctgtc agtggagcc

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2161 cggatagcat gaatgcctct cgacttagcc agcctgggca gctgatgtct cagccctcca
2221 cggcctccaa cagcttacct gagccagcca agaagagtga agaactggtg gctgaagcac
2281 ataacctctg caccctgcta gaaaatgcc aacagagcac agctgcttgg
2341 gtttcacggc cctagactgg agctgggtac agacggaaga agaagagcac agctgcttgg
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2521 tggggctgcc tggccgggc tctcacatgg tggttcctgc tgactgtatg gccaggggt
2581 ctctgggtatc cagatggagc tctcgcttcc tcagcagctg tgactttcac ccaggacca
2641 ggacgcagcc ctccgtgggc actgcccggc ccttgtctgc aactggagg tcctccatta
2701 cagaggccca ggcacatcg ctggccccc aaacgttcag ggtacagcc atggcagctc
2761 ctctctctgc cgtgagaaaa gtgcttggag tacggttgc cacacacgtg actggacagt
2821 gtccaattca aatctttcag ggcagagtcc gagcagcgtt tggtagacgc ctgtcctctc
2881 ctgctctcca aaggccctgc tccctgtcct ctctcacttt acagcttgtg tttcttctgg
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3001 cctcttttta tttcactgct gctaaaattg tgtttttacc taaaaaaaa aaaaaaaa
1 ggcacgagca tggcccttgt gatccagggt gggaaactaa ggcccagaga agtgaggacc
61 ccgcagacta tcaatcccag tctcttccc tcactccctg tgaagctctc cagcatcatc
121 gaggtcccat cagcccttgc cctgttggat gaataggcac ctctggaaga gccaaactgtg
181 tgagatggtg cagcccagtg gtggccggc agcagatcag gacgtactgg gcgaagagtc
241 tcctctgggg aagccagcca tgctgcacct gccttcagaa cagggcgctc ctgagacctt
301 ccagcgtgc ctggaggaga atcaagagct ccgagatgcc atccggcaga gcaaccagat
361 tctcggggag cgctgcgagg agcttctgca tttccaagcc agccagaggg agggaagga
421 gttcctcatg tgcaagtccc aggaggccag gaaactggtg gagagactcg gcctggagaa
481 gctcgatctg aagaggcaga aggagcaggc tctgcgggag gtggagcacc tgaagagatg
541 ccagcagcag atggctgagg acaaggcctc tgtgaaagcc caggtgacgt ccttgctcgg
601 ggagctgcag gagagccaga gtcgttggg ggctgccact aaggaaatgcc aggtcttggg
661 gggtcggggc cgggcggcca ggcagcaggc gcggcagctg gagagtgagc gcgaggcgtc
721 gcagcagcag cacagcgtgc aggtggacca gctgcgcagc cagggccaga gcgtggaggc
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1981 aaaaaaaaaa aaaa

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## (2) INFORMATION FOR SEQ ID NO:2718:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2718

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121 ctgaaagtac actgctggcg gatcctacgg aagttatgga aaaggcaag cgagagcca
181 cgccgtagtg tgtgccgccc ccttgggat ggaatgaaat gcagtcgagc cgtgggtaa
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301 ggtcctctgg agtgactatg ggcggtgaga gcttgtcctt gctccagttg cgtcatcat
361 gactacgccc gcctcccgca gacctgttc catgtttctt ttaggtatat ctttgactt
421 cctcccctga tccttgttct gttgcaagta gcatcatctg attgtgatat tgaaggtaaa
481 gatggcaaac aatatgagag tgttctaatt gtcagcatcg atcaattatt ggacagcatg
541 aaagaaattg gtagcaattg cctgaataat gaatttaact tttttaaag acatatctgt
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721 atactgttga actgcactgg ccagggttaaa ggaagaaaac cagctgcctt ggggtgaagcc  
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961 tcctccaaga atctatctgc ttatgcagtt tttcagagt gaaatgcttc tagaagttac  
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1381 tgttttagag ttaacaatga tatatggata atgccggtga gaataagaga gtcataaacc  
1441 ttaagtaagc aacagcataa caaggtccaa gatacctaaa agagatttca agagatttaa  
1501 ttaatcatga atgtgtaaca cagtgccttc aataaatggt atagcaaatg ttttgacatg  
1561 aaaaaaggac aatttcaaaa aaataaaat

## (2) INFORMATION FOR SEQ ID NO:2719:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2719

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121 tgagttaaag aaatcagacc aaagaacata tactgaaaga ttctctctat atacaaagtt  
181 caaaaatagg tggaccaatt catggtggtg ttagaaatca gaagagaggg tacctttgtg  
241 gggaggggac agtttaatgc ccagaagcgg taaataagga atcctctggg gagtggtaat  
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## (2) INFORMATION FOR SEQ ID NO:2720:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: \_ base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2720

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181 tgttcatatg cttgggcaa ccaagaaac aagtgggtga caaatggcac cttttggata  
241 gtggtattga ctttgaagt ttgggtcagg aagctgggga ggaagggtg gcaggctgtg

301 ggcaagtcctg ggccgaagac caggcagggc tatgtgctca ctgagcctcc gccctcttcc  
361 tttgaatctc tgatagactt ctgcctccta cttctccttt tctgcccttc tttgctttgg  
421 tggcttcctt gtggttcctc agtgggtgct gcaaccctg gttcacctcc ttcagggttc  
481 tggctccttc cagccatggc tctcagagtc cttctgttaa cagggtgcatg ggg

## (2) INFORMATION FOR SEQ ID NO:2721:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2721

1 gaattccgtg gttcctcagt ggtgcctgca acccctgggt cacctccttc caggttctgg  
61 ctccctccag ccatggctct cagagtcctt ctgttaacag ccttgacctt atgtcatggg  
121 ttaactttgg aactgaaaa cgcaatgacc ttccaagaga acgcaagggg cttcgggcag  
181 agcgtgggtc agcttcaggg atccagggtg gtggttgag cccccaggga gatagtggct  
241 gccaaccaaa ggggcagcct ctaccagtgc gactacagca caggctcatg cgagcccatc  
301 cgcttgagg tccccgtgga ggccgtgaac atgtccctgg gcctgtccct ggcagccacc  
361 accagccccc ctacgtgctt ggcctgtggt cccaccgtgc accagacttg cagtgagaac  
421 acgtatgtga aagggctctg cttcctgttt ggatccaacc tacggcagca gcccagaag  
481 ttcccagagg ccctccgagg gtgtcctcaa gaggatagt acattgcctt cttgattgat  
541 ggctctggtg gcatcatccc acatgacttt cggcgatga aggagtgtgt ctcaactgtg  
601 atggagcaat taaaaaagtc caaaaccttg ttctctttga tgcagtactc tgaagaattc  
661 cggattcact ttacctcaa agagttccag aacaacccta acccaagatc actggtgaag  
721 ccaataacgc agctgcttgg gcggacacac acggccacgg gcatccgcaa agtggtacga  
781 gagctgttta acatcaccaa cggagccgga aagaatgcct ttaagatcct agttgtcatc  
841 acggatggag aaaagtgttg cgatcccttg ggatatgagg atgtcatccc tgaggcagac  
901 agagagggag tcattcgcta cgtcatgggg gtgggagatg ccttcccgag tgagaaatcc  
961 cgccaagagc ttaataccat cgcatccaag ccgcctcgtg atcacgtgtt ccaggatgaat  
1021 aactttgagg ctctgaagac cattcagaac cagcttcggg agaagatctt tgcgatcgag  
1081 ggtactcaga caggaagttag cagctccttt gagcatgaga tgtctcagga aggttcagc  
1141 gctgccatca cctctaattg ccccttgctg agcactgtgg ggagctatga ctgggctggg  
1201 ggagtccttc tatatacatc aaaggagaaa agcaccttca tcaacatgac cagagtggat  
1261 tcagacatga atgatgctta cttgggttat gctgccgcca tcatcttacg gaaccgggtg  
1321 caaagcctgg ttctgggggc acctcgatat cagcacatcg gcctggtagc gatgttcagg  
1381 cagaacactg gcatgtggga gtccaacgct aatgtcaagg gcacccagat cggcgccctac  
1441 ttccggggcct ccctctgctc cgtggacgtg gacagcaacg gcagcaccga cctggtcctc  
1501 atcggggccc cccattacta cgagcagacc cgagggggcc aggtgtccgt gtgccccttg  
1561 cccagggggc agagggctcg gtggcagtgat gatgctgttc tctacgggga gcaggggcaa  
1621 ccctggggcc gctttggggc agccctaaca gtgctggggg acgtaaatgg ggacaagctg  
1681 acggacgtgg ccattggggc cccaggagag gaggacaacc ggggtgctgt ttacctgttt  
1741 cacggaacct caggatctgg catcagcccc tcccatagcc agcggtagc aggtccaag  
1801 ctctctccca ggctccagta ttttggtcag tcaactgagt ggggcccagga cctcacatg  
1861 gatggactgg tagacctgac ttaggagacc caggggcacg tgctgctgct caggtccag  
1921 ccagtactga gagtcaaggc aatcatggag ttcaatcca ggaagtggc aaggaatgta  
1981 tttgagtgtg atgatcaggt ggtgaaaggc aaggaagccg gagaggtcag agtctgcctc  
2041 catgtccaga agagcacacg ggatcggcta agagaaggac agatccagag tgtgtgact  
2101 tatgacctgg ctctggactc cggccgcccc cattcccgcg ccgtcttcaa tgagacaaag  
2161 aacagcacac gcagacagac acaggtcctt gggctgacct agacttgtga gacctgaaa  
2221 ctacagttgc cgaattgcat cgaggcccca gtgagcccca ttgtgctgcg cctggaactc  
2281 tctctggtgg gaacgccatt gtctgctttc gggaacctcc ggccagtgtt ggcggaggat  
2341 gctcagagac tcttcacagc cttgtttccc tttgagaaga attgtggcaa tgacaacatc  
2401 tgccaggatg acctcagcat cacttcagat tcatagagcc tggactgcct cgtggtgggt  
2461 gggccccggg agttcaacgt gacagtgaat gtgagaaatg atggtgagga ctctacagg  
2521 acacaggtca ccttctctt cccgcttgac ctgtcctacc ggaaggtgtc cacactccag  
2581 aaccagcgtc cacagcgatc ctggcgctg gcctgtgagt ctgcctcctc caccgaagtg  
2641 tctggggcct tgaagagcac cagctgcagc ataaaccacc ccatcttccc ggaactca  
2701 gaggtcacct ttaatatcac gtttgatgta gactctaagg cttcccttgg aaacaaactg  
2761 ctctcaagg ccaatgtgac cagtgagaac aacatgcccc gaaccaacaa aaccgaattc  
2821 caactggagc tgccggtgaa atatgctgtc tacatggtgg tcaccagcca tggggtctcc  
2881 actaaatata tcaactcac ggctcagag aataccagtc gggcatgca gcatcaatat  
2941 caggctagca acctggggca gaggagcctc cccatcagcc tgggtgtctt ggtgcccgtc  
3001 cggctgaacc agactgtcat atgggaccgc ccccagggtc ccttctccga gaacctctcg  
3061 agtacgtgcc acaccaagga gcgcttgccc tctcactccg actttctggc tgagcttcgg  
3121 aaggcccccgt tggtgactg ctccatcgct gtctgccaga gaatccagtg tgacatccc  
3181 ttctttggca tccaggaaga attcaatgct accctcaaag gcaacctctc gtttgactgg  
3241 tacatcaaga cctcgcataa ccacctctg atcgtgagca cagctgagat cttgtttaac  
3301 gattccgtgt tcacctgct gccgggacag gggcggtttg tgaggtccca gacggagacc  
3361 aaagtggagc cgttcgaggt ccccaacccc ctgccgctca tctgtggcag ctctgtcggg

3421 ggactgctgc tcttggccct catcacccgc gcgctgtaca agctcggctt cttcaagcgg  
3481 caatacaagg acatgatgag tgaagggggt ccccggggg ccgaacccca gtacgggctc  
3541 cttcccgaca gagctgcctc tcggtggcca gcaggactct gccagacca cagctagccc  
3601 ccaggctgct ggacacgtcg gacagcgaag tatccccgac aggacgggct tgggcttcca  
3661 tttgtgtgtg tgcaagtgtg tatgtgcgtg tgtgcgagt tgtgcaagt tctgtgtgca  
3721 agtgtgtgca cgtgtgcgtg tgcgtgcattg tgcactcgca cgcctatgtg tgagtgtgtg  
3781 caagtattgt agtgtgtcca gtgtgtgtgc gtgtgtccat gtgtgtgcag tgtgtgcattg  
3841 tgtgcgagt tgtgcattg tgtgtcagg ggctgtggct cactgtgtg actcagagt  
3901 tctctggcgt gtgggtaggt gacggcagcg tagcctctcc ggagaaagg aactgcctgg  
3961 gctcccttgt gcgtgggtaa gccgctgctg ggttttcctc cgggagagg gacggccaat  
4021 cctgtgggtg aagagagagg gaaacacagc agcatctctc cactgaaaga agtgggactt  
4081 cccgtgcctc gcgagcctgc ggctgtctg agcctgcgca gcttgatgg atactccatg  
4141 agaaaaagcc tgggtggaac caggagcctc ctccacacca gcgctgatgc ccaataaaga  
4201 tgcccactga ggaatcatga agcttccttt ctggattcat ttattatttc aatgtgactt  
4261 taattttttg gatggataag cctgtctatg gtacaaaaat cacaaggcat tcaagtgtac  
4321 agtgaaaagt ctccctttcc agatattcaa gtcacctctc taaaggtagt caagattgtg  
4381 ttttgagggt tctctcagac agattccagg cgatgtgcaa gtgtatgcac gtgtgcacac  
4441 accacacaca tacacacaca caagcttttt tacacaaatg gtagcatact ttatattggt  
4501 ctgtatcttg ctttttttca ccaatatttc tcagacatcg gttcatatta agacataaat  
4561 tactttttca ttcttttata ccgctgcata gtattccatt gtgtgagtgt accataatgt  
4621 atttaaccag tcttcttttg atatactatt ttcatctctt gttattgcat ctgctgagtt  
4681 aataaatcaa atatattgtc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa

## (2) INFORMATION FOR SEQ ID NO:2722:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2722

1 ggttcaagt attctgctgc ctcagcctcc caggcgggat tacaggtgcc tgccaccacg  
61 cctggctaatt tttttgtct ttttagtaaa gatgaggttt caccatgttg ggcaggctgg  
121 tttcaattgc tgacctcaag tgagccaccc cgctcagcc tccaaaatgc taggattaca  
181 ggcatgagcc accgcaccca gccaaagttg tacatatatt ttgactaca cttcttaact  
241 attcttagga taaattacta gaagtgaaaa ttcttgggtg aagagcttga ggcctttaca  
301 cacacacaca cacacacaca cacacacaca caaataggct ggatcgagt gctcacacct  
361 gtaatctcag cagtttgga ggctgaggaa ggaggatcac ttgagtcag gaggttgaga  
421 atagcctgaa caacatagca agatctgtgc tctacaaaa agtttaaaaa aaattagctg  
481 gccatggcag catgtgcctg tagtaccagc tactcggaag gctgaggtag gaggatcgct  
541 tgagcccagg aggtgattga agctgcagtg agctgtgatt acaccactgc actccagcct  
601 gggcaacaga gctagactct gtctctaaaa aaaggcacia aataatattt aaaaagcacc  
661 aggtatgcct gtacttgagt tgtctttgtt gatggctaca aatgagacag ccttggtga  
721 agggcggtt ccatctccat gggctggaag aggacatttt gcaaagtgtg ttttcaggaa  
781 gacacagagt ttacctcct acactgtttt gatctgtatt aatgtttgct tatttattta  
841 tttaattttt tttttgagac agagtctcac tctgtcacct gggctggagt gcagtgcat  
901 tattgaggct cattgcagtc tcagactcct gagctcaaac aatcctctg cctcagcctc  
961 tggagtagct agactacag gcatgtgcca ccatgcctgg ctaatttttt aaatgtattt  
1021 tttgttagag tcggggtctc cctatgttgc ccaggctgga gtgcagtggt gtgacctaag  
1081 ctactgcag cctggacctc gggctcaaga aattctcaca cctcagcctg tccagtagca  
1141 ggggctacag gcgcgcacca ccatccagc taattaaaaa ttttttttgg tagagacagg  
1201 gtctctctat gttgccagg ctggtttcaa actcccaggc tcaagcaatc ctctgcctt  
1261 gcctcccaaa tgacatcgga ttacaggcgt gagccactga gcctggcccg tattaatgtt  
1321 tagaacacga attccaggag gcaggctaag tctattcagc ttgttcatat gcttgggcca  
1381 acccaagaaa caagtgggtg acaaatggca ccttttgat agtggtattg actttgaaag  
1441 tttgggtcag gagctgggga ggaaggggtg gcaggctgtg ggcagtcctg ggcggaagac  
1501 caggcagggc tatgtgtca ctgagcctcc gccctcttcc tttgaatctc tgatagactt  
1561 ctgcctccta cttctcctt tctgccttc tttgcttttg tggcttctct gtggtctctc  
1621 agtgggtgct gcaaccctg ttcactctc caggttctg ctccttcag ccatgctctc  
1681 cagagtcctt ctgttaacag gtgcattggg gtggggtggg ggactctggg tggggaggag  
1741 ggtaactttt ggtctgtca taaatagagg gcc

## (2) INFORMATION FOR SEQ ID NO:2723:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2723

1 attttttgt agagacaggg tctctctatg ttgccaggc tggtttcaaa ctcccaggct



61 caagcaatcc tccctgcttg gcctcccaaa gtgctggcat tacaggcgtg agccactgcg  
121 cctggcccgt attaatgttt agaacacgaa ttccaggagg caggctaagt ctattcagct  
181 tgttcataatg cttgggcca cccaagaaac aagtgggtga caaatggcac cttttggata  
241 gtggtattga ctttgaaagt ttgggtcagg aagctgggga ggaaggggtg gcaggctgtg  
301 ggcagtcctg ggcggaagac caggcagggc tatgtgctca ctgagcctcc gccctcttcc  
361 tttgaatctc tgatagactt ctgcctccta cttctccttt tctgcccttc tttgctttgg  
421 tggcttcctt gtggttcctc agtgggtgct gcaaccctg gttcacctcc ttccaggttc  
481 tggctccttc cagccatggc tctcagagtc cttctgttaa cagggtgcatg ggg  
1 gaattccgtg gttcctcagt ggtgctgca acccctggtt caccctcttc caggttctgg  
61 ctccttcag ccatggctct cagagtcctt ctgttaacag ccttgacctt atgtcatggg  
121 ttcaacttg aactgaaaa cgcaatgacc ttccaagaga acgcaagggg cttcgggcag  
181 agcgtggtcc agcttcaggg atccagggtg gtggttgagg cccccagga gatagtggct  
241 gccaaacaaa ggggcagcct ctaccagtgc gactacagca caggctcatg cgagcccatc  
301 cgctgcagg tccccgtgga ggccgtgaac atgtccctg gcctgtccct ggcagccacc  
361 accagccccc ctgagctgct ggccgtgtgt cccaccgtgc accagactg cagtgagaac  
421 acgtatgtga aagggtctg cttcctgttt ggatccaacc tacggcagca gccccagaag  
481 ttcccaggagg ccctccgagg gtgtcctcaa gaggatagtg acattgcctt cttgattgat  
541 ggctctggtg gcatcatccc acatgacttt cggcggatga aggagtttgt ctcaactgtg  
601 atggagcaat taaaaaagtc caaaaccttg ttctctttga tgcagtactc tgaagaattc  
661 cggattcact ttaccttcaa agagttccag aacaacccta acccaagatc actggtgaag  
721 ccaataaccg agctgcttg gcgacacac acggccacg gcatccgcaa agtggtagca  
781 gagctgttta acatcaccaa cggagcccg aagaatgcct ttaagatcct agttgtcatc  
841 aggatggag aaaagtgtg cgatccctg ggatagagg atgtcatccc tgaggcagac  
901 agagaggag tcattcgcta cgtcattggg gtgggagatg ccttccgag cttgaaatcc  
961 cgccaagagc ttaataccat cgcattccaag ccgcctcgtg atcacgtgtt ccaggtgaat  
1021 aactttgagg ctctgaagac cattcagaac cagcttcggg agaagatctt tgcgacgag  
1081 ggtactcaga caggaagtag cagctccttt gagcatgaga tgtctcagga aggcttcagc  
1141 gctgccatca cctctaattg ccccttgctg agcactgtgg ggagctatga ctgggctggt  
1201 ggagtcttcc tatatacatc aaaggagaaa agcaccctca tcaacatgac cagagtggat  
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1381 cagaacactg gcatgtggga gtccaacgct aatgtcaagg gcaccagat cggcgctac  
1441 ttccgggccc cctctgctc cgtggacgtg gacagcaacg gcagaccga cctggtcctc  
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1561 cccagggggc agagggtctg gtggcagtg gatgctgttc tctacgggga gcagggccaa  
1621 ccctggggcc gctttggggc agccctaaca gtgctggggg acgtaaatgg ggacaaactg  
1681 acggacgtgg ccattggggc cccaggagag gaggacaacc ggggtgctgt ttacctgtt  
1741 cccggaacct caggatctgg catcagcccc tcccatagcc agcggatagc aggtccaag  
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1861 gatggactgg tagacctgac tgtaggagcc caggggcacg tgctgctgct caggtccag  
1921 ccagtactga gagtcaaggc aatcatggag ttcaatccca gggaagtggc aaggaatgta  
1981 tttgagtgtg atgatcaggt ggtgaaaggc aaggaaaggc gagaggtcag agtctgcctc  
2041 catgtccaga agagcacacg ggatcggcta agagaaggac agatccagag tgttgtgact  
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2161 aacagcacac gcagacagac acaggtcttg gggctgacct agacttgtga gacctgaaa  
2221 ctacagttgc cgaattgcat cgaggacca gtgagcccca ttgtgctgc cctgaacttc  
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2581 aaccagcgt cagacgacat ctggcgctg gcctgtgagt ctgcctctc caccgaagtg  
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2701 gaggtcacct ttaatatcac gtttgatgta gactctaagg cttccttgg aaacaaactg  
2761 ctcctcaagg ccaatgtgac cagtgaagac aacatgcccga gaaccaacaa aaccgaattc  
2821 caactggagc tgccggtgaa atatgctgtc tacatggtgg tcaccagcca tggggtctcc  
2881 actaaatatc tcaacttcac ggcctcagag aataccagtc gggctcatga gcatcaatat  
2941 caggtcagca acctggggca gaggagcctc cccatcagcc tgggtgttctt ggtgccgctc  
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3121 aaggcccccg tggggaactg ctccactcgt gtctgcccga gaatccagt tgacatcccg  
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3241 tacatcaaga cctcgcataa ccacctctg atcgtgagca cagctgagat cttgtttaac  
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3361 aaagtggagc cgttcgaggt ccccaacccc ctgcccgtca tctgtggcag ctctgtcggg  
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3481 caatacaagg acatgatgag tgaaggggg ccccggggg ccgaacccca gtagcggtc  
3541 cttcccgaca gagctgcctc tcggtggcca gcaggactct gccagacca cacgtagccc



3601 ccaggctgct ggacacgtcg gacagcgaag tatccccgac aggacgggct tgggcttcca  
3661 tttgtgtgtg tgcaagtgtg tatgtgctgt tgtgcgagtg tgtgcaagtg tctgtgtgca  
3721 agtgtgtgca cgtgtgctgt tgcgtgcatg tgcactcgca cgcccatgtg tgagtgtgtg  
3781 caagtattgtg agtgtgtcca gtgtgtgtgc gtgtgtccat gtgtgtgagc tgtgtgcatg  
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3901 tctctggcgt gtgggtaggt gacggcagcg tagcctctcc ggcaagaagg aactgccttg  
3961 gctcccttgt gcgtgggtaa gccgtgtctg ggttttcttc cgggagaggg gacggtcaat  
4021 cctgtgggtg aagagagagg gaaacacagc agcatctctc cactgaaaga agtgggactt  
4081 cccgtcgcct gcgagcctgc ggctgtctgg agcctgcgca gcttggatgg atactccatg  
4141 agaaaagccg tgggtggaac caggagcctc ctccacacca gcgctgatgc ccaataaaga  
4201 tgccactga ggaatcatga agcttccttt ctggattcat ttattatttc aatgtgactt  
4261 taattttttg gatggataag cctgtctatg gtacaaaaat cacaaggcat tcaagtgtac  
4321 agtgaaaagt ctcccttttc agatattcaa gtcacctcct taaaggtagt caagattgtg  
4381 ttttgaggtt tccttcagac agattccagg cgatgtgcaa gtgtatgcac gtgtgcacac  
4441 accacacaca tacacacaca caagcttttt tacacaaatg gtatgatact ttatttgggt  
4501 ctgtatcttg ctttttttca ccaatatttc tcagacatcg gttcatatta agacataaat  
4561 tactttttca ttcttttata ccgctgcata gtattccatt gtgtgagtg accataatgt  
4621 atttaaccag tcttcttttg atatactatt ttcactcttt gttattgcat ctgctgagtt  
4681 aataaatcaa atatatgtca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa  
1 ggttcaagtg attctgctgc ctcagcctcc caggcgggat tacaggtgct tgcaccacg  
61 cctggctaatt tttttgtct ttttagtaaa gatgagggtt caccatgttg ggcaggcttg  
121 tttcaattgc tgacctcaag tgagccaccc cgctcagc tccaaaatgc taggattaca  
181 ggcatgagcc accgcaccca gccaaagtgt tacatatatt tttgactaca cttcttaact  
241 attcttagga taaattacta gaagtgaata ttcttgggtg aagagcttga ggcctttaca  
301 cacacacaca cacacacaca cacacacaca caaataggct ggatcgagtg gctcacacct  
361 gtaatctcag cagtgtggga ggctgaggaa ggaggatcac ttgagtcag gaggttgaga  
421 atagcctgaa caacatagca agatcttctc tctacaaaaa agtttaaaaa aaattagctg  
481 gccatggcag catgtgcttg tagtaccagc tactcggaag gctgaggtag gaggatcgct  
541 tgagcccagg aggtgattga agctgcagtg agctgtgatt acaccactgc actccagcct  
601 gggcaacaga gctagactct gtctctaaaa aaaggcacaa aataatattt aaaaagcacc  
661 aggtatgcct gtacttgagt tgtcttgggt gatggctaca aatgagacag cctctggctga  
721 agggcggctt ccatttccat gggctggagg aggcattttt gcaaagtgtg ttttcaggaa  
781 gacacagagt tttacctct acactgtttt gatctgtatt aatgtttgct tatttattta  
841 ttttaatttt tttttgagac agagtctcac tctgtcacct gggctggagt gcagtggcat  
901 tattgaggct cattgcagtc tcagactcct gagctcaaac aatcctcctg cctcagcctc  
961 tggagtagct aggactacag gcatgtgcca ccagcctgg ctaatttttt aaatgtattt  
1021 tttgttagag tcggggtctc cctatgttgc ccaggctgga gtgcagtgtg gtgacctag  
1081 ctactgcag cctggacctc gggctcaaga aattctcaca cctcagcctg tccagtagca  
1141 ggggtacag gcgcgcacca ccateccagc taattaaaaa ttttttttg tagagacagg  
1201 gtctctctat gttgccagg ctggtttcaa actccaggc tcaagcaatc ctctgcctt  
1261 gcctcccaaa tgacatcgga ttacaggcgt gagccactga gcctggcccg tattaatgtt  
1321 tagaacacga attccaggag gcaggctaag tctattcagc ttgttcatat gcttgggcca  
1381 acccaagaaa caagtgggtg acaaatggca ccttttggat agtggatttg actttgaaag  
1441 tttgggtcag gagctgggga ggaagggtgg gcaggctgtg ggcagtcctg ggcggaagac  
1501 caggcagggc tatgtgtcga ctgagcctcc gccctcttcc tttgaatctc tgatagactt  
1561 ctgcctccta cttctccttt tctgccttcc tttgctttgg tggcttccct gtggttccct  
1621 agtgggtgct gcaaccctgg ttcactcttc caggttctgg ctccctccag ccatggctct  
1681 cagagtcctt ctgttaacag gtgcatgggg gtggggtggg ggactctggg tggggaggag  
1741 ggtaactttt ggtctgtca taaatagagg gcc

## (2) INFORMATION FOR SEQ ID NO:2724:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: \_ base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2724

1 ctgcagctcc ggaacggggg ggggtgtctc tccaccgcc ctgtgcccgc gccgggaaa  
61 gtgcaggcgg gccgggcgcg gtggtcagc cctgtgatct cagcactttg ggaggccgag  
121 gtgggcggat cacctgaggt cgggagttcg aggccagcct gcccaacatg gagaaacctt  
181 gtcttacta aagatacaaa attagccagg cgtggtgacg catgcctgta atcccagcta  
241 ctggagtggc tgaggcagga gaatcgcttg agcccgggag acagaggttg cggtagagctg  
301 agatcgacac attgcactcc agcctgggca acaagagcga aactcagaaa aaaaagaaaa  
361 gaaagtgcag gggaccgcc gtcgggggtg gggcggcgct gccagcctc tgtccactt  
421 ccatgcactt gacctcgacc ctccggcctc cgtctcgat cttcccgctc ctgaatatga  
481 ggcttggaac agaccagac cttcctgctt gccgctcctg agtggccccg ggaccgccgc  
541 ccatcttttg cccccagccc ctgcctctct gccgctcca ggtcggggg tcaggccagg  
601 aaagccccctt gggaagcccc cggggagcag ctggagcggg gtcgcccggc ggcgggaagg  
661 agtgggcgcc tctatttaag cggttcccc gccgcctcgg gacagagggg actgagcatg

721 gatttcggac tggccctcct gctggcgggg cttctggggc tctcctcgg tgagaagg

(2) INFORMATION FOR SEQ ID NO:2725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2725

1 atggatttcg gactggccct cctgctggcg gggcttctgg ggctcctcct cggccagtc  
61 ctccagggtga agccctgca ggtggagccc ccggagccgg tggtgcccg ggcttgggg  
121 gcctcgcgcc agctcacctg ccgcctggcc tgcgcggacc gggggccctc ggtgcagtgg  
181 cggggcctgg acaccagcct gggcgccggg cagtcggaca cgggcccag cgctcctacc  
241 gtgcgcaacg cctcgtctgc ggcggccggg acccgctgt gcgtgggctc ctgcggggg  
301 cgcaccttcc agcacaccgt gcagctcctt gtgtacgct tcccggacca gctgaccgtc  
361 tcccagcag ccttggtgcc tggtagcccg gaggtggcct gtacggccca caaagtcacg  
421 ccctgggacc ccaacgcgt ctccttctcc ctgctcgtc ggggccagga actggagggg  
481 gcgcaagccc tgggcccggg ggtgcaggag gaggaggagg agccccagg ggacgaggac  
541 gtgctgttca gggtagaca gcgtggcg ctgcccgc tggggacccc tgtcccgc  
601 gccctctact gccaggccac gatgaggctg cctggcttgg agctcagcca ccgccaggcc  
661 atccccgtcc tgcacagccc gacctcccc gagcctccc acaccacct cccggagcct  
721 cccaacacca cctccccgga gtctccgac accacctccc cggagtctcc cgacaccacc  
781 tcccaggagc ctcccgacac cacctcccag gagcctccc acaccacct ccaggagcct  
841 cccgacacca cctccccgga gcctccgac aagacctccc cggagccgc ccccagcag  
901 ggctccacac acaccccag gagcccaggc tccaccagga ctgcgcgcc tgagatctcc  
961 caggctgggc ccacgcaggg agaagtgat ccaacaggt cgtccaaacc tgcgggtgac  
1021 cagctgcccg cggctctgtg gaccagcagt gcggtgctgg gactgctgt cctggcctt  
1081 cccagctatc acctctgaa acgctgcgg cacctggctg aggacgac ccaccacca  
1141 gcttctctga ggttctgccc ccaggtgtcg gcctgggctg ggttaagggg gaccggccag  
1201 gtgcggatca gcccctctg agtgccagc ctttccccct gtgaaagcaa aatagcttgg  
1261 accccttcaa gttgagaact ggtcagggca aacctgcctc ccattctact caaagtcac  
1321 cctctgctca cagagatgga tgcattgtt gattgcctt ttggagaagc tcatcagaaa  
1381 ctcaaaagaa ggccactgtt tgtctcacct acccatgacc tgaagccct ccctgagtgg  
1441 tccccacctt tctggacgga accacgtact tttacatac attgattcat gtctcacgtc  
1501 tccctaaaaa tgcgtaagac caagctgtgc cctgaccacc ctgggcccct gtcgtcagga  
1561 cctcctgagg ctttgcaaaa taaacctcct aaaatgat

(2) INFORMATION FOR SEQ ID NO:2726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2726

1 tccatcacag cttccccgga ccagctgacc gtctccccag cagccctggt gcctggtgac  
61 ccggaggtgg cctgtacggc ccacaaagtc acgcccgtgg accccaacgc gctctccttc  
121 tccctgctcg tcgggggcca ggaactggag gggcgcaag ccctgggccc ggaggtgcag  
181 gaggaggagg aggagcccca gggggacgag gacgtgctgt tcagggtgac agagcgtgg  
241 cggctgccgc ccctggggac ccctgtcccg ccgcccctct actgccaggc cacgatgagg  
301 ctgcctggct tggagctcag ccaccgccag gccatccccg gtgagtccgc

(2) INFORMATION FOR SEQ ID NO:2727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2727

1 gtgcgcgac gccagtcct ccaggtgaag cccctgcagg tggagcccc ggagccggtg  
61 gtggccgtgg ccttgggcgc ctgcgccag ctacactgcc gcctggcctg cgcgaccgc  
121 ggggctcgg tgcagtggcg gggcctggac accagcctgg gcgcggtgca gtcggacag  
181 ggccgcagcg tctcaccgt gcgcaacgcc tcgctgtcgg cgccggggac ccgctgtgc  
241 gtgggctcct gcgggggccc caccttcag cacaccgtgc agctccttgt gtacgggtgag  
301 gcgtc

(2) INFORMATION FOR SEQ ID NO:2728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2728

```
1 ctgtttccag tctgcacag cccgacctcc ccggagcctc ccgacaccac ctccccggag
61 cctcccaaca ccacctcccc ggagtctccc gacaccacct ccccgagatc tcccgacacc
121 acctcccagg agcctcccca caccacctcc caggagcctc ccgacaccac ctcccaggag
181 cctcccgaca ccacctcccc ggagcctccc gacaagacct ccccgagacc cgccccccag
241 caggggtcca cacacacccc caggagccca ggctccacca ggactcgccg cctgagatc
301 tcccaggctg ggcccacgca gggagaagtg atcccaacag gctgtgagtt ctg
```

(2) INFORMATION FOR SEQ ID NO:2729:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2729

```
1 ctctccccag cgtccaaacc tgcgggtgac cagctgcccg cggtctgtg gaccagcagt
61 gcgggtgtgg gactgtgtgt cctggccttg cccacgtatc acctctgaa acgtgcccg
121 cacctggctg aggacgacac ccacccacca gcttctctga ggcttctgcc ccagggtctg
181 gcctgggctg ggttaagggg gaccggccag gtcgggatca gccctctctg agtggccagc
241 ctttccccct gtgaaagcaa aatagcttgg accccttcaa gttgagaact ggtcagggca
301 aacctgcctc ccattctact caaagtcata cctctgttca cagagatgga tgcattgtct
361 gattgcctct ttggagaagc tcatcagaaa ctcaaaagaa ggccactgtt tgtctcacct
421 acccatgacc tgaagcccct ccctgagtgg tccccacctt tctggacgga accacgtact
481 ttttacatac attgattcat gtctcacgtc tccctaaaaa tgcgtaagac caagctgtgc
541 cctgaccacc ctgggcccct gtcgtcagga cctctgagg ctttgcaaa taaacctcct
601 aaaatgat
```

(2) INFORMATION FOR SEQ ID NO:2730:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2730

```
1 gggactgagc atggatttcg gactggccct cctgctggcg gggcttctgg ggctcctcct
61 cggccagtcc ctccaggtag agcccctgca ggtggagccc ccggagccgg tgggtggcgt
121 ggcccttggc gcctcgcgcc agctcacctg ccgcctggcc tgcgaggacc gcggggcctc
181 ggtgcagtgg cggggcctgg acaccagcct gggcgcggtg cagtcggaca cgggcccagc
241 cgtcctcacc gtgcgcaacg cctcgctgtc ggcggccggg acccgcggtg gcgtgggctc
301 ctgcgggggc cgcaccttcc agcacaccgt gcagtcctt gtgtacgcct tcccggacca
361 gctgaccgtc tcccagcag ccctgggtgc tgggtgacccg gaggtggcct gtacggccca
421 caaagtcacg cccgtggacc ccaacgcgct ctcttctcct ctgctcgctg ggggcccagga
481 actggagggg gcgcaagccc tgggcccggg ggtgcaggag gaggaggagg agccccaggg
541 ggacgaggac gtgctgttca ggggtgacaga gcgctggcgg ctgccgcccc tggggacccc
601 tgtcccgccc gccctctact gccaggccac gatgaggctg cctggcttgg agctcagcca
661 ccgccaggcc atccccgtcc tgcacagccc gacctccccg gaggctcccc acaccacctc
721 cccggagtct cccgacacca cctccccgga gtctcccgac accacctccc cggagcctcc
781 cgacaccacc tcccggagc ctcccagaaa gacctccccg gagcccggcc cccagcaggg
841 ctccacacac acccccagga gccagggtc caccaggact cgccgcccct agatctccca
901 ggctgggccc acgcaggagg aagtgatccc aacaggctcg tccaaacctg cgggtgacca
961 gctgcccggc gctctgtgga ccagcagtgc ggtgtgggga ctgctgtccc tggccttgcc
1021 caggtatcac ctctgaaac gctgccggca cctggctgag gacgacaccc acccaccagc
1081 ttctctgagg cttctgcccc aggtgtcggc ctgggctggg ttaaggggga ccggccaggt
1141 cgggatcagc ccctctgag tggccagcct tccccctgt gaaagcaaaa tagcttgga
1201 cccttcaagt tgagaactgg tcagggcaaaa cctgcctccc attctactca aagtcatccc
1261 tctgttcaca gagatggatg catgttctga ttgcctctt ggagaagtc atcagaaact
1321 caaaagaagg cactgtttg tctcacctac ccatgacctg aagcccctcc ctgagtgtc
1381 cccaccttcc tggacggaac cagctacttt ttacatacat tgattcatgt ctcacgtctc
1441 cctaaaaatg cgtaagacca agctgtgccc tgaccacctt gggcccctgt cgtcaggacc
1501 tcctgaggct ttggcaata aacctcctaa aatgataaaa aaaaaa
```

(2) INFORMATION FOR SEQ ID NO:2731:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2731

```
1 ctgcagctcc ggaacggggg ggggctgctc tccaccgcc ctgtgcggcc gcccgggaaa
```

61 gtgcaggcgg gccgggagcg gtggctcacg cctgtgatct cagcactttg ggaggccgag  
121 gtggggcgat cacctgaggt cgggagttcg agggcagcct gcccaacatg gagaaccctt  
181 gtctctacta aagatacaaa attagccagg cgtggtagcg catgcctgta atcccgata  
241 ctggagtggtc tgaggcagga gaatcgcttg agcccgaggag acagaggttg cggtagctg  
301 agatcgacac attgactccc agcctgggca acaagagcga aactcagaaa aaaaagaaaa  
361 gaaagtgcag gggaccgccc gtcgggggtg gggcgggcgt gccagcctc tgtcccactt  
421 ccatgcactt gacctcgacc ctccggcctc cgtctgcgat ctcccgctgc ctgaatatga  
481 ggcttggaac agaccagacc ctctctgctt gcccgctcct agtgggcccg ggaccgccg  
541 ccatctttgg ccccgagccc ctgctctctt gccgctcca ggtcgggggg tcaggccagg  
601 aaagcccctt gggagcccc cggggagcag ctggagcggg gtcggcgggg ggcggaagg  
661 agtgggagcc tctatttaag cggcttcccc gcggcctcgg gacagagggg actgagcatg  
721 gatttcggac tggccctcct gctggcgggg cttctggggc tctcctcgg tgagaaggg  
1 atggatttgg gactggccct cctgctggcg gggcttctgg ggctcctcct cggccagtc  
61 ctccagggtga agcccctgca ggtggagccc ccggagccgg tggtgccctt ggccttggg  
121 gcctcgcgcc agctcacctg ccgctggccc tgcgaggacc gcggggcctc ggtgagtg  
181 cggggcctgg acaccagcct gggcgcggtg cagtcggaca cgggcccag cgtcctcacc  
241 gtgcgcaacg cctcgctgct ggcggcgggg acccgctgtg gcgtgggctc ctgcccggg  
301 cgcaccttcc agcacaccgt gcagctcctt gtgtacgctt tccggacca gctgaccgtc  
361 tccccagcag ccttggtgcc tggtagcccg gaggtggcct gtacggccca caaagtcacg  
421 cccgtggacc ccaacgcgct ctcttctctc ctgctcgctg ggggcccagga actggagggg  
481 gcgcaagccc tggggccgga ggtgcaggag gaggaggagg agccccagg ggacgaggac  
541 gtgctgttca gggtagacaga gcgctggcgg ctgcccggcc tggggacccc tgtcccggcc  
601 gccctctact gccaggccac gatgaggctg cctggcttgg agctcagcca ccgccaggcc  
661 atcccgttcc tgcacagccc gacctccccg gacctccccg acaccacctc cccggagcct  
721 cccaacacca cctccccgga gtctcccggc accacctccc cggagctctc cgacaccacc  
781 tcccaggagc ctcccagacc cactcccag gacctcccg acaccacctc ccaggagcct  
841 cccgacacca cctccccgga gcctcccagc aagacctccc cggagcccgc cccccagcag  
901 ggctccacac acacccccag gagcccaggc tccaccagga ctgcggccc tgagatctcc  
961 caggctgggg ccacgcaggg agaagtgate ccaacaggct cgtccaaacc tgcgggtgac  
1021 cagctgcccg cggtctgtg gaccagcagt gcggtgctgg gactgctgct cctggccttg  
1081 cccagctatc acctctgga acgctgcccg cactggtgct agggagacac ccaccacca  
1141 gcttctctga gcttctgccc ccaggtgtcg gcctgggctg ggttaagggg gaccggccag  
1201 gtggggatca gcccctcctg agtggccagc ctttccccct gtgaaagcaa aatagcttgg  
1261 acccttcaa gttgagaact ggtcagggca aacctgcctc ccattctact caaagtcac  
1321 cctctgctca cagagatgga tgcagtgtct gattgcctct ttggagaagc tcatcagaaa  
1381 ctcaaaagaa ggcactgtt tgtctcacct accatgacc tgaagccct cctgagtg  
1441 tccccacctt tctggacgga accacgtact tttacatac attgattcat gtctcacgtc  
1501 tccctaaaaa tgcgtaagac caagctgtgc cctgaccacc ctggggccct gtcgtcagga  
1561 cctctgagg cttggcaaa taaactcct aaaatgat  
1 tccatcacag cttcccggga ccagctgacc gtctcccag cagccctggt gctggtgac  
61 ccggaggtgg cctgtacggc ccacaaagtc acgcccgtgg accccaacgc gctctcctc  
121 tccctgctcg tcgggggcca ggaactggag gggcgcaag ccctggggcc ggaggtgac  
181 gaggagagg aggagcccca gggggacgag gacgtgctgt tcagggtgac agagcgtg  
241 cggctgccc ccctggggac ccctgtccc cccgcccctt actgccaggc cagcatgagg  
301 ctgcccgtt tggagctcag ccaccgccg gccatccccg gtgagtcgc  
1 gtcgcccag gccagtcct ccagtgaa gcccctgagg tggagcccc ggagccggtg  
61 gtggccgtgg cttggggcg ctgcgccag ctacctgcc gctggcctg cgcggaccgc  
121 ggggcccctg tgcagtggcg gggcctggac accagcctgg gcgcggtgca gtcggacacg  
181 ggccgagcg tctcaccgt gcgcaacgcc tcgctgtcgg cggccgggac ccgctgtgc  
241 gtgggctcct gcgggggccc cacttccag cacaccgtgc agctcctgt gtacggtgag  
301 gcgtc  
1 ctgtttccag tctgacag cccgacctc ccggagcctc ccgacaccac ctccccggag  
61 cctcccaaca ccacctccc ggagtctccc gacaccacct ccccggagtc tcccagacc  
121 acctcccagg agcctcccga caccacctc caggagcctc ccgacaccac ctcccaggag  
181 cctcccgaca ccacctccc ggagcctccc gacaagacct ccccggagcc cgcctccag  
241 cagggtcca cacacacccc caggagccca ggctccacca ggactcgccg cctgagatc  
301 tcccaggctg gggccacgca gggagaagt atcccaacag gctgtgagtt ctg  
1 ctctcccag cgtccaaacc tgcgggtgac cagctgccc cggctctgtg gaccagcagt  
61 gcggtgctgg gactgctgct cctggcctt cccacgtatc acctctgga acgctgccc  
121 cactggctg aggacgacac ccaccacca gcttctctga ggttctgccc ccaggtgtg  
181 gcctgggctg ggttaaggg gaccggccag gtcgggatca gcccctcct agtgccagc  
241 ctttccccct gtgaaagcaa aatagcttgg accccttcaa gttgagaact ggtcaggga  
301 aacctgcctc ccattctact caaagtcac cctctgttca cagagatgga tgcatttct  
361 gattgcctct ttggagaagc tcatcagaaa ctcaaaagaa ggccactgtt tgtctcact  
421 acctatgacc tgaagccct cctgagtggt tccccacct tctggacgga accacgtact  
481 tttacatac attgattcat gtctcacgtc tccctaaaaa tgcgtaagac caagctgtgc  
541 cctgaccacc ctggggccct gtcgtcagga cctcctgagg ctttggcaaa taaactcct  
601 aaaatgat

1 gggactgagc atggatttcg gactggccct cctgctggcg gggcttctgg ggctcctcct  
61 cgccaggtcc ctccaggtga agccctgca ggtggagccc ccggagccgg tgggtggccgt  
121 ggccttgggc gcctcgccgc agctcacctg ccgcctggcc tgcgcggacc gcggggcctc  
181 ggtgcagtgg cggggcctgg acaccagcct gggcgcggtg cagtcggaca cggggccgag  
241 cgtcctcacc gtgcgcaacg cctcgtgtgc ggccggccggg acccgcgtgt gcgtgggctc  
301 ctgcggggggc cgcaccttcc agcacaccgt gcagctcctt gtgtacgcct tcccggacca  
361 gctgaccgtc tccccagcag ccctggtgcc tggtagcccg gaggtggcct gtacggccca  
421 caaagtcacg. cccgtggacc ccaacgcgct ctccttctcc ctgctcgtcg ggggccagga  
481 actggagggg gcgcaagccc tgggcccggg ggtgcaggag gaggaggagg agccccaggg  
541 ggacgaggac gtgctgttca gggtagacaga gcgctggcgg ctgccgccc tggggacccc  
601 tgtcccggccc gccctctact gccaggccac gatgaggctg cctggcttgg agctcagcca  
661 ccgcccaggcc atccccgtcc tgcacagccc gacctccccg gagcctcccc acaccacctc  
721 cccggagtct cccgacacca cctcccggga gtctcccagc accacctccc cggagcctcc  
781 cgacaccacc tcccggagc ctcccagaca gacctccccg gagcccgccc cccagcaggg  
841 ctccacacac acccccagga gccagggtc caccaggact cgccgcccgt agatctccca  
901 ggctggggccc acgcaggag aagtgtatccc aacaggctcg tccaaacctg cgggtgacca  
961 gctgcccgcg gctctgttga ccagcagtg ggtgctggga ctgctgtccc tggcttggc  
1021 cacgtatcac ctctggaaac gctgccggca cctggctgag gacgacccc accaccagc  
1081 ttctctgagg cttctgcccc aggtgtcggc ctgggctggg ttaaggggga ccggccagggt  
1141 cgggatcagc cctcctgag tggccagcct tccccctgt gaaagcaaaa tagcttggac  
1201 cccttcaagt tgagaactgg tcagggcaaaa cctgcctccc atttactca aagtcatccc  
1261 tctgttcaca gagatggatg catgttctga ttgcctctt ggagaagctc atcagaaact  
1321 caaaagaagg ccactgtttg tctcacctac ccatgacctg aagccccctc ctgagtggtc  
1381 cccaccttcc tggacggaac cacgtacttt ttacatacat tgattcatt ctcacgtctc  
1441 cctaataatg cgtaagacca agctgtgccc tgaccacctt gggccccgt cgtcaggacc  
1501 tcctgaggct ttggcaata aacctcctaa aatgataaaa aaaaaa

## (2) INFORMATION FOR SEQ ID NO:2732:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2732

1 ggaattccgg gcccggtctt tcctcccggc gcccgccggc tggccccggg gactggcctc  
61 cacgtccgac tcgtccgagc tgaagcccag cagcactttg ctgccagccg cgggggcccg  
121 ggaggcggcc ccgggcccct ccaggaggct ctctgggcca gaggccgaga ttccggcacag  
181 gccccccagga gtccgtaagt aggagagggt gcccgagacc ggccggaccc ccatccccgc  
241 ggccgcccgc gccgctgtgc ccgcggctgc gaccgtggcg gctgccgctg gaaaatgtct  
301 caggagaggg ccacgttcta ccggcaggag ctgaacaaga caatctggga ggtgcccgag  
361 cgttaccaga acctgtctcc agtgggctct ggccgctatg gctctgtgtg tgctgctttt  
421 gacacaaaaa cgggggttacg tgtggcagtg aagaagctct ccagaccatt tcagtcctac  
481 attcatgcga aaagaacctc cagagaactg cggttactta aacatatgaa acatgaaat  
541 gtgattggtc tgttggacgt ttttacacct gcaaggctc tggaggaatt caatgatgtg  
601 tatctggtga cccatctcat gggggcagat ctgaacaaca ttgtgaaatg tcagaagctt  
661 acagatgacc atgttcagtt cttatctac caaattctcc gaggtctaaa gtatatacat  
721 tcagctgaca taattcacag ggacctaaaa cctagtaatc tagctgtgaa tgaagactgt  
781 gagctgaaga ttctggattt tggactggct cggcacacag atgatgaaat gacaggctac  
841 gtggccacta ggtggtacag ggctcctgag atcatgtga actggatgca ttacaaccag  
901 acagctgata tttggtcagt gggatgcata atggccgagc tgttgactgg aagaacctg  
961 tttcctggta cagaccatat tgatcagttg aagctcattt taagactcgt tggaaaccca  
1021 ggggctgagc ttttgaagaa aatctcctca gactctgcaa gaaactatat tcagtctttg  
1081 actcagatgc cgaagatgaa ctttgcgaat gtattttatt gtgccaatcc cctggctgtc  
1141 gacttgctgg agaagatgct tgtattggac tcagataaga gaattacagc ggcccaagcc  
1201 cttgcacatg cctactttgc tcagtaccac gatcctgatg atgaaccagt ggccgatcct  
1261 tatgatcagt cctttgaaag cagggacctc cttatagatg agtggaaaag cctgacctat  
1321 gatgaagtca tcagctttgt gccaccacc cttgaccaag aagagatgga ctcctgagca  
1381 cctgggtttct gttctgttga tcccacttca ctgtgagggg aaggcctttt cccgggaact  
1441 ctccaaatat tattcaagt cctctgttg cagagatttc ctccatggtg gaaggggggtg  
1501 tgcgtgcgtg tgcgtgcgtg ttagtgtgtg tgcattgtg

## (2) INFORMATION FOR SEQ ID NO:2733:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2733

1 aattaacct cactaaagg agtcgactcg atccccccgc ctacgccct tttttctttt

```

61 ttttttcatt ttcagttcag gagagtttta gcttaattat aggctacaga accagctttg
121 ggcttcatct atcctttcta atattttactg tttcctattt ctctaactct agctctttat
181 ttcttccctt tacttttact gggcttattt tgctatagtg gaatgcagag ggatgagtat
241 tccaggaagg cacaaaaact gtgccaagtc ttggagctag ggatgagtg gaaagggaca
301 tgttcaacca ttttaggcca ttccctcccc acctcccagc tcccagatat gtgcccctcg
361 caggaggagc ccaggaatgg gccaaacacc tcacttcttt gctctgaggg ccaccccagc
421 cctcccatca acagctctag aaacccaatg gtccttcttg gaaacacggg gcctgcatca
481 atcagaggtg tttgaacctg gtcctctctg gcctgagggg cagaagggga cacaatatgt
541 aatgtaagga gcccctgtca tcagaaatct gacttaatct gtttccagat attagacttc
601 cacataaaag ttgacttgga aaaagacttc tgctgctaaa caaaagttag aactgccttg
661 gtgataaaat ataagcagac cagctttctc ttctagcttt cctctctatt tcccataaga
721 ttttggtcaa gttatttaat ctctctgcat ccgtttcctc ttctatgaaa tgggcatgat
781 aataatggta tatacctcct caaggggggt ataacgtgaa cagagtcctt agcacagcac
841 tctgtctcta cgggagtgaa ttttcattgt ttttctcttt cctgttggag aaagtaagaa
901 gaaaacagcg cctttatggc ttcccatggg gaatggctgg ggcgcgtctg tgtccctgtc
961 tctctctctg ctccttctgg cctgaacagc cagaaggaag ccattgccat ctgtttcagc
1021 cctcagcttc cctcttgcatt ttcttagaaa agtcttttgg gccagctcc agctcagcag
1081 attcaggatc ccccttcatc atgacttggg caacgccctg ctcaggccaa ggctccttga
1141 gagttccaag cttctccact cctataaaaa ggccggcgga acagccagag gagcagagag
1201 gcaaagaaac attgtgaaat ctccaactct taaccttcaa catgaaagtc tctgcagtgc
1261 ttctgtgcct gctgctcatg acagcagctt tcaaccccca gggacttgct cagccaggta
1321 agtcacctcc cttcgactct cctctctctt cctctctgtt ctctattcaa ggaagacctt
1381 agcccagtg ctcctccact ttttttttag attgagctct attatgttgc ccaggctgaa
1441 gtgcaggggt gcatcttgg ctcattgcaa ccttcacctc ccaggttcaa gcgattctct
1501 tgccctcagc ttctgagtag ctgtgattac aggcaccgcc atcacgtgca gctaattttt
1561 gtatttttag tagagaaggg gtttcaactat gttggccagg ctggtctcaa actcttgacc
1621 tcaagtgate ctcccgtctc ggctcccaa agtgctggga ttacaggcgt gagcaccagg
1681 cccagccaag tgcccactt ctaagccac cagaatagta aggcctctca gaggttcaact
1741 ttaacatcta attttaaaga tagaaagctg aagcccatgt tggaggcaga agggacccta
1801 gccatccacc tccaggttat tgcagagcaa gaatgaaacc taagcttctg actccagatt
1861 tagggccttt tctttgacct catctgatcg tcccaaaactc tgcagatctg gaccacacc
1921 agaccttccc actggccttg cccgtggcct cccctagatg gctgtgacat gtctccacca
1981 tgcagctgag cctttgagah cctgaggcac atgtcacagg tcccacctca cctcagggtc
2041 taggggtgga gtgctgggct tgggggtgag taagatctac ttcttctctt ttgctttgca
2101 tcccatacag atgctccctg ctgtattcaa gctgagaaaa gcctaacaca tctcaaaagt
2161 ctttttcttt gtaactatct ctgatgcac tcaacgtccc atctacttgc tgcttcacat
2221 tttagcagta gaagatctcc ttgcagaggc tgaagagcta tgtgatcacc accagcaggt
2281 gtcccagaa ggctgtcatg tgggtagaaa aatccctgct cgctggctc ctcccactc
2341 ccacattccc caatccaaag ttctgcccc aagagacagac gtcagactga cttgagatct
2401 taggatgaga tctagccaga ctgtgtgatg caaaatcctc caattttggc tgcacaacag
2461 gtccaaagag gacctataat ttcccacacc ttgtttctct gatgggcacc agcccacacc
2521 ctttagcaga tgcaggatc agtttcccag gggcagcaag agcagtggct gcctccagag
2581 accccttctg tccacacacc tctacttcc tgtcctggag ggggtcccct tcacctgtag
2641 taggtggacc aggcaggttt agaaccaggt gtgtcatctc ctaggtaaac cctcaaaggy
2701 ttccatctaa ctgtgccaga tctccttctt ccacagcttc agaaccacac tgggcaagga
2761 gatctgtgct gaccacaaag agaagtgggt ccagaattat atgaaacacc tgggcccggaa
2821 agctcacacc ctgaagactt gaactctgct acccctactg aaatcaagct ggagtagctg
2881 aaatgacttt tccattctcc tctggcctcc tcttctatgc tttggaatac ttctaccata
2941 attttcaaat aggatgcatt cggttttgg attcaaaatg tactatgtgt taagtaatat
3001 tggctattat ttgacttgtt gctggtttgg agtttatttg agtattgctg atcttttcta
3061 aagcaaggcc ttgagcaagt aggttggctg ctctaagccc ccttcccttc cactatgagc
3121 tgctggcagt gggtttgtat tcggttccca ggggttgagc

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## (2) INFORMATION FOR SEQ ID NO:2734:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2734

```

1 ggcaaagaaa cattgtgaaa tctccaactc ttaaccttca acatgaaagt ctctgcagtg
61 cttctgtgcc tgctgtcat gacagcagct ttcaaccccc agggacttgc tcagccagat
121 gcaactcaacg tcccattctac ttgtgtctc acatttagca gtaagaagat ctccttgca
181 aggtggaaga gctatgtgat caccaccagc aggtgtcccc agaaggctgt catcttcaga
241 accaaactgg gcaaggagat ctgtgtgac ccaaaggaga agtgggtcac gaattatatg
301 aaacacctgg gccggaaagc tcacacctg aagacttgaa ctctgctacc cctactgaaa
361 tcaagctgga gtacgtgaaa tgacttttcc atttctctct ggcctctct tctatgcttt
421 ggaatacttc taccataatt ttcaaatagg atgcattcgg ttttgtgatt caaaatgtac
481 tatgtgttaa gtaattattg ctattatttg acttgttgcg gtttggagt ttatttgagt

```

541 attgctgctc ttttctatag caaggccttg agcaagtagg ttgctgtctc taagccccct  
 601 tcccttccac tatgagctgc tggcagtgagg tttgtattcg gttcccagg gttgagagca  
 661 tgcctgtggg agtcatggac atgaagggat gccgcaatgt aggaaggaga gctctttgtg  
 721 aatgtgaggt gttgctaaat atgttattgt ggaaagatga atgcaatagt aggactgctg  
 781 acattttgca gaaaatacat tttattttaa aatctcctaa aaaaaaaaaa aaaaaaaaaa  
 841 aagaaaaaaaa aaaaa

## (2) INFORMATION FOR SEQ ID NO:2735:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2735

1 acattgtgaa atctccaact cttaaccttc aacatgaaag tctctgcagt gcttctgtgc  
 61 ctgctgctca tgacagcagc tttcaacccc cagggacttg ctacagccaga tgcactcaac  
 121 gtcccactta ctgctgctt cacatttagc agtaagaaga tctccttgca gaggctgaag  
 181 agctatgtga tcaccaccag caggtgtccc cagaaggctg tcatcttcag aaccaaactg  
 241 ggcaaggaga tctgtgctga cccaaaggag aagtgggtcc agaattatat gaaacacctg  
 301 ggccggaaag ctacacacct gaagacttga actctgtac cctactgaa atcaagctgg  
 361 agtacgtgaa atgacttttc cattctcttc tggcctctc ttctatgctt tggaaactt  
 421 ctaccataat tttcaaatag gatgcattcg gttttgtgat tcaaaatgta ctatgtgta  
 481 agtaatatg gctattattt gacttgttgc tggtttgag tttatttgag tattgctgat  
 541 cttttctaaa gcaaggcctt gagcaagtag gttgctgtct ctaagcccc ttcccttcca  
 601 ctatgagctg ctggcagtg gttgtattcg gttcccagg gttgagagca tgctgtggg  
 661 agtcatggac atgaagggat gctgcaatgt aggaaggaga gctctttgtg aatgtgaggt  
 721 tgttgctaaa ttattgttta ttgtgaaag atgaatgcaa tagtaggact gctgacattt  
 781 tgcagaaaat acattttatt taaaatctcc taaaaaaaaa aaaaa

## (2) INFORMATION FOR SEQ ID NO:2736:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2736

1 aaaaggccgg cggaacagcc agaggagcag agaggcaaag aaacattgtg aaatctccaa  
 61 ctcttaacct tcaacatgaa agtctctgca gtgcttctgt gcctgctgct catgacagca  
 121 gctttcaacc ccagggact tgcacagcca gatgactca acgtcccatc tacttgctgc  
 181 ttcacattta gcagtaagaa gatctccttg cagaggctga agagctatgt gatcaccacc  
 241 agcaggtgtc ccagaaggc tgtcatcttc agaaccaaac tgggcaaggga gatctgtgct  
 301 gacccaaagg agaagtgggt ccagaattat atgaacacc tgggccggaa agctcacacc  
 361 ctgaagactt gaactctgct acccctactg aaatcaagct ggagtacgtg aaatgacttt  
 421 tccattctcc tctggcctcc tcttctatgc tttggaatac ttctaccata attttcaaat  
 481 aggatgcatt cggttttggg attcaaaatg tactatgtgt taagtaatat tggctattat  
 541 ttgacttggt gctggtttgg agtttatttg agtattgctg atcttttcta aagcaaggcc  
 601 ttgagcaagt aggttgctgt ctctaagccc ccttcccttc cactatgagc tgctggcagt  
 661 gggtttgat tgggttccca ggggttgaga gcattgctgt gggagtcatg gacatgaagg  
 721 gatgctgcaa ttaggaagg agagctcttt gtgaatgtga ggtgttgcta aatatgttat  
 781 tgtggaagaa tgaatgcaat agtaggactg ctgacatttt gcagaaaata cattttattt  
 841 aaatctcca aaaaaaaaaa

## (2) INFORMATION FOR SEQ ID NO:2737:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2737

1 aattaacct cactaaagg agtcgactcg atccccccgc ctacagcccc tttttctttt  
 61 ttttttcatt ttcatgtcag gagagtttta gcttaattat aggctacaga accagctttg  
 121 ggcttcatct atcctttcta atatttactg tttctattt ctctaactct agctctttat  
 181 ttcttccctt tacttttact gggcttattt tgctatagt gaatgcagag ggatgagat  
 241 tccaggaagg cacaaaaact gtgccaaatc ttggagctag ggatgagtg gaaaggagaca  
 301 tgttcaacca ttttaggcca ttccctcccc acctcccagc tcccagatat gtgcccctcg  
 361 caggaggagc ccaggaatgg gccaaacacc tcacttcttt gctctgaggg ccaccccagc  
 421 cctcccatca acagctctag aaacccaatg gtccttctcg gaaacacggg gcctgcatca  
 481 atcagaggtg tttgaacat gtccctctgg gcctgagggg cagaagggga cacaatatgt  
 541 aatgtaagga gccctgtca tcagaaatct gacttaactt gttttcagat attagacttc

601 cacatcaaaag ttgacttggg aaaagacttc tgctgctaaa caaaagtga aactgccttg  
661 gtgataaaat ataagcagac cagctttctc ttctagcttt cctctcatt tcccataaga  
721 ttttgggtcaa gttatttaat ctctctgcat ccgtttcctc ttctatgaaa tgggcatgat  
781 aataatggta tatacctcct caaggggggt ataacgtgaa cagagtcctt agcacagcac  
841 tctgtctcta cgggagtga ttttcattgt ttttctcttt cctgttggag aaagtaagaa  
901 gaaaacagcg cctttatggc ttcccatggg gaatggctgg ggcgcgtctg tgtccctgtc  
961 tcctctctgg ctctcttggg cctgaacagc cagaaggaag ccattgccatg ctgtttcagc  
1021 cctcagcttc cctcttgcat ttccatagaaa agtctttggg gccagctcc agctcagcag  
1081 attcaggatc ccccttcac atgacttggg caacgccctg ctcaggccaa ggtcctctga  
1141 gagttccaag cttctccact ccctataaaa ggccggcgga acagccagag gacgagagag  
1201 gcaaagaaac attgtgaaat ctccaactct taaccttcaa catgaaagtc tctgcagtgc  
1261 ttctgtgcct gctgctcatg acagcagctt tcaaccccca gggacttgtc cagccaggta  
1321 agtcacctcc ctteactct cctctctctt cctctgttt ctctattcaa ggaagacctt  
1381 agcccagagt ctctccact ttttttttag attgagtctc attatgttgc ccaggctgaa  
1441 gtgcaggggt gcatcttgg ctcatgcaa ccttcacctc ccagggtcaa gcgattctct  
1501 tgcctcagcc ttctgagtag ctgtgattac aggcaccgcc atcacgtgca gctaattttt  
1561 gtatttttag tagagaagg gtttcaactat gttggccagg ctggtctcaa actcttgacc  
1621 tcaagtgatc ctcccgctc ggccctccaa agtgctggga ttacaggcgt gaggaccagg  
1681 cccagccaa tgccccactt ctaagccac cagaatagta aggtcctca gaggttcact  
1741 ttaacatcta attttaaga tagaaagctg aagcccatgt tggaggcaga agggacccta  
1801 gccatccacc tccaggttat tgcagagcaa gaatgaaacc taagcttctg actccagatt  
1861 tagggcctt tctttgacct catctgatcg tcccaaactc tgcagatctg gaccacacc  
1921 agaccttccc actggcctt cccgtggcct cccctagatg gctgtgacat gtctccacca  
1981 tgcagctgag cctttgagah cctgaggcac atgtcacagg tcccactca cctcagggtc  
2041 taggggtggga gtgctgggct tgggggtgag taagatctac ttcttctct tttgtttgca  
2101 tcccatcac atgtccctg ctgtattcaa gctgagaaaa gcctaacaca tctcaaagt  
2161 ctttttctt gtaactatt ctgatgcac tcaacgtccc atctacttg tgtttcacat  
2221 ttagcagtaa gaagatctc ttgcagaggc tgaagagcta tgtgatcacc accagcagg  
2281 gtccccagaa ggctgtcatg tgggtagaaa aatccctgtc cgcttggtc ctccccactc  
2341 ccacattccc caatccaaag ttctgcccc ggagacagac gtcagactga cttgagatct  
2401 taggatgaga tctagccaga ctgtgtgatg caaaatcctc caattttggc tgcacaacag  
2461 gtccaaagag gacctataat ttccacaccc ttgtttcctg gatgggcacc agccacacc  
2521 ctttagcaga tgcaggatc agtttccag gggcagcaag agcagtggt gcctccagag  
2581 accccttctg tccacacacc tctacttcc tgtcctggag ggggtcccct tcacctgtg  
2641 taggtggacc aggcaggtt agaaccaggt gtgtcatctc ctaggtaaac cctcaaagg  
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2761 gatctgtgct gacccaaagg agaagtgggt ccagaattat atgaaacacc tgggcccggaa  
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2881 aaatgacttt tccattctc tctggcctcc tcttctatgc tttggaatac ttctaccata  
2941 attttcaaat aggatgcatt cggttttgtg attcaaatg tactatgtgt taagtaatat  
3001 tggctattat ttgacttgtt gctggttgg agtttatttg agtattgtg atcttttcta  
3061 aagcaaggcc ttgagcaagt aggttgtgt ctctaagccc ccttccctc cactatgagc  
3121 tgctggcagt gggtttgtat tcggttccca ggggttgagc  
1 ggcaaaagaa cattgtgaaa tctccaactc ttaaccttca acatgaaagt ctctgcagtg  
61 cttctgtgcc tgctgtcat gacagcagct ttcaaccccc agggacttgc tcagccagat  
121 gactcaacg tcccatctac ttgtgtctt acatttagca gtaagaagt ctcttgcag  
181 aggtgaaga gctatgtgat caccaccagc aggtgtccc agaaggctgt catctcaga  
241 accaaactgg gcaaggagat ctgtgtgac ccaaaggaga agtgggtcca gaattatag  
301 aaacacctgg gccggaaagc tcacacctg aagacttgaa ctctgtacc cctactgaa  
361 tcaagctgga gtacgtgaaa tgacttttc attctcctc ggctcctct tctatgctt  
421 ggaatacttc taccataatt ttcaaatagg atgcattcgg ttttgtgatt caaatgtac  
481 tatgtgttaa gtaatatgg ctattattg acttgttct ggttggagt ttatttgagt  
541 attgtgatc ttttctatag caaggcctg agcaagtagg ttgtgtctc taagccccct  
601 tcccttccac tatgagctgc tggcagtggt tttgtattcg gttcccagg gttgagagca  
661 tgcctgtgg agtcatggac atgaaggat gccgcaatgt aggaaggaga gctctttgtg  
721 aatgtgaggt gttgctaaat atgttattgt ggaaagatga atgcaatagt aggactgtg  
781 acattttgca gaaaatacat tttattttaa aatctcctaa aaaaaaaaa aaaaaaaaa  
841 aagaaaaaaa aaaaa  
1 acattgtgaa atctccaact cttaacctc aacatgaaag tctctgcagt gcttctgtg  
61 ctgtgtctca tgacagcagc tttcaacccc cagggacttg ctcagccaga tgcactcaac  
121 gtcccatcta ctgtgtctt cacatttagc agtaagaaga tctccttga gaggctgaag  
181 agctatgtga tcaccaccag cagggtgtccc cagaaggctg tcatcttcag aaccacactg  
241 ggcaaggaga tctgtgtgta ccaaaggag aagtgggtcc agaattatat gaaacacctg  
301 ggccggaaag ctacacacct gaagacttga actctgtac ccctactgaa atcaagctgg  
361 agtacgtgaa atgactttt cattctctc tggcctcctc ttctatgctt tggaaactt  
421 ctaccataat tttcaaatag gatgcattcg gttttgtgat tcaaatgta ctatgtgta  
481 agtaaatatt gctattattt gacttgttgc tggtttggag tttatttgag tattgtgat  
541 cttttctaaa gcaaggcctt gagcaagtag gttgtgtct ctaagcccc tcccttcca



601 ctatgagctg ctggcagtggt gttgtattcgt gttcccaggg gttgagagca tgcctgtggg  
661 agtcatggac atgaagggat gctgcaatgt aggaaggaga gctctttgtg aatgtgaggt  
721 tgttgctaaa ttattgttta ttgtggaaag atgaatgcaa tagtaggact gctgacattt  
781 tgcagaaaaat acattttatt taaaatctcc taaaaaaaaa aaaaa  
1 aaaaggccgg cggaacagcc agaggagcag agaggcaaag aaacattgtg aaatctccaa  
61 ctcttaacct tcaacatgaa agtctctgca gtgcttctgt gcctgctgct catgacagca  
121 gctttcaacc cccagggact tgctcagcca gatgactca acgtcccacg tacttgctgc  
181 ttcacattta gcagtaagaa gatctccttg cagaggctga agagctatgt gatcaccacc  
241 agcaggtgtc cccagaaggc tgtcatcttc agaaccaaac tgggcaagga gatctgtgct  
301 gacccaaagg agaagtgggt ccagaattat atgaaacacc tgggccggaa agctcacacc  
361 ctgaagactt gaactctgct acccctactg aaatcaagct ggagtacgtg aaatgacttt  
421 tccattctcc tctggcctcc tcttctatgc tttggaatac ttctaccata attttcaaat  
481 aggatgcatt cggttttgtg attcaaaatg tactatgtgt taagtaatat tggctattat  
541 ttgacttgtt gctggtttgg agtttatttg agtattgctg atcttttcta aagcaaggcc  
601 ttgagcaagt aggttgctgt ctctaagccc ccttcccttc cactatgagc tgctggcagt  
661 gggtttgtat tcggttccca ggggttgaga gcattgcctgt gggagtcagt gacatgaagg  
721 gatgctgcaa tgtaggaagg agagctcttt gtgaatgtga ggtgttgcta aatatgttat  
781 tgtggaaaga tgaatgcaat agtaggactg ctgacatttt gcagaaaata cattttattt  
841 aaaatctcca aaaaaaaaaa

## (2) INFORMATION FOR SEQ ID NO:2738:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: \_ base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2738

1 cgcccgaggca ggtcctctgc ctgactctgc tcccccaagg ctcccagaaa tctcaggtca  
61 gaggcacgga cagcctctgg agctctctgc tgggtgggacc atgaactgcc agcagctgtg  
121 gctgggcttc ctactcccca tgacagtctc aggcggggtc ctggggcttg cagaggtggc  
181 gcccgaggac tacctgtcac aatatgggta cctacagaag cctctagaag gatctaataa  
241 cttcaagcca gaagatatca ccgaggctct gagagctttt caggaagcat ctgaacttcc  
301 agtctcaggt cagctggatg atgccacaag ggcgcgcatg aggcagcttc gttgtggcct  
361 agaggatccc ttcaaccaga agacccttaa atacctgttg ctgggcccgt ggagaaagaa  
421 gcacctgact ttccgcatct tgaacctgcc ctccaccctt ccaccccaca cagcccgggc  
481 agccctgcgt caagccttcc aggactggag caatgtggct cccttgacct tccaagaggt  
541 gcaggctggt gcggctgaca tccgcctctc cttccatggc cgccaaagct cgtactgttc  
601 caatactttt gatgggcctg ggagagtctt ggcccatgcc gacatcccag agctgggcag  
661 tgtgcacttc gacgaagacg agttctggac tgaggggacc taccgtgggg tgaacctgcy  
721 catcattgca gcccatgaag tgggccatgc tctggggctt gggcactccc gatattccca  
781 ggccctcatg gccccagtct acgagggtta ccggcccccac tttaagctgc acccagatga  
841 tgtggcaggg atccaggctc tctatggcaa gaagagtcca gtgataaggg atgaggaaga  
901 agaagagaca gagctgcccc ctgtgcccc agtgcccaca gaaccagtc ccatgccaga  
961 cccttgcaat agtgaactgg atgccatgat gctggggccc cgtgggaaga cctatgcttt  
1021 caagggggac tatgtgtgga ctgtatcaga ttcaggaccg ggccccttgt tccgagtgtc  
1081 tgccctttgg gaggggctcc ccgaaaacct ggatgctgct gtctactcgc ctccgaacaca  
1141 atggattcac ttctttaagg gagacaaggt gtggcgctac attaatcca agatgtctcc  
1201 tggcttcccc aagaagctga ataggtcaga acctaacctg gatgcagctc tctattggcc  
1261 tctcaaccaa aaggtgttcc tctttaaggg ctccgggtac tggcagtgg acgagctagc  
1321 ccgaactgac ttcagcagct accccaaacc aatcaagggt ttgtttacgg gagtgcctaa  
1381 ccagccctcg gctgctatga gttggcaaga tggccgagtc tacttcttca agggcaaggt  
1441 ctactggcgc ctcaaccagc agcttcgagt agagaaaggc tatcccagaa atatttccca  
1501 caactggatg cactgtcgtc ccggactat agacactacc ccatcaggtg ggaataccac  
1561 tccctcaggt acgggcataa ccttggtatc cactctctca gccacagaaa ccacgtttga  
1621 atactgactg ctcaaccaca gacacaatct tggacattaa cccctgagge tccaccacc  
1681 accctttcat ttcccccca gaagcctaag gcctaatagc tgaatgaat acctgtctgc  
1741 tcagtagaac cttgcagggt ctgtagcagg cgcaagaccg tagatctcag gctctcaaca  
1801 cttccaactc cagccaccac tttctgtgct attttcactc ctgagaagtg ctccccctaac  
1861 tcagatcccc taacttagat ttggcccca actccatttc ctgtctgtct tagacagccc  
1921 ttccaactgt gtcattctct ctctggaggt caatgggtga gggagatgcc tgggtcctgt  
1981 tcttccctaca taaaatgcaa gaaaacagca tggccagtaa actgagcaag ggccttggaa  
2041 tcccttgagaa tcacatttat gtgcttatga ttacgggcaa gctaattaac cttgttgaat  
2101 ctgagattcc ccatttgcaa cattaggtta agaccagtac tgcaggattg ttgactaaa  
2161 tgaataactg tatgtgaagt gcctggcaca gtgtctggta catttgtgtt taataaaagc  
2221 taactccatg ttcataagaa aaaaaaaaaa

## (2) INFORMATION FOR SEQ ID NO:2739:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: \_ base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2739

```
1 ggagaccggc cgcattggacc cagggacagt ggccaccatg cgtaagcccc gctgctccct
61 gcctgacgtg ctgggggttg cggggctggt caggcggcgt cgccgggtacg ctctgagcgg
121 cagcgtgttg aagaagcgaa ccttgacatg gagggtagct tccttcccc agagctccca
181 gctgagccag gagaccgtgc gggtcctcat gagctatgcc ctgatggcct ggggcatgga
241 gtcaggcctc acatttcatg aggtggattc cccccagggc caggagcccc acatcctcat
301 cgactttgcc cgcgccttc accaggacag ctaccccttc gacgggttg ggggcaccct
361 agcccatgcc ttcttccctg gggagcacc catctccgg gacactcact ttgacgatga
421 ggagacctg acttttgggt caaaagcctc tcagcagctg gagcaggagc tggcaggcgg
481 ctcaccggtt gatgaggagc tgggcttcag ccggggctg cgtgtgaatc ctctgggtcc
541 tggcagtcct gagcgcctga gctgaataca gagggaagag gctgggagca aggccgggtg
601 ctggggccgg caggctgtgt tctgaga
```

## (2) INFORMATION FOR SEQ ID NO:2740:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: \_ base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2740

```
1 atgatcttac tcacattcag cactggaaga cggttggatt tcgtgcatca ttccgggggtg
61 tttttcttgc aaaccttgct ttggatttta tgtgctacag tctgcggaac ggagcagtat
121 ttcaatgttg aggtttggtt acaaaagtac ggctacctc caccgactga cccgaagt
181 tcagtgtgct gctctgcaga gaccatgcag tctgccctag ctgccatgca gcagttctat
241 ggcattaaca tgacaggaaa agtggacaga aacacaattg actggatgaa gaagccccga
301 tgcggtgtac ctgaccagac aagaggtagc tccaaatttc atattcgtcg aaagcgatat
361 gcattgacag gacagaaatg gcagcacaag cacatcactt acagtataaa gaacgtaact
421 ccaaaaagtag gagacctga gactcgtaaa gctattcggc gtgcctttga tgtgtggcag
481 aatgtaactc ctctgacatt tgaagaagtt ccctacagt aattagaaaa tggcaaacgt
541 gatgtggata taaccattat ttttgcatct ggtttccatg gggacagctc tccctttgat
601 ggagagggag gatttttggc acatgcctac ttccctggac caggaaattg aggagatacc
661 cattttgact cagatgagcc atggacacta ggaaatccta atcatgatg aaatgactta
721 tttctttag cagtccatga actgggacat gctctgggat tggagcattc caatgacccc
781 actgccatca tggctccatt ttaccagtac atggaaacag acaacttcaa actaccta
841 gatgatttac agggcatcca gaagatatat ggtccacctg acaagattcc tccacctaca
901 agacctctac cgacagtgc cccacaccgc tctattcctc cgctgaccc aaggaaaaat
961 gacaggccaa aacctcctcg gcctccaacc ggcagaccct cctatcccg agccaaaccc
1021 aacatctgtg atgggaactt taacactcta gctattcttc gtcgtgagat gttgttttc
1081 aaggaccagt ggttttggcg agtgagaaac aacagggtga tggatggata cccaatgcaa
1141 attacttact tctggcgggg ctgacctcct agtatcgatg cagtttatga aaatagcgac
1201 gggaattttg tgttctttaa agtgaaggga gacactctat ctgtaatcca agatgggttg
1261 ctctacaaat accattggaa atggattcta gaacaaaggc agtcagtgcc tgtgctctca
1321 agacaaactg aaaagcaca gacctatgaa gaattatctt ccatcacata ctaacaaaga
1381 acaatcagga attgaaaatt taaaataaaa ggccatttac aattgcattc gaaaacacca
1441 aataccgagg gatcaatctg caaaaaatgt gcatgacctc tacattgaaa acaacaaac
1501 actactaaat gtttgtcttt aaaggcagct gg
```

## (2) INFORMATION FOR SEQ ID NO:2741:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: \_ base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2741

```
1 tagaagttaa caatgaagtt tcttctaata ctgctcctgc aggccactgc ttctggagct
61 cttcccctga acagctctac aagcctggaa aaaaataatg tgctatttgg tgagagatac
121 ttgaaaaaat tttatggcct tgagataaac aaacttcag tgacaaaaat gaaatatagt
181 ggaaacttaa tgaaggaaaa aatccaagaa atgcagcact tcttgggtct gaaagtgacc
241 gggcaactgg acacatctac cctggagatg atgcacgcac ctcgatgtgg agtccccgat
301 ctccatcatt tcagggaat gccagggggg ccggtatgga ggaacatta tatcacctac
361 agaatcaata attacacacc tgacatgaac cgtgaggatg ttgactacgc aatccggaaa
421 gctttccaag tatggagtaa tgttaccctt ttgaaattca gcaagattaa cacaggcatg
481 gctgacattt tgggtggttt tgcccgtgga gctcatggag acttccatgc ttttgatggc
541 aaagggtgaa tctagccca tgcctttgga cctggatctg gcattggagg ggaatgcacat
601 ttcgatgagg acgaattctg gactacacat tcaggaggca caaacttgtt cctcactgct
661 gttcacgaga ttggccattc cttaggtctt ggccattcta gtgatccaaa ggctgtaatg
721 tttccacact acaaatatgt cgacatcaac acatttcgcc tctctgctga tgacatacgt
```

```

781 ggcattcagt cctgtatgg agacccaaaa gagaaccaac gcttgccaaa tcctgacaat
841 tcagaaccag ctctctgtga cccaatttg agttttgatg ctgtcactac cgtgggaaat
901 aagatctttt tcttcaaaga caggttcttc tggctgaagg tttctgagag accaaagacc
961 agtgtaattt taatttcttc cttatggcca accttgccat ctggcattga agctgcttat
1021 gaaattgaag ccagaaatca agtttttctt tttaaagatg acaaatactg gtttaattagc
1081 aatttaagac cagagccaaa ttatcccaag agcatacatt cttttggttt tcctaacttt
1141 gtgaaaaaaa ttgatgcagc tgtttttaac ccacgttttt ataggacctt cttctttgta
1201 ggaaccaggt attggaggta tgatgaaagg agacagatga tggaccctgg ttatcccaaa
1261 ctgattacca agaacttcca aggaatcggg cctaaaattg atgcagtctt ctatttctaaa
1321 aacaaatact actatttctt ccaaggatct aaccaatttg aatatgactt cctactccaa
1381 cgtatcacca aaacactgaa aagcaatagc tggtttggtt gttagaaatg gtgtaattaa
1441 tggtttttgt tagttcactt cagcttaata agtatttatt gcatatttgc tatgtcctca
1501 gtgtaccact acttagagat atgtatcata aaaaataaaa ctgtaaacca taggtaatga
1561 ttatataaaa tacataarat ttttcaattt tgaaaactct aattgtccat tcttgcttga
1621 ctctactatt aagtttgaaa atagttacct tcaaagcaag ataattctat ttgaagcatg
1681 ctctgtaagt tgcttcttaa catccttggg ctgagaaatt atacttactt ctggcataac
1741 taaaattaag tatatatatt ttggctcaaa taaaattg

```

## (2) INFORMATION FOR SEQ ID NO:2742:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2742

```

1 aaagaaggta agggcagtga gaatgatgca tcttgcatc cttgtgctgt tgtgtctgcc
61 agtctgctct gcctatcctc tgagtggggc agcaaaaagag gaggactcca acaaggatct
121 tgcccagcaa tacctagaaa agtactacaa cctcgaaaag gatgtgaaac agtttagaag
181 aaaggacagt aatctcattg ttaaaaaaat ccaaggaaatg cagaagtcc ttgggttgga
241 ggtgacaggg aagctagaca ctgacactct ggaggtgatg cgcaagccca ggtgtggagt
301 tcctgacgtt ggtcacttca gctcctttcc tggcatgccg aagtggagga aaaccacct
361 tacatacagg attgtgaatt atacaccaga ttgccaaga gatgtgttg attctgccat
421 tgagaaagct ctgaaagtct gggaagaggt gactccactc acattctcca ggtgtatga
481 aggagaggct gatataatga tctcttcgc agttaaaaga catggagact tttactcttt
541 tgatggccca ggacacagtt tggctcatgc ctaccacct ggacctgggc tttatggaga
601 tattcacttt gatgatgatg aaaaatggac agaagatgca tcaggcacca atttattcct
661 cgttgctgct catgaacttg gccactccct ggggctcttt cactcagcca aactgaagc
721 tttgatgtac cactctaca actcattcac agagctcgcc cagttccgcc tttcgcaaga
781 tgatgtgaat ggcattcagt ctctctacgg acctccccct gcctctactg aggaaccctt
841 ggtgcccaca aaatctgttc cttcgggagc tgagatgcca gccaaagtgt atcctgcttt
901 gctcttcgat gccatcagca ctctgagggg agaatactg tcttttaaag acagatattt
961 ttggcgaaag tccactgga accctgaacc tgaatttcat ttgatttctg cattttggcc
1021 ctctcttcca tcatatttgg atgctgcata tgaagttaac agcagggaca ccgtttttat
1081 ttttaaagga aatgagttct gggccatcag aggaaatgag gtacaagcag gttatccaag
1141 aggcattccat accctgggtt ttctccaac cataaggaaa attgatgcag ctgtttctga
1201 caaggaaaag aagaaaacat acttctttgc agcggacaaa tactggagat ttgatgaaaa
1261 tagccagtc atggagcaag gcttccttag actaatagct gatgacttca caggagttag
1321 gcctaagggt gatgctgtat tacaggcatt tggatttttc tacttcttca gtggatcatc
1381 acagtttgag tttgaccca agccagagat ggtgacacac atattaaaga gtaacagctg
1441 gttacattgc taggcgagat agggggaaga cagatatggg tgtttttaat aaatctaata
1501 attattcatc taatgtatta tgagccaaaa tggttaattt ttctgcatg ttctgtgact
1561 gaagaagatg agccttgcat atatctgcat gtgtcatgaa gaatgtttct ggaattcttc
1621 acttgctttt gaattgcact gaacagaatt aagaaatact catgtgcaat aggtgagaga
1681 atgtattttc atagatgtgt tattacttcc tcaataaaaa gttttatttt gggcctgttc
1741 ctt

```

## (2) INFORMATION FOR SEQ ID NO:2743:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2743

```

1 ctgaggtggg taagagtaca atggctaaat cttaacacac tcttacgtgt acaccctacc
61 gtacaccatc cagactcgtc cccatacaat caggagtgat cagtacgtaa atgcttatgg
121 tgtgatttga aggggtgtta gagtagatca tctctcacac cgcagcagca ctgcttccaa
181 ttcacctttt ggaattttat tccctgactg ttaaaagtgt ttagtgctta aatattctct
241 attagggtaa gagacagatt ctgtgcaatg ggacaattag gtcaagaggg aaagaagctg
301 aggtgatagg cagatagatt ccagaggcaa acttttccca tctgctaaag ttgaaaagag

```

361 taacctacat cctaccaacg ctagacaatc taggatgtag ggaaagtgtg tctctggaat  
421 ctatccaggt acccaggtgg gactgagctt cagcttagat gtctgaagat gtttaagtatt  
481 agaatcaggt ttaagtctga agatgttaag ttatagaatc aggatctgag ccggtacaac  
541 acgtggataa acaatgaagt cgatgttaca aatttttttt tgctacttgt aaaatctctg  
601 tatcacattt ctctaggagg ctggattccg tttaggagca ctcatctact ccaggaaaag  
661 gattttattt aatctttcaa cttttacttt aaaaactttt tttatctata atgaatataa  
721 ggaagtatta taatgaaaac caagttatca ggctttaaga aaatatattt taagttctcc  
781 ttctctttta gttgcttgat atttctttta caagggtcta tttttagat aggtggacgt  
841 agaggcttat ttatcatttt gaaggtagat actctgaatt gcttgagtga tggactagat  
901 gctaattgat ccattgtcgt ctgaataaag tcatgctttt gtttgcatgt ttttagagat  
961 agtcaaggga tgatatcaac tatgagtcac tcataggatt catattcaca gaaccggac  
1021 taagggttat ataaagagga acagttcagg aacttaggct agaaaggaca cagtaaaactg  
1081 aattgatccg tttagaagtt tacaatgaag tttcttctaa tactgtctct gcaggccact  
1141 gcttctggag ctcttccccct gaacagctct acaagcctgg aaaaaataa tgtgctattg  
1201 ggtgagaga

## (2) INFORMATION FOR SEQ ID NO:2744:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2744

1 cgccccgggca ggtcctctgc ctagcactgc tcccccaagg ctcccagaaa tctcaggtca  
61 gaggcacgga cagcctcttg agctctcgtc tgggtgggacc atgaactgcc agcagctgtg  
121 gctgggcttc ctactcccca tgacagcttc aggcggggtc ctggggcttg cagaggtggc  
181 gcccggtggac tacctgtcac aatatgggta cctacagaag cctctagaag gatctaataa  
241 cttcaagcca gaagatatca ccgaggctct gagagctttt cagggaagat ctgaacttcc  
301 agtctcaggt cagctggatg atgccacaag ggccccgatg aggcagcctc gttgtggcct  
361 agaggatccc ttcaaccaga agacccttaa atacctgttg ctggggccgt ggagaaagaa  
421 gcacctgact ttccgcatct tgaacctgcc ctccaccctt ccaccaccaca cagcccgggc  
481 agccctgcgt caagccttcc aggactggag caatgtgggt cccttgacct tccaagaggt  
541 gcaggctggt gcggctgaca tccgcctctc ctcccatggc cgccaaagct cgtactgttc  
601 caatactttt gatggcctg ggagagctct ggcccatgcc gacatcccag agctgggcag  
661 tgtgcacttc gacgaagacg agttctggac tgagggggacc taccgtggg tgaactgcg  
721 catcattgca gcccatgaag tgggccatgc tctggggctt gggcactccc gatattccca  
781 ggccctcatg gccccagtct acgaggggta ccggcccccac ttttaagctgc acccagatga  
841 tgtggcaggg atccaggctc tctatggcaa gaagagtcca gtgataaggg atgaggaaga  
901 agaagagaca gagctgcccc ctgtgcccc agtgccaca gaaccagtc ccatgccaga  
961 cccttgagct agtgaactgg atgccatgat gctggggccc cgtgggaaga cctatgcttt  
1021 caagggggac tatgtgtgga ctgtatcaga ttcaggaccg ggccccttgt tccgagtgtc  
1081 tgccccttgg gaggggctcc ccggaacctt ggatgctgct gtctactgca ctgcaacaca  
1141 atggattcac ttctttaagg gagacaaggt gtggcgctac attaatctca agatgtctcc  
1201 tggcttcccc aagaagctga ataggtcaga acctaacctg gatgcagctc tctattggcc  
1261 tctcaaccaa aaggtgttcc tctttaaggg ctccgggtac tggcagtggt acgagctagc  
1321 ccgaactgac ttcagcagct accccaaacc aatcaagggt ttgtttacgg gagtgcacaa  
1381 ccagccctcg gctgctatga gttggcaaga tggccgagtc tacttcttca agggcaaaat  
1441 ctactggcgc ctcaaccagc agcttcgagt agagaaaggg tatcccagaa atatttccca  
1501 caactggatg cactgtcgtc cccggactat agacactacc ccatacaggtt ggaataccac  
1561 tccctcaggt acgggcataa ccttggtatc cactctctca gccacagaaa ccagtttga  
1621 atactgactg ctcaccaccaca gacacaatct tggacattaa cccttgaggc tccaccacc  
1681 accctttcat ttcccccca gaagcctaag gcctaatagc tgaatgaaat acctgtctgc  
1741 tcagtagaac cttgcagggt ctgtagcagg cgcaagaccg tagatctcag gcctctaaca  
1801 cttccaactc cagccaccac tttctgtgct attttcactc ctgagaagtg ctcccctaac  
1861 tcagatcccc taacttagat ttggccccc actccatttc ctgtctgtct tagacagccc  
1921 ttccaactgt gtcattctct ctctggaggt caatgggtga gggagatgcc tgggtctgtg  
1981 tcttctctaca taaaatgcaa gaaaacagca tggccagtaa actgagcaag ggccttgga  
2041 tcttgagaa tcacatttat gtgcttatga ttacgggcaa gctaattaac cttgttgaa  
2101 ctacagattcc ccatttgcaa cattaggtta agaccagtag tgcaggattg ttgactaaa  
2161 tgaaatactg tatgtgaagt gcctggcaca gtgtctggta cattgtgtt taataaaagc  
2221 taactccatg ttcataagaa aaaaaaaa  
1 ggagaccggc cgcattggacc cagggacagt ggccaccatg cgtaagcccc gctgctccct  
61 gcctgacgtg ctgggggttg cggggctggt caggcggtcgt cgccgggtacg ctctgagcgg  
121 cagcgtgttg aagaagcgaa cctgacatg gaggtacgt tcttcccccc agagctccca  
181 gctgagccag gagaccgtgc gggtcctcat gagctatgcc ctgatggcct ggggcatgga  
241 gtcaggcctc acatttcatg aggtggattc cccccagggc caggagcccc acatcctcat  
301 cgactttgcc cgcgccttcc accaggacag ctacccttcc gacgggttg ggggaccct  
361 agcccatgcc ttcttccctg gggagcacc catctccggg gacactcact ttgacgatga  
421 ggagacctgg acttttgggt caaaagcctc tcagcagctg gagcaggagc tggcaggcgg

481 ctcaccgggt gatgaggagc tgggcttcag cgggggctgg cgtgtgaatc ctctgggtcc  
541 tggcagtcct gagcgctga gctgaatata gagggaagag gctgggagca aggccgggtg  
601 ctggggccgg caggctgtgt tctgaga  
1 atgatcttac tcacattcag cactggaaga cggttggatt tctgtcatca ttcgggggtg  
61 tttttcttgc aaaccttgct ttggatttta tgtgctacag tctgcggaac ggagcagtat  
121 ttcaatgtgg aggtttggtt acaaaagtac ggctaccttc caccgactga ccccagaatg  
181 tcagtgtctg gctctgcaga gaccatgcag tctgccctag ctgccatgca gcagttctat  
241 ggcattaaca tgacaggaaa agtggacaga aacacaattg actggatgaa gaagccccga  
301 tgcggtgtac ctgaccagac aagaggtagc tccaaatttc atattcgtcg aaagcgatat  
361 gcattgacag gacagaaatg gcagcacaag cacatcactt acagtataaa gaacgtaact  
421 ccaaaagttag gagacctga gactcgtaaa gctattcgcc gtgcctttga tgtgtggcag  
481 aatgtaactc ctctgacatt tgaagaagt ccctacagt aattagaaaa tggcaaacgt  
541 gatgtggata taaccattat tttgcatct ggtttccatg gggacagctc tccctttgat  
601 ggagagggag gatttttggc acatgcctac ttcctgggac caggaattgg aggagatacc  
661 cattttgact cagatgagcc atggacacta ggaaatccta atcatgatgg aaatgactta  
721 tttctttagc cagtccatga actgggacat gctctgggat tggagcattc caatgacccc  
781 actgccaatc tggctccatt ttaccagtac atggaaacag acaacttcaa actaccta  
841 gatgatttac agggcatcca gaagatatat ggtccacctg acaagattcc tccacctaca  
901 agacctctac cgacagtgc cccacaccgc tctattcctc cggtgaccc aaggaaaaat  
961 gacaggccaa aacctcctcg gcctccaacc ggcagacct cctatcccg agccaaaccc  
1021 aacatctgtg atgggaactt taacactcta gctattcttc gtcgtgagat gtttgttttc  
1081 aaggaccagt ggttttggcg agtgagaaac aacagggtga tggatggata cccaatgcaa  
1141 attacttact tctggcgggg ctgacctct agtatcgatg cagtattatg aaatagcgac  
1201 gggaaatttg tgttctttaa agtgaaggga gacactctat ctgtaatcca agatggttgg  
1261 cttcacaaat accattggaa atggattcta gaacaaaggc agtcagtgc tgtgctctca  
1321 agacaaactg aaaagcacia gacctatgaa gaattatctt ccatcacata ctaacaaaga  
1381 acaatcagga attgaaaatt taaaataaaa ggccatttac aattgcattc gaaaacacca  
1441 aataccgagg gatcaatctg caaaaaatgt gcatgacctc tacattgaaa acaacaaaac  
1501 actactaaat gtttgtcttt aaaggcagct gg  
1 tagaagttta caatgaagt tcttctaata ctgctcctgc aggccactgc ttctggagct  
61 ctccccctga acagctctac aagcctggaa aaaaataatg tgctatttgg tgagagatac  
121 tttagaaaaat tttatggcct tgagataaac aaacttcag tgacaaaaat gaaatatagt  
181 ggaacttaaa tgaaggaaaa aatccaagaa atgcagcact tcttgggtct gaaagtgacc  
241 gggcaactgg acacatctac cctggagatg atgcacgcac ctcgatgtgg agtccccgat  
301 ctccatcatt tcagggaat gccagggggg cccgtatgga ggaacatta tatcacctac  
361 agaatcaata attacacacc tgacatgaac cgtgaggatg ttgactacgc aatccggaaa  
421 gctttccaag tatggagtaa tgttaccctt ttgaaattca gcaagattaa cacaggcatg  
481 gctgacattt tgggtggttt tgcccgtgga gctcatggag acttccatgc tttgatggc  
541 aaaggtgga tcttagccca tgcttttggg cctggatctg gcattggagg ggatgcacat  
601 ttcgatgagg acgaattctg gactacacat tcaggaggca caaacttgtt cctcactgct  
661 gttcacgaga ttggccattc cttaggtctt ggccattcta gtgatccaaa ggctgtaatg  
721 tccccacct acaaatatgt cgacatcaac acatttcgcc tctctgctga tgacatacgt  
781 ggcattcagt ccctgtatgg agaccacaaa gagaaccaac gcttgccaaa tcttgacaat  
841 tcagaaccag ctctctgtga ccccaatttg agttttgatg ctgtcactac cgtgggaaat  
901 aagatctttt tcttcaaaga caggttcttc tggctgaagg tttctgagag accaaagacc  
961 agtgttaatt taatttcttc cttatggcca accttgccat ctggcattga agctgcttat  
1021 gaaattgaag ccagaaatca agtttttctt ttaaagatg acaataactg gtttaattagc  
1081 aatttaagac cagagccaaa ttatcccaag agcatacatt cttttggttt tcttaacttt  
1141 gtgaaaaaaa ttgatgcagc tgtttttaac ccacgttttt ataggacctt cttctttgta  
1201 gataaccagt attggaggtg tgatgaaagg agacagatga tggaccttgg ttatcccaaa  
1261 ctgattacca agaacttcca aggaatcggg cctaaaattg atgcagtctt ctattctaaa  
1321 aacaaatact actatttctt ccaaggatct aaccaatttg aatatgactt cctactccaa  
1381 cgtatcacca aaacactgaa aagcaatagc tggttttggt gttagaaatg gtgtaattaa  
1441 tggtttttgt tagttcactt cagcttaata agtatttatt gcatatttgc tatgtcctca  
1501 tgttaccact acttagagat atgtatcata aaaaataaat ctgtaaacca taggtaatga  
1561 ttatataaaa tacataatat ttttcaattt tgaaaactct aattgtccat tcttgcttga  
1621 ctctactatt aagtttgaaa atagttacct tcaaagcaag ataattctat ttgaagcatg  
1681 ctctgtaagt tgcttcctaa cactccttga ctgagaaatt atacttactt ctggcataac  
1741 taaaattaag tatatatatt ttggctcaaa taaaattg  
1 aaagaaggta agggcagtg gaatgatga tcttgcttc cttgtgctgt tgtgtctgct  
61 agtctgctct gcctaccctc tgagtggggc agcaaaaagag gagactcca acaaggatct  
121 tgccccagaa tacctagaaa agtactacaa cctcgaaaag gatgtgaaac agtttagaag  
181 aaaggacagt aatctcattg ttaaaaaaat ccaaggaaat cagaagtcc ttgggttggg  
241 ggtgacaggg aagctagaca ctgacactct ggaggtgatg cgcaagccca ggtgtggagt  
301 tcttgacgtt ggtcacttca gctccttcc tggcatgccg aagtggagga aaaccacct  
361 tacatacagg attgtgaatt atacaccaga tttgccaaga gatgctgttg attctgccat  
421 tgagaaaagt ctgaaagtct gggaagaggt gactccactc acattctcca ggctgtatga  
481 aggagaggct gatataatga tctcttctgc agttaaagaa catggagact tttactcttt

541 tgatggccca ggacacagtt tggctcatgc ctaccacct ggacctgggc tttatggaga  
601 tattcacttt gatgatgatg aaaaatggac agaagatgca tcaggcacca atttattcct  
661 cgttgctgct catgaacttg gccactccct ggggctcttt cactcagcca acactgaagc  
721 tttgatgtac ccactctaca actcattcac agagctcgcc cagttccgcc tttcgcaaga  
781 tgatgtgaat ggcattcagt ctctctacgg acctccccct gcctctactg aggaaccctt  
841 ggtgcccaca aaatctgttc ctctgggagc tgagatgcca gccaaagtgt atcctgcttt  
901 gtccttcgat gccatcagca ctctgagggg agaatatctg ttctttaaag acagatatatt  
961 ttggcgaaga tcccactgga accctgaacc tgaatttcat ttgatttctg catttttgcc  
1021 ctctcttcca tcatatttgg atgctgcata tgaagttaac agcagggaca ccgttttat  
1081 ttttaaaggga aatgagttct gggccatcag aggaaatgag gtacaagcag gttatccaag  
1141 aggcattccat accctgggtt ttctccaac cataaggaaa attgatgcag ctgtttctga  
1201 caaggaaaag aagaaaacat acttctttgc agcggacaaa tactggagat ttgatgaaaa  
1261 tagccagtc atggagcaag gcttccttag actaatagct gatgactttc caggagtga  
1321 gcctaagggt gatgctgtat tacaggcatt tggatttttc tacttcttca gtggatcatc  
1381 acagtttgag ttgacccca atgccaggat ggtgacacac atattaaaga gtaacagctg  
1441 gttacattgc taggcgagat agggggaaga cagatatggg tgttttaaat aaactaata  
1501 attattcatc taatgtatta tgagccaaaa tggtaattt ttctgcatg ttctgtgact  
1561 gaagaagatg agccttgcat atatctgcat gtgtcatgaa gaatgtttct ggaattcttc  
1621 acttgctttt gaattgact gaacagaatt aagaaatact catgtgcaat aggtgagaga  
1681 atgtattttc atagatgtgt tattacttcc tcaataaaaa gttttatttt gggcctgttc  
1741 ctt

1 ctgaggtggg taagagtaca atggctaaat cttaacacac tcttacgtgt acaccctacc  
61 gtacaccatc cagactcgtc ccatacaat caggagtgat cagtacgtaa atgcttatgg  
121 tgtgatttga aggggtgtta gtagatgata tctctcacac cgacgagca ctgcttccaa  
181 ttcactcttt ggaattttat tccctgactg ttaaaagttt ttagtgctta aatattctct  
241 attgaggtaa gagacagatt ctgtgcaatg ggacaattag gtcaagaggg aaagaagctg  
301 aggtgatagg cagatagatt ccagaggcaa acttttccca tctgctaaag ttgaaaagag  
361 taaccacat cctaccaacg ctagacaatc taggatgtag ggaagtttg tctctggaat  
421 ctatccaggt acccagttgg gactgagctt cagcttagat gtctgaagat gtttaagttat  
481 agaatcaggt ttaagtctga agatgttaag ttatagaatc aggatctgag ccggtacaac  
541 acgtggataa acaatgaagt cgatgttaca aattttttt tgctacttgt aaaatctctg  
601 tatcacattt ctctagggag ctggattccg tttaggagca ctcatctact ccaggaaaag  
661 gattttattt aatctttcaa catttacttt aaaaactttt tttatctata atgaatataa  
721 ggaagtatta taatgaaaac caagttatca ggctttaaga aaatatattt taagttctcc  
781 ttctctttta gttgcttgat atttctttta caagggtta tttgtagat aggtggacgt  
841 agaggcttat ttatcatttt gaaggtagat actctgaatt gcttgagtga tggactagat  
901 gctaattgat ccattgtcgt ctgaataaag tcatgctttt gtttgcattg ttttagagat  
961 agtcaaggga tgatatcaac tatgagtcac tcataggatt catattcaca gaaccggac  
1021 taagggttat ataaagagga acagttcagg aacttaggct agaaaggaca cagtaaacg  
1081 aattgatccg tttagaagtt tacaatgaag tttcttctaa tactgtctct gcaggccact  
1141 gcttctggag ctcttccctt gaacagctct acaagcctgg aaaaaataa tgtgctattg  
1201 ggtgagaga

## (2) INFORMATION FOR SEQ ID NO:2745:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2745

1 aaggacacgg gcagcagaca gtggctcagtc ctttcttggc tctgctgaca ctcgagccca  
61 cattccgtca cctgctcaga atcatgcagg tctccactgc tgcccttgct gtccctctct  
121 gcaccatggc tctctgcaac cagttctctg catcacttgc tgctgacacg ccgaccgcct  
181 gctgcttcag ctacacctcc cggcagattc cacagaattt catagctgac tactttgaga  
241 cgagcagcca gtgctccaag cccggtgtca tcttccctaa caagcgaagc cggcaggtct  
301 gtgctgaccc cagtgaggag tgggtccaga aatatgtcag cgacctagag ctgagtgcct  
361 gaggggtcca gaagcttcga ggcccagcga cctcgggtgg ccagtgggga ggagcaggag  
421 cctgagcctt gggaaacatg cgtgtgacct ccacagctac ctcttctatg gactggttgt  
481 tgccaaacag ccacactgtg ggactcttct taacttaaat ttaattttat ttatactatt  
541 tagtttttgt aatttatttt cgatttcaca gtgtgtttgt gattgtttgc tctgagagtt  
601 cccctgtccc ctcccccttc cctcacaccg cgtctgtgta caaccgagtg gctgtcatca  
661 gcctgtgtag gcagtcagtg caccaaagcc accagactga caaatgtgta tcggatgctt  
721 ttgttcaggg ctgtgatcgg cctggggaaa taataaagca cgctctttta aaaggt

## (2) INFORMATION FOR SEQ ID NO:2746:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2746

1 acagccttga ccttatgtca tgggttcaac ttggacactg aaaacgcaat gaccttccaa  
61 gagaacgcaa ggggcttcgg gcagagcgtg gtccagcttc agggatccag ggtgggtggtt  
121 ggagcccccc aggagatagt ggctgccaac caaaggggca gcctctacca gtgcgactac  
181 agcacaggct catgcgagcc catccgcctg cagggtccccg tggaggccgtg gaacatgtcc  
241 ctgggacctgt ccctggcagc caccaccagc cccctcagc tgctggcctg tggccccacc  
301 gtgcaccaga cttgcagtga gaacacgtat gtgaaagggc tctgcttctt gtttggatcc  
361 aacctacggc agcagcccca gaagtcccca gagggccctcc gaggggtgtcc tcaagaggat  
421 agtgacattg ccttcttgat tgatggctct ggtagcatca tcccacatga ctttcggcgg  
481 atgaaggagt ttgtctcaac tgtgatggag caattaaaaa agtccaaaac cttgttctct  
541 ttgatgcagt actctgaaga attccggatt cactttacct tcaaaagatt ccagaacaac  
601 cctaacccaa gatcactggt gaagccaata acgcagctgc ttgggcggac acacacggcc  
661 acgggcatcc gcaaagtgtt acgagagctg ttaacatca ccaacggagc ccgaaagaat  
721 gcctttaaga tcctagtgt catcacggat ggagaaaagt ttggcgatcc cttgggatat  
781 gaggatgtca tccctgaggg agacagagag ggagtcatte gctacgtcat tggggtgga  
841 gatgccttcc gcagtgaaga atcccgccaa gagcttaata ccatcgatc caagccgcct  
901 cgtgatcacg tgttccaggt gaataacttt gaggtcttga agaccattca gaaccagctt  
961 cgggagaaga tctttgcgat cgagggtact cagacaggaa gtacgagctc ctttgagcat  
1021 gagatgtctc aggaaggctt cagcgctgcc atcacctcta atggccccct gctgagcact  
1081 gtggggagct atgactgggc tgggtggagtc tttctatata catcaaagga gaaaagcacc  
1141 ttcatacaaca tgaccagagt ggattcagac atgaatgatg cttacttggg ttatgtgcc  
1201 gccatcatct tacggaaccg ggtgcaaagc ctggttctgg gggcacctcg atatcagcac  
1261 atcggcctgg tagcgatgtt caggcagaac actggcatgt gggagtccaa cgtaatgtc  
1321 aagggcaccc agatcggcgc ctacttcggg gcctccctct gctccgtgga cgtggacagc  
1381 aacggcagca ccgacctggt cctcatcggg gccccccatt actacgagca gaccggaggg  
1441 ggccagggtg ccgtgtgccc cttgccagg gggcagaggg ctcggtggca gtgtgatgct  
1501 gttctctacg gggagcaggg ccaaccctgg ggcgccttg gggcagccct aacagtgtg  
1561 ggggacgtaa atggggacaa gctgacggac gtggccattg gggccccagg agaggaggac  
1621 aaccggggtg ctgtttacct gtttcacgga acctcaggat ctggcatcag cccctcccat  
1681 agccagcgga tagcaggtc caagctctct cccaggctcc agtatttttg tcagtcactg  
1741 agtgggggac aggacctcac aatggatgga ctggtagacc tgactgtagg agcccagggg  
1801 cacgtgctgc tgctcaggtc ccagccagta ctgagagtca aggcaatcat ggagttcaat  
1861 cccagggaag tggcaaggaa tgtatttgag tgtaatgatc aggtgggtgaa aggcaaggaa  
1921 gccggagagg tcagagtctg cctccatgtc cagaagagca cacgggatcg gctaagagaa  
1981 ggacagatcc agagtgtgtg gacttatgac ctggctctgg actccggccg cccacattcc  
2041 cgcgcctctc tcaatgagac aaagaacagc acacgcagac agacacaggt cttggggctg  
2101 acccagactt gtgagacctt gaaactacag ttgccgaatt gcatcgagga cccagtgagc  
2161 cccattgtgc tgcgcctgaa cttctctctg gtgggaacgc cattgtctgc tttcgggaac  
2221 ctccggccag tgctggcgga ggatgctcag agactcttca cagccttggt tccctttgag  
2281 aagaattgtg gcaatgacaa catctgccag gatgacctca gcatcacctt cagtttcatg  
2341 agcctggact gcctcgtggt ggggtggccc cgggagtcca acgtgacagt gactgtgaga  
2401 aatgatgggt aggaactccta caggacacag gtcaccttct tcttcccgct tgacctgtcc  
2461 taccggaagg tgtccacgct ccagaaccag cgctcacagc gatcctggcg cctggcctgt  
2521 gagtctgcct cctccaccga agtgtctggg gccttgaaga gcaccagctg cagcataaac  
2581 caccatctct tcccggaaaa ctcagagggtc acctttaata tcacgtttga tgtagactct  
2641 aaggcttccc ttggaaacaa actgtctctc aaggccaatg tgaccagtga gaacaacatg  
2701 ccagaacca acaaaaccga attccaactg gagctgccgg tgaatatgca tgtctacatg  
2761 gtggtcacca gccatggggt ctcactaaa tatctcaact tcacggcctc agagaatacc  
2821 agtcgggtca tgcagcatca atatcagggtc agcaacctgg ggcagaggag cctccccatc  
2881 agcctgggtg tcttgggtgc cgtccggctg aaccagactg tcatatggga ccgccccag  
2941 gtcaccttct ccgagaacct ctcgagtacg tgccacacca aggagcgctt gccctctcac  
3001 tccgactttc tggctgagct tcggaaggcc cccgtggtga actgctccat cgctgtctgc  
3061 cagagaatcc agtgtgacat cccgttcttt ggcattccagg aagaattcaa tgtaccctc  
3121 aaaggcaacc tctcgtttga ctggtacatc aagacctcgc ataaccacct cctgatcgtg  
3181 agcacagctg agatcttgtt taacgattcc gtgttcaccc tgctgccggg acagggggcg  
3241 tttgtgaggt cccagacgga gaccaaagtg gagccgttcg aggtcccaa cccctgccg  
3301 ctcatcgtgg gcagctctgt cgggggactg ctgctcctgg ccctcatcac cgccgcctg  
3361 tacaagctcg gcttctcaa gcggcaatac aaggacatga tgagtgaagg gggcccccg  
3421 ggggccgaac cccagttagc gtccttccc gacagagctg cctctcgggt gccagcagga  
3481 ctctgccag accacacgta gccccaggc tgctggacac gtcggacagc gaagtatccc  
3541 cgacaggacg ggcttgggct tccatttgtg tgtgtgcaag tgtgtatgtg cgtgtgtgag  
3601 agtgtgtgca agtgtctgtg tgcaagtgtg tgcacgtgtc ggtgtgctgt catgtgact  
3661 cgcacgcccc tgtgtgagtg tgtgcaagta tgtgagtggt tccaagtgtg tgtgctgtg  
3721 tccatgtgtg tgcaagtgtg tgcatgtgtg cgagtgtgtg catgtgtgtg ctcaggggag  
3781 tgtggtctac gtgtgtgact cagatgtctc tggcggtgtg gtaggtgacg gccagcgtag  
3841 cctctccggc agaagggaac tgcctgggct ccttgtgctg tgggtggaag cgctgctggg  
3901 ttttccctcg ggagagggga cggtaaatcc tgtgggtgaa gacagaggga aacacagcag

3961 cttctctcca ctgaaagaag tgggacttcc cgtcgcctgc agcctgcggc ctgctggagc  
4021 ctgcgcagct tggatggaga ctccatgaga agcctggtt ggaaccagga gcctcctcca  
4081 caccagcgct gatgcccaat aaagatgccc actgaggaat gatg

## (2) INFORMATION FOR SEQ ID NO:2747:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2747

1 agcaggaagc tcgcgccgcc gtcgcccgcg ccgctcagct tccccggggc cgtccaggac  
61 cgcgtgcgcc aggcgcgcgc tccccggacc cggcgtgcgt ccctacgagg aaagggaccc  
121 cgccgctcga gccgcctccg ccagcccccac tgcgaggggt cccagagcca gccgcgccc  
181 ccctcgcccc cggccccgca gccttccgc cctgcgcgcc atgaacgccc ccgagcggca  
241 gcccacccc gacggcggg acgccccagg ccacgagcct gggggcagcc cccaagacga  
301 gcttgacttc tccatcctct tcgactatga gtatttgaat ccgaacgaag aagagccgaa  
361 tgcacataag gtcgccagcc caccctccg acccgcatatc cccgatgatg taatggacta  
421 tggcctcaag ccatacagcc cccttgctag tctctctggc gagccccccg gccgattcgg  
481 agagccggat agggtagggc cgcagaagtt tctgagcgcg gccaaagccag caggggcctc  
541 gggcctgagc cctcgatcg agatcactcc gtcccacgaa ctgatccagg cagtggggcc  
601 cctccgcag agagacgcgg gcctcctggt ggagcagcct cccctggcgc ggggtggcgc  
661 cagcccgagg ttcaccctgc cgtgcccgc cttcagggc taccgcgagc cgctttgctt  
721 gagccccgct agcagcggct cctctgccag cttcatttct gacaccttct cccctacac  
781 ctgcgccctgc gtctcgccca ataacggcgg gcccgacgac ctgtgtccgc agtttcaaaa  
841 catccctgct cattattccc ccagaacctc gccataaatg tcacctcgaa ccagcctcgc  
901 cgaggacagc tgcctgggccc gccactgcgc cgtgccccgt ccggcctccc gtcctcate  
961 gcctgggtgcc aagcggaggc attcgtgcgc cgaggccttg gttgccctgc cgccggagc  
1021 ctcaccccag cgtcccggga gccctcgccc gcagccctca tctcacgttg caccacagga  
1081 ccacggctcc cgggtgggt acccccctgt ggctggctct gccgtgatca tggatgccct  
1141 gaacagcctc gccacggact cgccttggtg gatccccccc aagatgtgga agaccagccc  
1201 tgacccctcg ccggtgtctg ccgccccatc caaggccggc ctgcctcgcc acatctaccc  
1261 ggccgtggag ttccctggggc cctgcgagca gggcgagagg agaaactcgg ctccagaatc  
1321 catcctgctg gttccgcccc cttggcccaa gccgctggtg cctgccattc ccatctgcag  
1381 catcccagtg actgcattcc tccctccact tgagtggcgg ctgtccagtc agtcaggctc  
1441 ttacgagctg cggatcgagg tgcagcccaa gccacatcac cgggccactc atgacagaga  
1501 aggcagccga ggggtgtgca aagctccaac tggaggccac cctgtggttc agctccatgg  
1561 ctacatggaa aacaagcctc tgggacttca gatcttcatt gggacagctg atgagcggat  
1621 ccttaagccg cagccttct accaggtgca ccgaatcac gggaaaactg tcaccaccac  
1681 cagctatgag aagatagtg gcaacaccaa agtcctggag atcccccttg agcccaaaaa  
1741 caacatgagg gcaaccatcg actgtgcggg gatcttgaag cttagaaacg ccgacattga  
1801 cgtgcggaaa ggcgagacgg acattggaag aaagaacacg cgggtgagac tggttttccg  
1861 agttcacatc ccagagtcga gtggcagaat cgtctcttta cagactgcat ctaaccccat  
1921 cgagtgtctc cagcgatctg ctcacgagct gccatgggtt gaaagacaag acacagacag  
1981 ctgcctggtc tatggcggcc agcaaatgat cctcacgggg cagaacttta catccgagtc  
2041 caaagtgtg tttactgaga agaccacaga tggacagcaa atttgggaga tggagccac  
2101 ggtggataag gacaagagcc agcccaacat gctttttgtt gagatccctg aatatcgga  
2161 caagcatatc cgcacacctg taaaagtga cttctacgtc atcaatggga agagaaaacg  
2221 aagtcagcct cagcacttta cctaccaccc agtcccagcc atcaagacgg agcccacgga  
2281 tgaatatgac cccactctga tctgcagccc caccatgga ggcctgggga gccagcctta  
2341 ctacccccag caccgatgg tggccgagtc cccctcctgc ctggtggcca ccatggctcc  
2401 ctgccagcag ttccgcacgg ggctctcatc ccctgacgcc cgtaccagc aacagaaccc  
2461 agcggccgta ctctaccagc ggagcaagag cctgagcccc agcctgcttg gctatcagca  
2521 gccggccctc atggccgccc cgtgtccct tgcggacgct caccgctctg tctgtgtgca  
2581 cgccggctcc cagggccaga gctcagccct gctccacccc tctccgacca accagcaggc  
2641 ctgcctgtg atccactact caccaccaa ccagcagctg cgtgcggaa gccaccagga  
2701 gttccagcac atcatgtact gcgagaattt cgcaccagc accaccagac ctggcccgc  
2761 cccggtcagt caaggtcaga ggctgagccc gggttcctac cccacagtca ttcagcagca  
2821 gaatgccacg agccaaagag ccgcaaaaaa cggacccccg gtcagtgacc aaaaggaagt  
2881 attacctgcg ggggtgacca ttaaacagga gcagaacttg gaccagacct acttgatga  
2941 tgtaaatgaa attatcagga aggagtttcc aggacctct gccagaaatc agacgtaa

## (2) INFORMATION FOR SEQ ID NO:2748:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2748



1 gctgcagcac cctggggccac gccgatgact actgcaaact gtggcgccca cgacgagctc  
61 gacttcaaac tcgtctttgg cgaggacggg gcgcgggcgc cgccgcccc gggctcgcg  
121 cctgcagatc ttgagccaga tgattgtgca tccatttaca tctttaatgt agatccacct  
181 ccactctact taaccacacc actttgctta ccacatcatg gattaccgtc tcaactctct  
241 gttttgtcac catcgtttca gtcctaaagt cacaaaaact atgaaggaaac ttgtgagatt  
301 cctgaatcta aatatagccc attaggtggg cccaaaccct ttgagtgcgc aagtattcaa  
361 attacatcta tctctcctaa ctgtcatcaa gaattagatg cacatgaaga tgacctacag  
421 ataaatgacc cagaacggga atttttggaa aggccttcta gagatcatct ctatcttctc  
481 cttgagccat cctaccggga gtcttctctt agtcctagt ctgccagcag catctcttct  
541 aggagttggg tctctgatgc atcttcttgt gaatcgcttt cacatattta tgatgatgtg  
601 gactcagagt tgaatgaagc tgcagcccga tttacccttg gatccctct gacttctctc  
661 ggtggctctc cagggggctg ccctggagaa gaaacttggc atcaacagta tggacttggg  
721 cactcattat caccagga cactccttgc cactctccta gatccagtgt cactgatgag  
781 aattggctga gcccaggcc agcctcagga cctcatcaa ggccacatc cccctgtggg  
841 aaacggaggc actccagtgc tgaagtttgt tatgtgggt cctttcacc ccatactca  
901 cctgttccct cacctgttca ctccccagg ggaagtgtga cagaagata ttggctcaat  
961 gcttctgtcc atgggtgggc aggccttggc cctgcagttt ttccatttca gtactgtgta  
1021 gagactgaca tccctctcaa aacaaggaaa acttctgaag atcaagctgc catactacca  
1081 ggaaaattag agctgtgttc agatgaccaa gggagtttat caccagcccg ggagacttca  
1141 atagatgatg gccttgatc tcagtatcct ttaaagaaag attcatgtgg tgatcagttt  
1201 ctttcagttc cttcaccctt tacctggagc aaaccaaagc ctggccacac ccttatattt  
1261 cgcacatctt cattacctcc actagactgg cctttaccag ctcattttg acaatgtgaa  
1321 ctgaaatag aagtgaacc taaaactcat catcgagccc attatgaaag tgaagtgagc  
1381 cgaggggcag taaaagcatc tactggggga catcctgttg tgaagctcct gggctataac  
1441 gaaaagccaa taaatctaca aatgtttatt gggacagcag atgatcgata tttacgacct  
1501 catgcatttt accaggtgca tcgaatcact ggaagacag tcgctactgc aagccaagag  
1561 ataataattg ccagtacaaa agttctggaa attccactc ttcctgaaaa taatatgtca  
1621 gccagtattg attgtgcagg tattttgaaa ctccgcaatt cagatataga acttcgaaaa  
1681 ggagaaactg atattggcag aaagaatact agagtacgac ttgtgtttcg tgtacacatc  
1741 ccacagccca gtggaaaagt cctttctctg cagatagcct ctatacccg tgagtgtctc  
1801 cagcgtgtcg ctcaagaact tcctcatatt gagaagtaca gtatcaacag ttgtctgtga  
1861 aatggaggtc atgaaatggg tgtgactgga tctaattttc ttccagaatc caaaatcatt  
1921 tttcttgaaa aaggacaaga tggacgacct cagtgggagg tagaaggga gataatcagg  
1981 gaaaaatgtc aaggggtc caattgtcctt gaagttcctc catatcataa cccagcagtt  
2041 acagctgcag tgcaggtgca cttttatctt tgcaatggca agaggaaaaa aagccagttc  
2101 caacgtttta cttatacacc agttttgtcg aagcaagaac acagagaaga gattgatttg  
2161 tcttcagttc catctttgcc tgtgcctcat cctgtcaga cccagaggcc ttcctctgat  
2221 tcagggtgtt cacatgcagc tgtactgtca ggacagagaa gtttgatttg ttccatccca  
2281 caaacatatg catccatggt gacctcatcc catctgccac agttgcagtg tagagatgag  
2341 agtgtagta aagaacagca tatgattcct tctccaattg tacaccagcc ttttcaagtc  
2401 acaccaacac ctctgtggg gtcttctctat cagcctatgc aaactaatgt tgtgtacaat  
2461 ggaccaactt gtcttctctat taatgtctgc tctagtcaag aatttgattc agtttggtt  
2521 cagcaggatg caactctttc tggtttagtg aatcttggct gtcaaccact gtcattccata  
2581 ccatttcatt cttcaaatc aggtcaaca ggacatctct tagcccatc acctcattct  
2641 gtgcataccc tgcctcatct gcaatcaatg ggatattcatt gttcaaatc aggacaaga  
2701 tctctttctt ctccagtggtg taccagatt acaggtcagc cttcgtctca gttacaacct  
2761 attacatatg gtccttcaca ttcagggtct gttacaacag cttccccagc agcttctcat  
2821 cccttgggta gttcaccgct ttctgggcca ccatctctc agtttcagcc tatgccttac  
2881 caatctccta gctcaggaa tggctcatca cgtctccaag ccaccagaat gcattctgga  
2941 cagcactcaa ctcaagcaca aagtacgggc caggggggtc tttctgcacc ttcactccta  
3001 atatgtcaca gtttgtgtga tccagcgtca tttccacctg atggggcaac tgtgagcatt  
3061 aaacctgaac cagaagatcg agagcctaac tttgcaacca ttggtctgca ggacatcact  
3121 ttagatgatg accaatttat atctgacttg gaacaccagc catcagggtt agcagagaaa  
3181 tggcctaacc acagtgtgct ctcatgtcca gctcctttct ggagaatcta gaggtgaacg  
3241 agataattgg gagagacatg tcccagattt ctgtttccca aggagcaggg gtgagcaggc  
3301 aggcctcccct cccgagtcct gagtccctgg atttaggaag atctgatggg ctctaacagt  
3361 gcttactgca gccttgtgtc caccaccaac ttctcagcat gtttctctcc ttggaccttg  
3421 ggtttccaac tcttcaacct tcaggtcttg ggccaggagt gggaccacc atttgtgggg  
3481 aaagtagcat tcttccacct caggccttgg gtagatttgg caaaagaaca ggagcagcat  
3541 aggtgttttg agctttgggg aaatgaactt tgctttttat atttaactag gatactttta  
3601 aatgatgggt gctttgagtg tgaatccagc aggtctctct gtttccgagg tgcgtctttt  
3661 gcaggtgacc tggttactta actaggagtg gtgatttga ctgctttatg gtcatttgaa  
3721 gggcccttta gtttttatga taatttttaa aataggaact tttgataaga ccttctagaa  
3781 gcaa

## (2) INFORMATION FOR SEQ ID NO:2749:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2749

1 gctgcagcac cctgggccac gccgatgact actgcaaact gtggcgccca cgacgagctc  
61 gacttcaaac tcgtctttgg cgaggacggg gcgcggggcg cgcgcggccc gggctcgagg  
121 cctgcagatc ttgagccaga tgattgtgca tccatttaca tctttaatgt agatccacct  
181 ccactctact taaccacacc accttgctta ccacatcatg gattaccgct tcactcttct  
241 gttttgtcac catcgtttca gctccaaagt cacaataact atgaaggaaac ttgtgagatt  
301 cctgaatcta aatatagccc attagggtgg cccaaaccct ttgagtggcc aagtattcaa  
361 attacatcta tctctcctaa ctgtcatcaa gaattagatg cacatgaaga tgacctacag  
421 ataaatgacc cagaacggga atttttggaa aggccttcta gagatcatct ctatcttctc  
481 cttgagccat cctaccggga gtcttctctt agtcctagt ctgccagcag catctcttct  
541 aggagttggt tctctgatgc atcttcttgt gaatcgctt cacatattta tgatgatgtg  
601 gactcagagt tgaatgaagc tgcagcccga tttacccttg gatccctct gacttctcct  
661 ggtggctctc cagggggctg ccttggaaga gaaacttggc caacaagta tggacttggg  
721 cactcattat caccagggca atctccttgc cactctccta gatccagtgt cactgtgag  
781 aattggctga gccccaggcc agcctcagga cctcatcaa ggccacatc cccctgtggg  
841 aaacggaggc actccagtgc tgaagtttgt tatgtgggt cctttcacc ccatcactca  
901 cctgttcctt cacctgttca ctccccagg ggaagtgtga cagaagatac gtggtcaat  
961 gcttctgtcc atggtgggtc aggccttggc cctgcagttt ttccatttca gtactgtgta  
1021 gagatgaca tccctctcaa aacaaggaaa acttctgaag atcaagctgc catactacca  
1081 ggaaaattag agctgtgttc agatgaccaa gggagtttat caccagcccg ggagacttca  
1141 atagatgatg gccttgatc tcagtatcct ttaaagaaag attcatgtgg tgactcagtt  
1201 ctttcagttc cttaccctt tacctggagc aaaccaaagc ctggccacac cctatatatt  
1261 cgcacatctt cattacctc actagactgg cctttaccag ctcattttgg acaatgtgaa  
1321 ctgaaaatag aagtgaacc taaaactcat catcgagccc attatgaac tgaaggtagc  
1381 cgaggggagc taaaagcatc tactggggga catcctgttg tgaagctcct gggctataac  
1441 gaaaagccaa taaatctaca aatgtttatt gggacagcag atgatcgata ttacgacct  
1501 catgcatttt accaggtgca tcgaatcact gggaagacag tcgctactgc aagccaagag  
1561 ataataattg ccagtacaaa agttctggaa attccactc ttctgaaaaa taatatgtca  
1621 gccagtattg attgtgcagg tattttgaaa ctccgcaatt cagatataga acttcgaaaa  
1681 ggagaaactg atattggcag aaagaatact agagtacgac ttgtgtttcg tgtacacatc  
1741 ccacagccca gtggaaaagt cctttctctg cagatagcct ctataccgt tgagtgtcc  
1801 cagcgtcttg ctcaagaact tctcatatt gagaagtaca gtatcaacag ttgttctgta  
1861 aatggaggtc atgaatggg tgtgactgga tctaattttc ttccagaatc caaaatcatt  
1921 tttcttgaag aaggacaaga tggacgacct cagtgggagg tagaagggaa gataatcagg  
1981 gaaaatgtc aaggggtcct cattgtcctt gaagttcctc catatcataa cccagcagtt  
2041 acagctgcag tgcaggtgca cttttatctt tgcaatggca agaggaaaaa aagccagttc  
2101 caacgtttta cttatacacc agttttgtcg aagcaagaac acagagaaga gattgatttg  
2161 tcttcagttc catctttgcc tgtgcctcat cctgctcaga cccagaggcc ttctctgat  
2221 tcagggtgtt cacatgacag tgtactgtca ggacagagaa gtttgatttg ctccatccca  
2281 caaacatag catccatggt gacctcatcc catctgccac agttgcagtg tagagatgag  
2341 agtggttagta aagaacagca tatgattcct tctccaattg tacaccagcc ttttcaagtc  
2401 acaccaacac ctctgtggg gtcttcttat cagcctatgc aaactaatgt tgtgtacaat  
2461 ggaccaactt gtcttcttat taatgtgcc tctagtcaag aatttgattc agtttgggtt  
2521 cagcaggatg caactcttct tgggttagtg aatcttggct gtcaaccact gtcatccata  
2581 ccatttcatt cttcaaattc aggtcaaca ggacatctct tagccatac acctcattct  
2641 gtgcataccc tgcctcatct gcaatcaatg ggatattcatt gttcaaatc aggacaaaga  
2701 tctctttctt ctccagtggt tgaccagatt acaggtcagc cttcgtctca gttacaacct  
2761 attacatag gtcttcaca ttcagggtct gttacaacag cttccccagc agcttctcat  
2821 cccttgggta gttcaccgct ttctgggcca ccatctcctc agtttcagcc tatgccttac  
2881 caatctccta gctcaggaac tggctcatca cgtctccag ccaccagaat gcattctgga  
2941 cagcactcaa ctcaagcaca aagtacgggc caggggggtc tttctgcacc ttcatcctta  
3001 atatgtcaca gtttgtgtga tccagcgtca tttccacctg atggggcaac tgtgagcatt  
3061 aaacctgaac cagaagatcg agagcctaac tttgcaacca ttggtctgca ggacatcact  
3121 ttagatgatg atttgtttac cagtaataat tttgacttgc ttcagttgag acctacgttt  
3181 tggccagtc cagcaggaag atatctgagg aatctagagt gaacgagata attgggagag  
3241 acatgtccca gatttctgtt tcccaaggag caggggtgag caggcaggct cccctccga  
3301 gtctgagtc cctggattta ggaagatctg atgggtctca acagtgttca ctgcagcctt  
3361 gtgtccacca ccaacttctc agcatgtttc tctccttggg ccttgggttt ccaactcttc  
3421 aaccttcagg tctggggcca ggagtgaggc ccaccatttg tggggaaagt agcatctctc  
3481 cacctcaggc cttgggtaga tttggcaaaa gaacaggagc agcataggct gtttgagctt  
3541 tggggaaatg aactttgctt tttatatatta actaggatac ttttaaatga tgggtgcttt  
3601 gagtgtgaat ccagcaggct ctcttgtttc cgaggtgctg cttttgcagg tgacctggtt  
3661 acttaactag gagtgggtgat ttgtactgct ttatgtcat ttgaagggcc ctttagtttt  
3721 tatgataatt tttaaaatag gaacttttga taagaccttc tagaagcaa

(2) INFORMATION FOR SEQ ID NO:2750:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: \_ base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2750

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1 gctgcagcac cctgggcccac gccgatgact actgcaaact gtggcgccca cgacgagctc
61 gacttcaaac tcgtcttttg cgaggacggg gcgcgggcgc cgccgcccc gggtcgcgg
121 cctgcagatc ttgagccaga tgattgtgca tccatttaca tctttaatgt agatccacct
181 ccatctactt taaccacacc actttgctta ccacatcatg gattaccgtc tcaactctct
241 gttttgtcac catcgtttca gctccaaagt cacaaaaact atgaaggaaac ttgtgagatt
301 cctgaatcta aatatagccc attaggtggg cccaaaccct ttgagtggcc aagtattcaa
361 attacatcta tctctcctaa ctgtcatcaa gaattagatg cacatgaaga tgacctacag
421 ataaatgacc cagaacggga atttttggaa aggccttcta gagatcatct ctatcttctt
481 cttgagccat cctaccggga gtcttctctt agtcttagtc ctgccagcag catctctctt
541 aggagtgggt tctctgatgc atcttcttgt gaatcgcttt cacatattta tgatgatgtg
601 gactcagagt tgaatgaagc tgcagcccga tttacccttg gatccctctt gacttctctt
661 ggtggctctc cagggggctg cctggagaa gaaacttggc atcaacagta tggacttggg
721 cactcattat caccagggca atctccttgc cactctccta gatccagtgt cactgatgag
781 aattggctga gccccaggcc agcctcagga cctcatcaa ggcccacat cccctgtggg
841 aaacgggagc actccaagtgc tgaagtttgt tatgctgggt cctttccacc ccatcactca
901 cctgttctctt cacctgggtca ctccccagg ggaagtgtga cagaagatac gtggctcaat
961 gcttctgtcc atggtgggtc aggccttggc cctgcagttt ttccatttca gtactgtgta
1021 gagactgaca tccctctcaa aacaaggaaa acttctgaag atcaagctgc catactacca
1081 ggaaaattag agctgtgttc agatgaccaa gggagtttat caccagcccc ggagacttca
1141 atagatgatg gccttggatc tcagtatcct ttaaagaaaag attcatgttg tgatcagttt
1201 ctttcagttc cttcaccctt tacctggagc aaaccaaaagc ctggccacac ccctatatct
1261 cgcacatctt cattacctcc actagactgg cctttaccag ctcatcttgg acaatgtgaa
1321 ctgaaaatag aagtgcaccc taaaactcat catcgagccc attatgaaac tgaagtgagc
1381 cgagggggcag taaaagcatc tactggggga catcctgttg tgaagctcct gggctataac
1441 gaaaagccaa taaatctaca aatgtttatt gggacagcag atgatcgata tttacgacct
1501 catgcatttt accaggtgca tcgaatcact ggggaagacag tcgctactgc aagccaagag
1561 ataataattg ccagtacaaa agttctggaa attccacttc ttcctgaaaa taatatgtca
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1801 cagcgggtctg ctcaagaact tcctcatatt gagaagtaca gtatcaacag ttgttctgta
1861 aatggaggtc atgaaatggg tgtgactgga tctaattttc ttccagaatc caaatcatt
1921 tttcttgaaa aaggacaaga tggacgacct cagtgggagg tagaagggaa gataatcagg
1981 gaaaaatgtc aagggggtca cattgtcctt gaagtccctc catatcataa cccagcagtt
2041 acagctgcag tgcaggtgca cttttatctt tgcaatggca agaggaaaaa aagccagttc
2101 caacgtttta cttatacacc agttttgtgt aagcaagaac acagagaaga gattgatttg
2161 tcttcagttc catctttgcc tgtgctctat cctgtctcaga cccagaggcc tctctctgat
2221 tcaggggtgtt cacatgacag tgtactgtca ggacagagaa gtttgatttg ctccatccca
2281 caaacatatg catccatggg gacctcatcc catctgccac agttgcagtg tagagatgag
2341 agtggttagta aagaacagca tatgattcct tctccaattg tacaccagcc ttttcaagtc
2401 acaccaacac ctctgtggg gtcttctctat cagcctatgc aaactaatgt tgtgtacaat
2461 ggaccaactt gtcttctctat taatgtctgc tctagtcaag aatttgattc agtttggttt
2521 cagcaggatg caactctttc tggtttagtg aatcttggct gtcaaccact gtcattccata
2581 ccatttcatt cttcaaattc aggcctcaaca ggacatctct tagccatac acctcattct
2641 gtgcataccc tgcctcatct gcaatcaatg ggatattcatt gttcaaatatc aggcacaaaga
2701 tctctttctt ctccagtggg tgaccagatt acaggtcagc ctctgtctca gttacaacct
2761 attacatatg gtctttcaca ttcagggtct gttacaacag cttccccagc agcttctcat
2821 cccttgggta gttcacgct ttctgggcca ccatctctc agtttcagcc tatgccttac
2881 caatctccta gctcaggaac tggctcatca ccgtctccag ccaccagaat gcattctgga
2941 cagcactcaa ctcaagcaca aagtacgggc caggggggtc tttctgcacc ttcattcctta
3001 atatgtcaca gtttgtgtga tccagcgtca tttccacctg atggggcaac tgtgagcatt
3061 aaacctgaac cagaagatcg agagcctaac tttgcaacca ttggtctgca ggacatcact
3121 ttagatgatg gtaagttcat ctctgatatg ttcttgaagt agtgaagatt cagggacttt
3181 attctcccaa gtgtcatgaa aaagtctcta tggattgctt attggcatat ggttgggctt
3241 ttaaataagt tgttattaga aatatatgtt aatatataac tttgccaggt accacggctc
3301 acgctgtgat cccagcactt tgggaaggctg aggcgggttg atcacaaggt caggagtcca
3361 agaccagcct ggccaacatg gtgtaacgct gtctctacta aaaatacaaa aaattagcca
3421 ggcatgggtg tgtgtgacta taatcccagc tactcgggag gctgagacag gagaatcact
3481 tgaacccggg aggtggcagt tgcaggagc taagatcgcg ccattgcact ccagcctggg
3541 cggcagagca agactccgtc tcgggaaaaa aaaaaaaaaa aaa
```

(2) INFORMATION FOR SEQ ID NO:2751:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: \_ base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2751

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1 gaattccggg ccgggagaac cgaaccctg gcggccgcga ccccggtcc cggccgggcc
61 cgggccgac ccgcatgac ggggtggag gaccaggagt tcgacttcga gttcctctt
121 gagtttaacc agcgcgacga gggcgccgc gcggccgccc cagaacacta tggctatgca
181 tcctccaacg tcagccccgc cctgccgtc cccacggcgc actccaccct gccggccccg
241 tgccacaacc ttcagacctc cacaccgggc atcatcccgc cggcgatca cccctcgggg
301 tacggagcag ctttggacgg tgggcctgc ggctacttcc tctcctcgg ccacaccagg
361 cctgatgggg ccctgccct ggagagtcct cgcacgaga taacctcgtg cttgggcctg
421 taccacaaca ataaccagtt ttccacgat gtggagggtg aagacgtcct ccctagctcc
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(2) INFORMATION FOR SEQ ID NO:2752:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: \_ base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2752

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361 attacatcta tctctcctaa ctgtcatcaa gaattagatg cacatgaaga tgacctacag  
421 ataaatgacc cagaacggga atttttggaa aggccttcta gagatcatct ctatcttctt  
481 cttgagccat cctaccggga gtcttctctt agtcctagtc ctgccagcag catctcttct  
541 aggagttggt tctctgatgc atcttcttgt gaatcgcttt cacatattta tgatgatgtg  
601 gactcagagt tgaatgaagc tgcagcccga tttacccttg gatccccctt gacttctcct  
661 ggtggtctc caggggggtc cctgggagaa gaaacttggc atcaacagta tggacttga  
721 cactcattat cccccaggca atctccttgc cactctccta gatccagtg cactgatgag  
781 aattggctga gccccaggcc agcctcagga cctcatcaa ggccccacac cccctgtggg  
841 aaacggaggc actccagtgc tgaagtttgt tatgtctggg ccctttcacc ccatcactca  
901 cctgttctct cactgtgtca ctccccagg ggaagtgtga cagaagatac gtggctcaat  
961 gcttctgtcc atggtgggtc aggccttggc cctgcagttt tccatttca gtactgtgta  
1021 gagactgaca tccctctcaa aacaaggaaa acttctgaag atcaagctgc catactacca  
1081 ggaaaattag agctgtgttc agatgaccaa gggagtttat caccagccc ggagacttca  
1141 atagatgatg gccttgatc tcagtatcct ttaaagaaaag attcatgtgg tgatcagttt  
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1261 cgcacatctt cattacctc actagactgg cctttaccag ctcattttg acaatgtgaa  
1321 ctgaaaatag aagtgaacc taaaactcat catcgagccc attatgaaac tgaaggtagc  
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1441 gaaaagccaa taaatctaca aatgtttatt gggacagcag atgatcgata tttacgacct  
1501 catgcatttt accaggtgca tcgaatcact ggggaagacag tcgctactgc aagccaagag  
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2041 acagctgcag tgcaggtgca cttttatctt tgcaatggca agaggaaaaa aagccagtct



2101 caacgtttta cttatacacc agttttgctg aagcaagaac acagagaaga gattgatttg  
2161 tcttcagttc catctttgcc tgtgctcat cctgctcaga cccagaggcc ttcctctgat  
2221 tcagggtgtt cacatgacag tgtactgtca ggacagagaa gtttgatttg ctccatccca  
2281 caaacatatg catccatggt gacctcatcc catctgccac agttgacgtg tagagatgag  
2341 agtgttagta aagaacagca tatgattcct tctccaattg tacaccagcc ttttcaagtc  
2401 acaccaacac ctccctgtggg gtcttccatc cagcctatgc aaactaatgt tgtgtacaat  
2461 ggaccaactt gtcttccatc taatgtctgc tctagtcaag aatttgattc agtttggtt  
2521 cagcaggatg caactctttc tgggttagtg aatcttggtc gtaaccactt gtcattccata  
2581 ccatttcatt cttcaaatcc aggtcacaac ggacatctct tagcccatcc accctattct  
2641 gtgcataccc tgcctcatct gcaatcaatg ggatatcatt gttcaaatac aggacaaaga  
2701 tctctttctt ctccagtggtg tgaccagatt acaggctcagc cttcgtctca gttacaacct  
2761 attacatatg gtccttcaca ttcagggtct gttacaacag cttccccagc agcttctcat  
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2881 caatctccta gctcaggaac tggctcatca ccgtctccag ccaccagaat gcattctgga  
2941 cagcactcaa ctcaagcaca aagtacgggc caggggggtc tttctgcacc ttcattcetta  
3001 atatgtcaca gtttgtgtga tccagcgtca tttccacctg atggggcaac tgtgagcatt  
3061 aaacctgaac cagaagatcg agagcctaac tttgcaacca ttggtctgca ggacatcact  
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3181 atttcccaa gtgtcatgaa aaagtctcta tggattgctt attggcatat ggttgggctt  
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3361 agaccagcct ggccaacatg gtgtaacgct gtctctacta aaaatacaaa aaattagcca  
3421 ggcatggtgg tgtgtgacta taatccagc tactcgggag gctgagacag gagaatcact  
3481 tgaacccggg aggtggcagt tgcagggagc taagatcgcg ccattgcact ccagcctggg  
3541 cggcagagca agactccgtc tcgggaaaaa aaaaaaaaaa aaa

1 gaattccggg cggggagaac cgaacccctg gcggccgcca ccccggtcc cgccccggcc  
61 cggccccgac ccgcatgac ggggctggag gaccaggagt tgcacttoga gttcctcttc  
121 gagtttaacc agcgcgacga gggcgccgcc gcggccgccc cagaacacta tggctatgca  
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241 tgcacacaac ttcagacctc cacaccgggc atcatccgc cgccggatca cccctcgggg  
301 tacggagcag ctttgagcgg tgggctgctg ggctacttcc tctcctccgg ccacaccagg  
361 cctgatgggg cccctgccct ggagagtcct cgcactcaga taacctcgtg cttgggctg  
421 taccacaaca ataaccagt tttccacgat gtggaggtgg aagacgtcct ccctagctcc  
481 aaacgggtccc cctccacggc cagcctgctc tcccggagct gcaactcaga ggcctcctcc  
541 tcgtgcttga gcccgccag cagcctgctc tcccggagct gcaactcaga ggcctcctcc  
601 tacgagtcca actactcgt cccgtacgcg tccccccaga cgtcgccatg gcagtctccc  
661 tgcgtgtctc ccaagaccac ggaccccgag gagggcttcc ccccggggtc gggggcctgc  
721 aactgctga gttccccgcg gactcccccc tccacctcgc ccccgccag cgctcactag  
781 gagagctggc tgggtgcccc ctctccaga ccccgctccc cttgcaacaa gaggaagtac  
841 agcctcaacg gccggcagcc gccctactca cccaccact cgccacgccc atccccgcac  
901 ggctccccgc gggtcagcgt gaccgacgac tcgtggttgg gcaacaccac ccagtacacc  
961 agctcggcca tcgtggccgc catcaacgcg ctgaccaccg acagcagcct ggacctggga  
1021 gatggcgctc ctgtcaagtc ccgcaagacc accctggagc agccgcccct agtggcgctc  
1081 aagggtggag ccgtcgggga ggacctgggc agccccccgc ccccgccga cttcgcgccc  
1141 gaagactact cctctttcca gcacatcagg aaggcggtc tctgcgacca gtacctggcg  
1201 gtgcccagc acccctacca gtgggcaag cccaagcccc tgtcccctac gtcctacatg  
1261 agcccagacc tggccgccct ggactggcag ctgcccctcc actcaggccc gtatgagctt  
1321 cggattgagg tgcagcccaa gtcccaccac cgagcccact acgagacgga gggcagccgg  
1381 ggggcccgtga aggcgtcggc cggaggacac cccatcgtgc agctgcatgg ctacttggag  
1441 aatgagccgc tgatgtgca gcttttcatt gggacggcgg acgaccgctt gctgcgcccg  
1501 cagccttct accagtgca ccgcatcaca ggggaagacc tgtccaccac cagccagcag  
1561 gccatcctct ccaacaccaa agtccctggag atccactcc tgcggagaa cagcatgcga  
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1681 ggagagacgg acatcgggag gaagaacaca cgggtacggc tgggttccg cgttcacgtc  
1741 ccgcaaccca gcggccgcac gctgtccctg cagggtggct ccaaccccat cgaatgctcc  
1801 cagcgtcag ctccagagct gcctctggtg gagaagcaga gcacggacag ctatccggtc  
1861 gtgggcccga agaagatggt cctgtctggc cacaacttcc tgaggactc caaggtcatt  
1921 ttcgtggaga aagccccaga tggccaccat gtctgggaga tggaaagcga aactgaccgg  
1981 gacctgtgca agccgaattc tctggtggtt gagatccgc cgtttcgaa tcagaggata  
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2101 cagcgtttca cctaccttcc cgccaacgtt ccaattataa aaacagaaacc cactgatgat  
2161 tatgagcctg ctccaacctg tggaccgggt agccagggtt taagtctct cccaagacca  
2221 tactacagcc agcagctcgc gatgccaccc gacccagct cctgcctcgt ggccggcttc  
2281 ccgccctgtc cgcagagaag caccctgatg ccagcggccc ctggcgtgag cccaagctc  
2341 cagacacctt ctcccgtgc ctacaccaag ggcgttgcca gcccgggcca ctgtcacctc  
2401 ggactcccgc agccggccgg agaggccccc gccgtccagg acgtgcccag gccagtggcc  
2461 acgacccccg gctcggcccgc gcagccacc cggccctgc tgccacagca gtaaatgaaa  
2521 taatacgaat tgacctctcc agcacgagca cccactccta gttgccacat tggagcactc



2581 agttcagcag gggtatgctg acctcagcag acaaagactt ttgaataaat aaactgaact  
2641 cacacctggt accactcaga acctccaact gactgaatgc caggagctga acattaatat  
2701 gtgcaaagat tggtctctcca acaagaagga aagcagggag gaaggagac cactgtgtcg  
2761 cctggaggag aagtcattct atgacaacag aaggagggtg gccgggctga gcacggagac  
2821 ccaccgtgca ggggccttct atgggaacgg cccacacgca gtttgacccc acgccagcc  
2881 cttctggcac ccctggggtt caatactgga agtgccttat ttaaccagac catca

## (2) INFORMATION FOR SEQ ID NO:2753:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2753

1 gaattcccaa ggcgcccccg accgctgct acgcgggggc cgcgccggcg ccctcgcagg  
61 tcaagagcaa ggccaagaag accgtggaca agcacagcga cgagtacaag atccggcgcg  
121 agcgcaacaa catcgccgtg cgcaagagcc gcgacaaggc caagatgcgc aacctggaga  
181 cgacgacaa ggtcctggag ctcacggccg agaacgagcg gctgcagaag aagggtggagc  
241 agctgtcgcg cgagggaatt c

## (2) INFORMATION FOR SEQ ID NO:2754:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2754

1 gtccttcgcg tcccggcggc gcggcgagg ggccggcggt acgcagcggg tgctacgggc  
61 cgcccttata aataaccggg ctcaggagaa actttagcga gtcagagccg cgcacgggac  
121 tgggaagggg acccaccgga ggtccagcc accagcccc tcactaatag cggccacccc  
181 ggcagcgggc gcagcagcag cagcgacgca gcggcgacag ctcagagcag ggaggcccg  
241 cacctgcccc cgggccggag cgggcagccc caggccccct ccccgggcac ccgcgttcat  
301 gcaacgcctg gtggcctggg acccagcatg tctccccctg ccgcgcgcgc gcctgcctt  
361 taaatccatg gaagtggcca acttctacta cgaggcgagc tgcttggtg ctgcgtacgg  
421 cggcaaggcg gcccccgcg cgcccccgcc ggccagaccc ggccgcgcgc cccccgcgg  
481 cgagctggcg agcatcgcg accacgagcg cgccatcgac ttcagcccg acctggagcc  
541 gctggggcg cgcgagcccc cgcgccccgc cagggccacg gacaccttc aggcggctcc  
601 gcccgcgcgc gcccccgcg ccgcctctc cgggcagcac cagcacttc tctccgacct  
661 cttctccgac gactacgggg gcaagaactg caagaagccg gccgagtac gctacgtgag  
721 cctggggcg ctgggggctg ccaagggcg gctgcacccc ggctgcttc cgccccgca  
781 cccaccgccc ccgcccgcgc cgccgcccgc cgagctcaag gcggagccg gcttcgagcc  
841 cgcggaactg aagcggaagg aggagggcgg ggccggggc ggccggcgag gcatggcgcg  
901 gggcttcccg tacgcgtgc cgcttacct cggctaccag gcggtgcga gcggcagcag  
961 cgggagcctc tccacgtct cctcgccag ccgccccgc acgcgagcc ccgctgacgc  
1021 caaggccccc ccgaccgct gctacgggg ggccggggcg gcgccctgc aggtcaagag  
1081 caaggccaag aagaccgtg acaagcacag cgacgagta aagatccgg gcgagcgcaa  
1141 caacatcgcc gtgcgcaaga gccgcgacaa ggccaagat cgcaacctg agacgcagca  
1201 caaggtcctg gagctcacg ccgagaacga gcggctcgag aagaaggtg agcagctgtc  
1261 gcgcgagctc agcaccctgc ggaacttgt caagcagct cccgagcccc tgctcgctc  
1321 ctccggccac tgctagcgcg gcccccgcg cgctccccct gggccggccg gggctgagac  
1381 tccggggagc gcccgcgcgc gcgcccctgc cccncccc nnnccgcaa aactttggca  
1441 ctggggcact tggcagcngg ggagcccgct ggtaatttta atattttat atatatat  
1501 atctatat tggcaaccaa ccgtacatg agatggctcc cgcccggtgt gtataaagaa  
1561 gaaatgtcta tgtgtacaga tgaatgataa actctctgct ctccctctgc ccctctccag  
1621 gcccgcggg cggggcccgt ttcgaagttg atgcaatcg tttaaactg gctgaacgcg  
1681 tgtgtacacg ggactgacgc aaccacgtg taactgtcag ccgggcccct agtaatcgct  
1741 taaagatgtt ctagggttg ttgctgttga tgttttgtt tgttttgtt tttgttctt  
1801 tttgttatta taaaaataa tctatttcta tgagaaaaga ggcgtctgta tattttggga  
1861 atcttttccg tttcaagcaa ttaagaacac ttttaataa ctttttttg

## (2) INFORMATION FOR SEQ ID NO:2755:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2755

1 gaattcccaa ggcgcccccg accgctgct acgcgggggc cgcgccggcg ccctcgcagg  
61 tcaagagcaa ggccaagaag accgtggaca agcacagcga cgagtacaag atccggcgcg  
121 agcgcaacaa catcgccgtg cgcaagagcc gcgacaaggc caagatgcgc aacctggaga

181 cgcagacaaa ggtcctggag ctcacggccg agaacgagcg gctgcagaag aaggtggagc  
241 agctgtcgcg cgagggaatt c  
1 gtccttcgcg tcccgccggc gcggcgagg ggccggcgtg acgcagcggg tgctacgggc  
61 cgcccttata aataaccggg ctcaggagaa acttttagcga gtcagagccg cgcacgggac  
121 tgggaagggg acccaccgga ggggtccagcc accagcccc tctaataag cgccaccgcc  
181 ggcagcgcg gcagcagcag cagcgacgca gcggcgacag ctcagagcag ggaggccgcg  
241 caccctgcgg ccggccggag cgggcagccc caggccccct ccccgggcac ccgcttcat  
301 gcaacgcctg gtggcctggg acccagcatg tctccccctg ccgcgcgcgc cgctgcctt  
361 taaatccatg gaagtggcca acttctacta cgaggcgagc tgcttggtg ctgctacgg  
421 cggcaaggcg gccccgcgg cggccccgc ggccagacc ggccgcgcgc ccccgccgg  
481 cgagctgggc agcatcggc accacgagcg cgccatcgac ttcagcccgt acctggagcc  
541 gctggcgcg ccgcaggccc cggcgcgcgc cagggccacg gacaccttcg aggcggctcc  
601 gcccgcgcgc gccccgcgc ccgcctctc cgggcagcac cagcatttc tctccgacct  
661 ctttccgac gactacgggg gcaagaactg caagaagccg gccgagtac gctacgtgag  
721 cctggggcgc ctgggggtg ccaaggcgcc gctgcacccc ggctgcttc cgccccgca  
781 cccaccgccc ccgcgcgcgc cgccgcgcgc cgagctcaag gcggagccgg gcttcgagcc  
841 cgcggactgc aagcggaaag aggaggccgg ggcccgggc ggccgcgcgc gcatggcgcc  
901 gggcttcccg tacgcgtgc gcgcttacct cggctaccag gcggtgccga gcggcagcag  
961 cgggagcctc tcacgtcct cctcgtccag cccgcccggc acgcccagcc ccgctgacgc  
1021 caaggccccc ccgaccgct gctacgcggg ggccggggcg gcgccctcg aggtcaagag  
1081 caaggccaag aagaccgtgg acaagcacag cgacgagtag aagatccggc gcgagcgcaa  
1141 caacatcgcc gtgcgcaaga gccgcgacaa ggccaagatg cgcaacctgg agacgcagca  
1201 caaggtcctg gagctcacgg ccgagaacga gcggtgcag aagaaggtag agcagctgtc  
1261 gcgcgagctc agcaccctgc ggaacttggt caagcagctg cccgagcccc tgctcgctc  
1321 ctccggccac tgctagcgcg gccccgcgg cgtccccctg ggccggggcg gggctgagac  
1381 tccggggagc gccgcgcgc gcgcctcgc cccncccc nnnccgcaa aactttggca  
1441 ctggggcact tggcagcngg ggagcccgtc ggtaatttta atattttatt atatatatat  
1501 atctatatat tgccaaccaa ccgtacatgc agatggctcc cgcccggtgt gtataaagaa  
1561 gaaatgtcta tgtgtacaga tgaatgata actctctgt ctccctctgc cctctccag  
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1681 tgtgtacacg ggactgacgc aaccacgtg taactgtcag ccgggcccgt agtaacgct  
1741 taaagatgtt ctagggttg ttgctgtga tgtttgttt tgtttgttt tttggtcttt  
1801 tttgtatta taaaaataa tctatttcta tgagaaaaga ggcgtctgta tttttggga  
1861 atcttttccg tttcaagcaa ttaagaacac ttttaataaa ctttttttg

## (2) INFORMATION FOR SEQ ID NO:2756:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2756

1 gaccagagca atttctgctt ttcacaggc gggtttctca acggtgactt gtgggcagtg  
61 ccttctgctg agcagtcac ggcccgaagg cagaactaac tgtgcctgca gtcttctc  
121 tcagatgca gccaggttg gcccaagggg ccacgatgtg gcttgagtc ctgctgacc  
181 ttctgctctg ttcaagcctt gaggtcaag aaaactctt cacaatcaac agtgttgaca  
241 tgaagacct gccggactg acggtgcaaa atgggaagaa cctgacctg cagtgttcg  
301 cggatgtcag caccacctc cagctcaag ctcagacca gatgctgtc tataaggatg  
361 acgtgctgtt ttacaacatc tctccatga agagcacaga gatttattt attcctgaag  
421 tccggtacta tgactcaggg acatataaat gtactgtgat tgtgaacaac aaagagaaaa  
481 cactgcaga gtaccagtg ttggtggaag gactgcccag tcccagggtg aactggaca  
541 agaaagaggc catccaaggt gggatcgtga ggtcaactg ttctgtcca gaggaagg  
601 cccaataca cttcacaatt gaaaaactg aactaaatga aaaaatgtc aagctgaaaa  
661 gagagaagaa ttctcgagac cagaattttg tgatactgga attccccgtt gaggaacagg  
721 acccggtttt atcttccga tgtcaagcta ggtatcttc tgggattcc atgcagacct  
781 cagaatctac caagagtga ctggtcacc tgacggaatc cttctctaca ccaagtcc  
841 acatcagccc caccggaatg atcatggaag gagctcagct ccacattaa tgcaccattc  
901 aagtgactca cctggcccag gagtttccag aaatcataat tcagaaggac aaggcgattg  
961 tggccacaa cagacatggc aacaaggctg tgtactcag catggccatg gtggagcaca  
1021 gtggcaacta cagtgcaaa gtggagtcca gccgcatatc caaggtcagc agcatcgtg  
1081 tcaacataac agaactattt tccaagccc aactggaatc ttccttcaca catctggacc  
1141 aagtgaaag actgaacctg tctgctcca tcccaggagc acctccagcc aacttcacca  
1201 tccagaagga agatcagatt gtgtcacaga ctcaagattt caccaagata gcctcaaagt  
1261 cggacagtg gacgtatatc tgactgcag gatttgaca agtggtcaag aaaagcaaca  
1321 cagtccagat agtcgtatgt gaaatgtct cccagcccag gatttcttat gatgccagt  
1381 ttgaggtcat aaaaggacag accatcgaag tccgttgca atcgatcagt ggaactttgc  
1441 ctatttctta ccaacttta aaaacaagta aagttttgga gaatagtagc aagaactcaa  
1501 atgatcctgc ggtattcaaa gacaaccca ctgaagacgt cgaataccag tgtgtgcag  
1561 ataattgcca tcccacgcc aaaatgttaa gtgaggttct gaggtgaaag gtgatagccc

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1621 cgggtggatga ggtccagatt tctatcctgt caagtaaggt ggtggagtct ggagaggaca
1681 ttgtgctgca atgtgctgtg aatgaagat ctggtcccat cacctataag ttttacagag
1741 aaaaagaggg caaaccttc tatcaaatga cctcaaatgc caccaggca ttttgacca
1801 agcagaaggc taacaaggaa caggaggag agtattactg cacagccttc aacagagcca
1861 accagcctc cagtgtcccc agaagcaaaa tactgacagt cagagtcatc cttgccccat
1921 ggaagaaagg acttattgca gtggttatca tcggagtgat cattgtcttc ttgatcattg
1981 cggccaaatg ttattttctg aggaagcca aggccaagca gatgccagt gaaatgtcca
2041 ggccagcagt accacttctg aactccaaca acgagaaaat gtcagatccc aatatggaa
2101 ctaacagtca ttacggtcac aatgacgatg tcggaaacca tgcaatgaaa ccaataaatg
2161 ataataaaga gcctctgaac tcagacgtgc agtacacgga agttcaagtg tcctcagctg
2221 agtctcacia agatctagga aagaaggaca cagagacagt gtacagtga gtcgggaaag
2281 ctgtccctga tgcggtggaa agcagatact ctagaacgga aggtccctt gatggaaact
2341 agacagcaag gccagatgca catccctgga aggacatcca tgttccgaga agaacagatg
2401 atccctgtat ttcaagacct ctgtcc

```

## (2) INFORMATION FOR SEQ ID NO:2757:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2757

```

1 gaattccggg agaagtgacc agagcaattt ctgcttttca cagggcgggt ttctcaacgg
61 tgacttgtgg gcagtgcctt ctgctgagcg agtcatggcc cgaaggcaga actaactgtg
121 cctgcagtct tcaactctcag gatgcagccg aggtgggccc aaggggccac gatgtggctt
181 ggagtcctgc tgacccttct gctctgttca agccttgagg gtcaagaaaa ctctttcaca
241 atcaacagtg ttgacatgaa gagcctgcg gactggacgg tgcaaaatgg gaagaacctg
301 accctgcagt gcttcgcgga tgtcagcacc acctctcagc tcaagcctca gcaccagatg
361 ctgtttctata aggatgacgt gctgttttac aacatctcct ccatgaagag cacagagagt
421 tattttattc ctgaagtccg gatctatgac tcagggacat ataaatgtac tgtgattgtg
481 aacaacaaag agaaaaccac tgcagagtac cagctgttgg tggaaggagt gccagtgccc
541 aggttgacac tggacaagaa agaggccatc caaggtggga tcgtgagggt caactgttct
601 gtcccagagg aaaaggcccc aatacacttc acaattgaaa aacttgaaaa aaatgaaaaa
661 atgtgtcaagc tgaaaagaga gaagaattct cgagaccaga attttgtgat actggaattc
721 cccgttgagg aacaggaccg cgttttatcc ttccgatgtc aagctaggat catttctggg
781 atccatagtc agacctcaga atctaccaag agtgaactgg tcaccgtgac ggaatccttc
841 tctacacca agttccacat cagccccacc ggaatgatca tggaaggagc tcagctccac
901 attaatgca ccattcaagt gactcacctg gccaggagt ttccagaaat cataattcag
961 aaggacaagg cgattgtggc ccacaacaga catggcaaca aggtgtgtga ctcagtcag
1021 gccatgggtg agcacagtgg caactacacg tgcaaaagtgg agtccagccg catatccaag
1081 gtccagcagca tcgtggtcaa cataacagaa ctattttcca agcccgaact ggaatcttcc
1141 ttcacacatc tggaccaagg tgaaagactg aacctgtcct gctccatccc aggagcacct
1201 ccagccaact tcaccatcca gaaggaagat acgatttgtt cacagactca agatttcacc
1261 aagatagcct caaagtcgga cagtgggacg tatatctgca ctgcaggtat tgacaaagtg
1321 gtcaagaaaa gcaacacagt ccagatagtc gtatgtgaaa tgctctccca gccaggatt
1381 tcttatgatg cccagtttga ggtcataaaa ggacagacca tcgaagtccg ttgcaaatcg
1441 atcagtggaa ctttgcttat ttcttaccaa cttttaaaaa caagtaaagt ttggagaat
1501 agtaccaga actcaaatga tcctgcggtt ttcaaagaca accccactga agacgtcgaa
1561 taccagtgtg ttgcagataa ttgccattcc catgccaaaa tgttaagtga ggttctgagg
1621 gtgaagggtg tagccccggg ggtgaggtc cagatttcta tcctgtcaag taaggtggtg
1681 gagtctggag aggacattgt gctgcaatgt gctgtgaatg aaggatctgg tccatcacc
1741 tataagtttt acagagaaaa agaggcaaaa cccttctatc aaatgacctc aaatgccacc
1801 caggcatttt ggaccaagca gaaggctagc aaggaacagg agggagagta ttactgcaca
1861 gccttcaaca gagccaacca cgcctccagt gtccccagaa gcaaaatact gacagtcaga
1921 gtcattcttg ccccatggaa gaaaggactt attgcagtgg ttatcatcgg agtgatcatt
1981 gctctcttga tcattgcggc caaatgttat tttctgagga aagccaaggc caagcagatg
2041 ccagtggaaa tgtccaggcc agcagtacca cttctgaact ccaacaacga gaaaatgtca
2101 gatcccaata tggagctaa cagtcattac ggtcacaatg acgatgtcag aaacctatga
2161 atgaaccaaa taaatgataa taaagagcct ctgaactcag acgtgcagta cacggaagtt
2221 caagtgtcct cagctgagtc tcacaagat ctaggaaaga aggacacaga gacagtgtac
2281 agtgaagtc ggaaagctgt ccctgatgcc gtggaaagca gatactctag aacggaaggc
2341 tcccttgatg gaacttagac agcaaggcca gatgcacatc cctggaagga catccatgtt
2401 ccagagaaga cagataatcc ctgtatttca agacctctgt gcacttattt atgaacctgc
2461 cctgtctcca cagaacacag caattcctca ggctaagctg ccggttctta aatccatcct
2521 gctaagttaa tgttgggtag aaagagatac agagggg

```

## (2) INFORMATION FOR SEQ ID NO:2758:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2758

```
1 cccgggttca agcgattctc ctgcctcagc ctcttgggta gctgggatta taggcgtgtg
61 ccaccgtgcc tggctaattt ttgtattttt attggaagaca gggtttcacc atgttggcca
121 ggctgggtctg aaactcctga cctcaggcaa tcctcctacc tcagcctctc aaagtgcctgg
181 gattaccggc atgagccacg actcccggcc ccaaaggcca atcttaaagc tacaaggtat
241 cttttaaaag gagtaggaat aacgtatttt gaggcctaaa ggagtaggaa tagtgtattt
301 ttagatttga agccatcttc taaagggtac gatatttggg taacatgtca ctccctatcg
361 ccattggaaga agttaattct attctttttt tttttttttt gagatggagt ctcaactctgt
421 tgcccaggct ggagtacaat ggtgtgatct cagctcactg caacctctgc ctccctgggtt
481 caagcaattc tcctgcctca gcctcctgag tagcagggat tacaggggtt ctccaccatg
541 cctgtctaat tttgtattt ttttttttag tagagggtga gtttcacatg gttggtcagg
601 ctggtctcaa acccctaacc tcatgatccg cccgccttgg cctcccaaag tgctgggatt
661 acaggcgtga gccaccatgc ccagccgtta attctattct tactgcttac tcccttattt
721 tgtatgttct tcttctatct tacatctttt gcttttgcta ttgcttaagc tagcctacgc
781 caagggtgct ctttgccttc tacttctctc gctattctcg cctcagttcc gctgcattcc
841 aagctcagcc tgcccagca gcaggtctct ttgacaaacc tgcaattttg gggaaaagtc
901 agccccaaga aaggcagggg gccagactt atgctgtgtg gcaaaagccc tctttgatgg
961 gggaagggga ggactggaaa agcagagaga tcttctgga tgcctggga gacagccct
1021 ttgggtggtg ggtggaggct ggaggcaggg aggaatcccc tcacagtgcc atgagaaggg
1081 cccccaacc caggcgagac agaggaggg tcaagaacgc caaggcaaat gtcacttgtg
1141 ccttgtttt tccctaaaga aactaaacaa agcggccgcg ttcggtggcc cctcaggaag
1201 gccggtcatt tctgaggag atatcaggcc agcccaggcc ccattgttcc cgtttccag
1261 ccattggctgc cattacctga ccagcgccac agccggtctc tctgcaggcg ccgggagaag
1321 tgaccagagc aatttctgct tttcacaggg cgggtttctc aacggtgact tgtgggcagt
1381 gccttctgct gagcagtcga tggcccgaag gcagaactaa ctgtgcctgc agtcttcact
1441 ctcaggatgc agccgaggtg ggcccaaggg gccacgatgt ggcttgaggt cctgctgacc
1501 cttctgctct gtgagtgtt actctgttcc cacatcactt taactccatg agcatcgaa
```

## (2) INFORMATION FOR SEQ ID NO:2759:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2759

```
1 gaattccggg agaagtgacc agagcaattt ctgcttttca caggggcgggt ttctcaacgg
61 tgacttgtgg gcagtgcctt ctgctgagcg agtcatggcc cgaaggcaga actaactgtg
121 cctgcagtct tcaactctcag gatgcagccg aggtgggccc aaggggccac gatgtggcctt
181 ggagtcctgc tgacccttct gctctgttca agccttgagg gtcaagaaaa ctctttcaca
241 atcaacagtg ttgacatgaa gagcctgccg gactggacgg tgcaaaatgg gaagaacctg
301 accctgcagt gcttcgcgga tgtcagcacc acctctcacg tcaagcctca gcaccagatg
361 ctgttctata aggatgacgt gctgttttac aacatctcct ccatgaagag cacagagagt
421 tattttattc ctgaagtccg gatctatgac tcagggacat ataatgtac tgtgattgtg
481 aacaacaaag agaaaaccac tgcagagtac cagctgttgg tggaaggagt gccagtcctc
541 agggtgacac tggacaagaa agaggccatc caagggtgga tctgtagggt caactgttct
601 gtcccagagg aaaaggcccc aatacacttc acaattgaaa aacttgaact aaatgaaaaa
661 atggtcaagc tgaaaagaga gaagaattct cgagaccaga attttgtgat actggaattc
721 ccggttgagg aacaggaccg cgttttatcc ttccgatgtc aagctaggat cattctcggg
781 atccatagtc agacctcaga atctaccaag agtgaactgg tcaccgtgac ggaatccttc
841 tctacacca agttccacat cagccccacc ggaatgatca tggaaggagc tcagctccac
901 attaagtgca ccattcaagt gactcacctg gccaggagt ttccagaaat cataattcag
961 aaggacaagg cgattgtggc ccacaacaga catggcaaca aggctgtgta ctcagtcatg
1021 gccatggtgg agcacagtgg caactacacg tgcaaaagtgg agtccagccg catatccaag
1081 gtacagcagc tcgtggtcaa cataacagaa ctattttcca agcccgaact ggaatcttcc
1141 ttcacacatc tggaccaagg tgaaagactg aacctgtcct gctccatccc aggagcactt
1201 ccagccaact tcaccatcca gaaggagat acgatttgtt cacagactca agatttcacc
1261 aagatagcct caaagtcgga cagtgggacg tatatctgca ctgcaggat tgacaaagtg
1321 gtcaagaaaa gcaacacagt ccagatagtc gtatgtgaaa tgctctccca gccaggattt
1381 tcttatgatg cccagtttga ggacagacca tcgaagtccg ttgcaatcg
1441 atcagtggaa ctttgcctat ttcttaccaa cttttaaaaa caagtaaaat tttggagaat
1501 agtaccaga actcaaatga tcctgcggtg ttcaaagaca accccactga agacgtcgaa
1561 taccagtgtg ttgcagataa ttgccattcc catgccaaaa tgttaagtga ggttctgagg
1621 gtgaagggtg tagccccggt ggatgaggtc cagatttcta tcctgtcaag taagggtgtg
1681 gagtctggag aggacattgt gctgcaatgt gctgtgaatg aaggatctgg tcccatcacc
1741 tataagtttt acagagaaaa agagggcaaa cccttctatc aaatgacctc aaatgccacc
1801 caggcatttt ggaccaagca gaaggctagc aaggaacagg agggagagta ttactgcaca
```

```

1861 gccttcaaca gagccaacca gcctccagt gtccccagaa gcaaaatact gacagtcaga
1921 gtcattcttg ccccatggaa gaaaggactt attgcagtgg ttatcatcgg agtgatcatt
1981 gctctcttga tcattgcggc caaatgttat tttctgagga aagccaaggc caagcagatg
2041 ccagtggaaa tgtccaggcc agcagtacca cttctgaact ccaacaacga gaaaatgtca
2101 gatcccaata tggaagctaa cagtcattac ggtcacaatg acgatgtcag aaaccatgca
2161 atgaaaccaa taaatgataa taaagagcct ctgaactcag acgtgcagta cacggaagtt
2221 caagtgtcct cagctgagtc tcacaaagat ctaggaaaga aggacacaga gacagtgtac
2281 agtgaagtcc ggaaagctgt ccctgatgcc gtggaagca gatacttag aacggaaggc
2341 tcccttgatg gaacttagac agcaaggcca gatgcacatc cctggaagga catccatggt
2401 ccgagaagaa cagataatcc ctgtatttca agacctctgt gcacttattt atgaacctgc
2461 cctgctccca cagaacacag caattcctca ggctaagctg ccggttctta aatccatcct
2521 gctaagttaa tgttgggtag aaagagatac agagggg

```

## (2) INFORMATION FOR SEQ ID NO:2760:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2760

```

1 tcttttggtt ttgctattgc ttaagctagc ctacgccaag ggtgctcttt gccccctact
61 tcctctgcta ttctcgcttc agttccgctg cattccaagc tcagcctgcc ccagcagcag
121 gtctctttga caaacctgca attttgggga aaagtcagcc caagaaaaggc agggggccca
181 gacttatgct gtgtggcaaa agccctcttt gatggggcaa gggtaggact ggaaaagcag
241 agagatcttt ctggatgtcc tgggagagca gccctttggg tgggtgggtg aggctggagg
301 cagggaggaa tccccacaca gtgagaaggg cccccaacc caggcgagac agagggaggg
361 tcaagaacgc caaggcaaat gtcacttgtg cctgtttttt tccctaaaga aactaaacaa
421 agcggccgcg ttcggtggcc cctcaggaag gccggtcatt tcctgaggag atatcaggcc
481 agcccaggcc ccattgttcc cggttccag ccattggtgc cattacctga ccagcgccac
541 agccggtctc tctgcaggcg ccgggagaag tgaccagagc aatttctgct tttcacaggg
601 cgggtttctc aacggtgact tgtgggcagt gccttctgct gagcgagtca tggcccgaa
661 gcagaactaa ctgtgcctgc agtcttcact ctcaggatgc agccgaggtg ggcccaaggg
721 gccacgatgt ggcttgaggt cctgctgacc cttctgctct gtgagtgttt actctgtttc
781 cacatcactt taactccatg agcatcgaag cttctggaat caacatgttt cttatgtttc
841 ttgcaggttc aagccttgag ggtcaagaaa actgtaagtc tgatgtttcc actgtaacag
901 atgtttctac ctggcttccct cctttctctt ctgtgatgcc taaaacgcac attaaattgc
961 tgggttttga tacttctaac aattaaggaa aagaatccaa ttgagaacta aagtttatcc
1021 catgtgggca tttttagaaa ggcttagatc taagccaagt tctggtcagt gtgttttaga
1081 agtagcacac gtttccttgg ctggtctgaa agtagtgggt tatcttgatg aattgtttag
1141 tcagttacag atcaaaactcc atgttctttt ctctgttctc acgactactc ttgactagtc
1201 taaaaatata ttaggttggt gaaaagtaat tgtggttttt gccattactt tttaaaagat
1261 ggcaaaaaac acaattataa gtagcacaca ttttcttttt ttttctctt tttttttgag
1321 acagagtctc tgttaccagc gctggagtgc agtggtgcaa tccggctctc tgcaaacctc
1381 gcctccaggg ttcaagggat tctcctgtct cagcctcctg ggctgctgga attagagg

```

## (2) INFORMATION FOR SEQ ID NO:2761:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2761

```

1 ttggcaggct ggtctcaaac tctgacctc aggtgatccg ctggcctcca cctcccaaag
61 tgctgggatt acaggtgtga gccaccacgc ccggcctcac attttctaga tttcagtgca
121 ttgctgtttt ttgggatggg gaagtgattt ttttatttta atgagcaatt ccataattag
181 ttttttggtg ttttaccata atggcttatt tgaatattgt aaggtatccc caactgtttt
241 tttttgcaaa tgagatataa ttgatttggt agacatatga agacagatcc tagtttaaat
301 tgttgctact ttttttactc ctaaatgata aaaatcacac actcagatcc

```

## (2) INFORMATION FOR SEQ ID NO:2762:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2762

```

1 ttggcaggct ggtctcaaac tctgacctc aggtgatccg ctggcctcca cctcccaaag
61 tgctgggatt acaggtgtga gccaccacgc ccggcctcac attttctaga tttcagtgca
121 ttgctgtttt ttgggatggg gaagtgattt ttttatttta atgagcaatt ccataattag
181 ttttttggtg ttttaccata atggcttatt tgaatattgt aaggtatccc caactgtttt
241 tttttgcaaa tgagatataa ttgatttggt agacatatga agacagatcc tagtttaaat

```

301 tgttgctact ttttttactc ctaaagtata aaaatcacac actcagagctc

## (2) INFORMATION FOR SEQ ID NO:2763:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2763

1 gctgtccac agcccaccct tcatcacaat agtcctgaaa ctttttgggt tcagtaagga  
61 aatctgtggg ctttctctcc agaaaaagca cacatttgca cacaattgga ggtagttgat  
121 gagctccta acaccaccc atgcacctcc caggggctgt gtcccccagg ttgtgaacag  
181 tcaactctgtg taaatagtga gacctacagg cagtaattca gtttggtgtg gcttggtgg  
241 tttattttaga aagatgataa tgttt

## (2) INFORMATION FOR SEQ ID NO:2764:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2764

1 gagctctcca agggcagaca ctgccagcct cactgttctc tgaacccccca gtatgggaca  
61 gtgcttgga cagaaaaacc cccttaaag tttgctatga atgggtgcta ggaagaaggc  
121 agagaatgtc aaccagaggc caggcactgg caatatatac acggcccc

## (2) INFORMATION FOR SEQ ID NO:2765:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2765

1 ataccttggc tcaactgcaac ctctgcctcc caggttcaag cagttctcct gcctcagtc  
61 cccaagtagc tgggattaca ggcgccacc accacaccgc gctaattttg tatttttagt  
121 agagatgagg ttccaccatg ttggccaggc tggcttgaa ctctgacct caagtgatcc  
181 acccgctcg gcctcccaaa gtgctgggat tacaggcata aaccaccgtg cccggtggt  
241 cca

## (2) INFORMATION FOR SEQ ID NO:2766:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2766

1 gagctcatcc agcaggcttc ttaaatcagg agcttgtaag ttgcatataa agacaaaaaa  
61 gggagttcca aagagtaatg ctgtgggaaa tgacttgaat ttaaaccgtc acctgtttg  
121 atctcatgga ctggtcagac accatttttg ttgtcgttgt tgttgtaaaa ttaattgctc  
181 agaatatagc agcaggcgca aattgtagta ctctgtttta aattgaagat taaattttta  
241 attacccaac aaaggcctaa ctttgtaaaa ag

## (2) INFORMATION FOR SEQ ID NO:2767:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2767

1 gaattctacc gacagcctat gggtactgga tataagccaa ttctgttctg gggacttgcc  
61 agaaatgaca caattggcca gttgaccac agcctagttc ctacgagaga ttggatagct  
121 gattgagcgt tgtggctgtt ttgaggcttg accagagatt cctgccgttg gcagagggga  
181 atctgtagtc tttgttctt ggtagcaggt gaggctgaaa acgcaagtag caggctaaaa  
241 actgggttca agtcctcacc atctggtgaa acctcagagc ccatcagata gaaaaagcca  
301 gctgggactg tgctaattcg gtaaggcctg ggtggagaag gagggcctgg gcacgaccat  
361 ctggtttcgg aatggaggta gcagtcattt attaatgact taatgtatat cgggcactgt  
421 acaggagacg ttctggctgt tctcctgtac atttctgca aagacctaag gagatatgat  
481 tactccatcc tacaggtaag gaaactgagc tcagagagtc tagctgcccc gggtcacaca  
541 gtaaatgatg agccaggact tgaacacttg actgcttgaa tctgtactc cctccagggg

```

601 ccaagatgtg gcagctcaca gaatgcctat atcttttttt ttttttgtct tttgagacag
661 tctcactctg ttgccaggc tggagtgcag tggtagatc tcacctcact gcaacccccg
721 cctcccaggt tcaagtgtt cttgtgcctc agcctctcaa gtagctgggt tacaggcctg
781 caccaccaaa cctggctaatt ttttgtattt ttagtagaga ggggggttca ccatgttggc
841 caggccagtc tctaactgtc gacctcaggt gatccacca ccttgggtctc ccaaagtgtc
901 gggattatag gcgtgagcca ccatacctag ctctacatct ttatcactct gttcctttgc
961 cttgggtggga aaagtgtgag cttagtacca actgcctcct gcttgagcca ctgtgcacag
1021 ttactatcag cctggccctg taggcacgta gaacccctgg actcaatact gcataggatg
1081 ggataagacc acatctgtat tgggtgaaggt caccgggatg atgtgttttc tgagataaca
1141 ggtatgtctg ccttccttcg ggttgcattt agctttcaca atcaacagtg ttacattgaa
1201 gagcctgccc gactggacgg tgcaaaatgg gaagaacctg accctgcagt gcttcgcgga
1261 tgtcagcacc acctctcagc tcaagcctca gcaccagatg ctgttctata aggatgacgt
1321 gctgttttac aacatctcct ccataagag cagagagagt tattttatcc ctgaagtccg
1381 gatctatgac tcagggacat ataaatgtac tgtgattgtg aacaacaaag agaaaaccac
1441 tgcagagtac cagctgttgg tggaaagtgta gtccttgga ctagcacag gcaagcagat
1501 ggagcatagc acacagtggc gtgaataaca gctgtgaatg aatagtgaac ctggacttaa
1561 ctctccaccc atcaccctct cattcatctg cctggcattt tccttacctg aatagctaag
1621 cactagacat attccccaat aggcaggccc ttcttctcct ccttctctcc ttcttctctt
1681 ccttctctcc ttcttctctt ccttctctcc ttcttctctt tctttgatgt agtctcactc
1741 tgtcaccag tctggagtgc agtgggtgat ctgggtcac tgcaacctgt gcttcccagg
1801 ttcaagcgat tctctgcct cagcctccca agtaattggg attacaggtg tgtgccacca
1861 cacctggcta atttgtatt tttagtagag atgggggttc actgtgttgg tcaggctggg
1921 ctggaactct gacctcaagt gatccacctg cctcccaaaa tgcttcttca tctcgctcta
1981 taaattacaa tttcttctt caagactcaa ctcaatgatg ttttgcaaaa acaaaatggg
2041 tctaccccag ggtgccagtc agtacagctc tggatgctct tctacaggca atggtatttg
2101 tgtgtataaa ggccacagcg gtgtgttaag acacctcgtt ctgcagtcac tctgcctggg
2161 tttcaatctt ggtcaagtc cttaacatgc tctaaacttc aaaatcctca ccagtaaaag
2221 gaagataaca acgataccca tttcaggcaa ttattgagag ggttaaaagt gtcattgtggg
2281 tagagtgtt agcaaaatct ccagcaccta gtgagttcct aataaataga aatgtattta
2341 tttatttgag acagagtctt cctctgtcac ccaggctaaa gagcaatggc gcgaccttgg
2401 ctcaactgaa cctctgtctc ctgggttcaa gcgattctcc tgtctcagcc tcccagaaa
2461 ctgggattac aggcacgcgc cactgtgcct ggctaatttt ttgtattttt agtaaggatg
2521 ggggtttacc atgttggcca gcctgtgtct gaactcctaa cttcaagtga tttaccacc
2581 ttggcctccc agagtgtcag gattacaggt gtgagccacc atgcccgtgc cacaaatatt
2641 ctatttctc cagtattggc atccgttctt acacatctgt ctgctcttct ggatagtga
2701 attgtaaaga cagagatggt gtttgggttt attcttatat cttgaacaat gaatctggct
2761 catagtaggc attcagtcaa tgttcatgga ataaattaaa gtcagtccta gcctgtgggt
2821 gcattcaata aagggttaaca acaatcacag tgacactgac aaatactggg ttacttttcc
2881 cctctaagca tcatctgttg ggaatctgat tgtgtcctct tcccaatagg attataaacc
2941 attgaaaaca ccaagtacat cttgaccata ttttattttt taaatttatt tatttattta
3001 tttattttatt tttagacaga gtctcactct gttgcccagg ctggagggca gtggcacgat
3061 ctcaagctcac tgcaacctct gccttcgggg ttcaagcaat tctcctgcct cagcctccaa
3121 gtagctggga ttacaggtgc ctgccaccat gccggctaatt tttgatttaa tagagatggg
3181 gttcgccatg ttggccaggc tgggtctcaa ctctgacct caggtgatcc acctgcctca
3241 gcctcccaaa gtgttgagat tacagatgtg agccacctcg cgtggcctta gtgtgattt
3301 tgggtggacc atcaccagag cagtgtacac tgtacctagt gtgtagtcat tttatccctc
3361 gctccctccc actctttccc ctgagtcctc aaagtcact gtatcattct tatgccttgg
3421 ttctctcata gcttagctcc cattgagcat attttatatt ttttcttctc ttttcttctc
3481 ttttttgaga cagggtctct gttgccagg ctggagtga gtgggtggat tactgtctac
3541 tgccgcctca acctcctagg ctcaagtgat tctccacct cggcctccca agtagctggg
3601 actaccagtg cacaccacta actacccctg gctaatttta atttttttt ttgtagagat
3661 agcatttcac cgtgttgccc aggtgtgtct ccaactcctg ggctcaagag atccaccac
3721 ctcagcctcc agattttata tatttcaag tgccatgtac tgtgtgtggc acatacctgt
3781 tcatattatta cctggttagt cgactgggt gttcagagaa caaaaaagag ccctctcatg
3841 ggatcaacta cagtactca gcggagggga gggctgtgt ctctcaatca ggctgatact
3901 gacagacttt cttcttcaat caggctgata ctgacatgac tttctacttt ccccgtagga
3961 gtgcccagtc ccagggtgac actggacaag aaagaggcca tccaaggtgg ctactgtagg
4021 gtcaactgtt ctgtcccaga ggaaaaggcc ccaatacact tcacaattga aaaacttgaa
4081 ctaaatgaaa aaatgggtcaa gctgaaaaga gagaagaatt ctcgagacca gaattttgtg
4141 atactggaat tcccgttga ggaacaggac cgcttttat ccttccgatg tcaagctagg
4201 atcatttctg ggtccatat gcagacctca gaatctacca agagtgaact ggtcaccgtg
4261 acgggtcagc atctgtctcc ttctcatcgt ttcttgggtg tttctggg

```

## (2) INFORMATION FOR SEQ ID NO:2768:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: \_ base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2768

```

1 gttctagaga agaaagggtg aattttaaag ttagttagga acaatagaaa agtttgaaaa
61 ggggaagcag caaaaagagc agaagaggct cctcttgccc aggtttgcac ctgagtccaa
121 ccagggtgtc ttctctctct gcagaatcct tctctacacc caagttccac atcagcccca
181 ccggaatgat catggaagga gctcagctcc acattaagtg caccattcaa gtgactcacc

```

```

241 tggcccagga gtttccagaa atcataattc agaaggacaa ggcgattgtg gcccaacaac
301 gacatggcaa caaggctgtg tactcagtc tggccatggt ggagcacagt ggcaactaca
361 cgtgcaaaagt ggagtcacag cgcataatcca aggtcagcag catcgtggtc aacataacag
421 gtagggtgtg tgctgccgga ggggtgtggc atatggcggg ctcaagaggc caccatgctg
481 caatccagca tggccaaaga gagctgatca tttcctgccc ctgcttatct gaatgaatgt
541 gctcagatgg ggcttgggtg ctctgtggag gaaaccactg cagagcgagt taacagtcta
601 ctgtgcgtgt tgagggtaca ggctccggca ccaaagctta accctgccgc tcaactgttc
661 tgtgaccttg ggtgagttat tgaacgtgcc gcagcgtgt gagatggta taatgacctt
721 ttaggactgc tataatgatt aatgagataa ctatactgta agcatgagct gagagatttg
781 tacagagtaa gactctgaaa cactgtgtaa tgttttcatt actctgttat atttctccat
841 cccctgtgac aagcactatg ctatgac

```

## (2) INFORMATION FOR SEQ ID NO:2769:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2769

```

1 gaattccggc ctgtgaatcc atctggttct tggacttttt ttggttggtg agctattgat
61 tattgccaca atttcagatc ccgttattgg tctattcaga gattcaactt cttcctgggt
121 tagtcttggg agagtgtgtg tgttgaggaa tttatccatt tctcctagat tttctagttt
181 atttgcgtag aggtgtttgt agatattctc tgatggtagt ttgtatttgt gtgggatcgg
241 tgatgatac ccctttatca ttttttattg cgtgtatttg attcttctct ctttttttct
301 ttattaggct tgctagcggg ctatcaattt tgttgatcct ttcaaaaaac cagctcctgg
361 attcattaat tttttgaagg gttttttgtg tctctatttc cttcagttct gctctgattt
421 tagttatttc ttgccttctg ctagcttaag gagtttcatt cttgttgccc aggtcggagt
481 gcagtggagc aatctcggt cactgcaatc tctgtctcct gggttcaagg gattctcttg
541 cctcagcttc ccgagtatct gggattacag gcgccacca ccatgctggc taattttata
601 tttttagtag agatggggtt tcaccatgtt gccaggctg gtctcaactc ctgacctcag
661 gtgatccacc cactctgcc tcccaaagt ctgggattac aggcattgagc caccacacct
721 ggccacaagt tgcaaaactt ttctaactct tgtcattgaa ataaattgga ttaacaagaa
781 aggaaaaact gccattggaa tcctaggcaa agaattgaacc ctagctcctt actgggggtg
841 tcgttaggta catgagaagc aaaggaaaac tttttgctgg aagttggaag ttggttctgc
901 caagagcacc tgagccaagg gcctctccag gaagggtctt tagggtgggt gccagacaca
961 tctcgctcca ttccactca ctgtttttca gaactatttt ccaagcccg aactggaatct
1021 tctttcacac atctggacca aggtgaaaga ctgaacctgt cctgctccat cccaggagca
1081 cctccagcca acttcaccat ccagaaggaa gatacgattg tgcacagag tcaagatttc
1141 accaagatag cctcaaagtc ggacagtggg acgtatatct gcactgcagg tattgacaaa
1201 gtggccaaga aaagcaacac agtccagata gtcgtatgtg gtgagtatat tgttgcgact
1261 cagaggacat ccggggttga atgggagaaa ggaaatttat ctgcagctgc cgccctctcc
1321 ggtctccggg ctgagcagac tcaggcaggg taagaactag agggagagaa gtgcgaaatc
1381 aaaggccaaa gaaacaagga ggtattcctg ctcagaacac tgattcactg atgatgatgt
1441 ggcctctgac ttgcaagatt ctggcaagat tctgcctcct ggagcaagac ccacccaaaa
1501 gtccaggaag gaaacactac ttagtcaatg ttaaactttt cttttttttt tttgagacgt
1561 gtcgccagg ctgagtgaca gtggcacgat agctcactgc aacctctgcc tcttaggttc
1621 aagtgatctc ctgcctcagc ctcccaagta gctgggatta caggtgcccc ccaccacgtc
1681 tgctctaattt ttgtattttt atttttatta cttttattta tttattttt tattttttt
1741 cggctctgtc cccaggctgg cagtgccagt ggcacaatct gggcatcact ggaaagcatc
1801 cgcactcctg ggtacacgag cattctcctg cctcagccct cccaagtggt tgtggactac
1861 aggcacacac gt

```

## (2) INFORMATION FOR SEQ ID NO:2770:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2770

```

1 tcacttgagt ccaggagtcc aagaccagcc tgagcacata gtgagacct gtctctacaa
61 aaaataaaga attagccagg tgtggtgtgc acctatagtc ccagctactc gggagggtga
121 ggtaggagga ttgcttgatt ctgggaggtt gtagtgagct gtcacgcac cagtgcactc
181 cagcctgggt aatagagtga gacctgtct caaatacaca cacacacaca cacacacaca
241 cattttgttg gctacttgtt gtacttttct tatgttttct gtgtctttgc tcaacacaa
301 aaaagtatat tatgtgtgca tgtgcgtgtg agatattgta aaatatgaac atgtatttct
361 ggggatgtaa tgttttctct gaatttctgt cattctctgt tttgcttatt gtacttctct
421 ttccctttcc cttctcacca cacacacaca cacacacaca cacacacaca cacagcctgt
481 cagtctcata ggtgtcctat aaaggtaaat ggcaggcagg catttgaaat tacagcaggg
541 atagaagca aaactcaggc tttggaggag gaacctcttg tgctggatgc tttgttttta
601 cttcagtgcc cttttggatt gtttctccct ctgttctaga aatgctctcc cagccaggga
661 tttcttatga tgcccagttt gaggtcataa aaggacagac catcgaagtc cgttgcgaa
721 cgatcagtg aactttgcct atttcttacc aacttttaaa aacaagttaa gttttggaga
781 atagtaccaa gaactcaaat gatcctgcgg tattcaagaa caacccactc gaagacgtcg

```



841 aataccagtg tgttcagat aattgccatt cccacgcaa aatgttaagt gaggttctga  
901 ggggtgaaggt gataggttaag ttgctgtgct gtgagaagaa atcatgtggg cttggggcat  
961 tcttttcaccc ccagggactg tggggacaat aagagaagta gggggccagg tgcggtggct  
1021 catgcctgta atcccagcac tttaggaggc caaggccggt gaatcattga ggccaggagt  
1081 tcaagaccag cctggccaac atggtgaaac cccatctcta ctaaaaaatc aaaaatttagc  
1141 tgggcatgat ggcgtgcgcc tataatccca gccactcggg aggctgaggc aggagaattg  
1201 cttgaaccca ggaagcacag gttgcactga gccaaagtgc gccattgcac tccagcctga  
1261 gcaacaagag cgaactcca tctaaaaaaa aaaaagcgag agaagtagtg ggtgcttatg  
1321 caaagtccat atactagata tgaccaaaag caggggcaag gttcagtaaa ggaggctgga  
1381 aaatatttgg gggctattga tgaggacaat ataactctct tccagaacct tccaacaaac  
1441 tgctaaaaaga tgataagcat gaaagtgtcc tgactgcagg aagcactgaa gttgtgcata  
1501 tgggcttccc ttagcacttt ctcttttca gatacactgt tctgagaatt gtagatcagg  
1561 actctgtctg tgtgactcct agccggggaa ccctgccttg tgtgaattcg agattagcct  
1621 ggccaacatg gtgaaatcct gtctctaata aaaatacaaa aaattagctg ggtgtgggtg  
1681 tgggcacctt taatgccagc tactcgggag gctgaggcac aagaatcatt tgaacctggg  
1741 aggcagaggc tgcagtgagc caatatcatt ccgctacact ccagcctggg caacggagca  
1801 agactccatc tcaaaaaaaa aaaaaattaa cattacatag actaagcacc taatggtgtg  
1861 aggcatacaa aaaagaagac atattctttg tttcaatgct gtggaagaa acacaagctc  
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1981 ttgggggtca tgtttggttgcacgtgaaac tatatcctta cagtgatggt gatagtaatt  
2041 tagggatgac cagacttcat ctacttaag tgggtaaaac ttgtgaaaaa gctgggctag  
2101 gtgccagggc ttgagaatgg gtggccagag aaggctgaag atggctgaac atctccagca  
2161 aacacatgag ccaaaaggtc ccattgggca cttcaaaaga ctgtgcgcag ccaggtgcgg  
2221 tggctcacgc ctataatccc agcactttgg gagaccgaat ggggtggatc acttgagccc  
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2341 attagccagc cgtggtggtg ggtgtcctgt agccccagct actcaggtg ctgaggtggt  
2401 agaatacatt gaatccagga ggcagaggtt gcagtgcagc aagatcgtgc cactgcactc  
2461 cagcctgggt gacagagtga gactctatct ccacaaaaaa aaaaaaatta atggagaatc  
2521 aaggactgtg gccaaatcag atggctggaa acaaaggctg gagtttggga gtgaggaatc  
2581 accggatatg agctgaaaaa gtggctgagc ctaagcgtga caggtgtcag gtgccagctc  
2641 caggagttag caattgtcct gcatgcagtg aaaagccaga agatggaagg aaggacagga  
2701 tgcaaatgag ttctcggaac gatccacctg gtggctgggt cagggagcag gcatggtgac  
2761 ttcagacctc atggtacgtt agaggctaat gtgaagccca tgtgaagctg ttggtttaa  
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2881 gtagtaaaatt gctccaatgg aaactcacia taaccacaga aggccagtaa cagcattgtc  
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3001 gattttgagc cactggtgtc ccaggcccg agcttggctt ctccattgt cttaccacag  
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3181 atggagctag gaaaagcggg tacaggaggt agccaaagttc tgcttgacc tgcagggagt  
3241 gaggtggcc gggctccagg tggaaatccc caggtgaaaa gggagacttg gagtccagga  
3301 aagtaacctg gactggagcc ataggtttag gtgtcagtgg ctgagagaca gaagctcagc  
3361 gtgtaggtga aatcacccag gaggagaatg gggatggaaa actgaggatt gaattttgca  
3421 aaatgttcat acttccgggg aaaacaaaga ataaccagt aataagaaag ggggtccagg  
3481 taagaaggga agagaatcag agtcatgagg aacccagaaa ccccgaaaaa agctgagttc  
3541 cacgtaagac ctgggcaaca gtgaagtatg gagagcccaa gattgggagc gtggaggaa  
3601 agcatccacc actgaattta atcagcccg gactcagggc cgttggttg ggaatcaagt  
3661 gaccttccca gtttcttcaa aacttgagag agagtgcagt gtcacaagat tgtgactaca  
3721 aaagagtga gtcagatttc aggggtaaca agaaagtgtg aaataaggga gtcaaagcat  
3781 aaaggaaaaa ggagaaaaaa tggccgatag cttagagaagg cgtgggtcaa gattgtctgt  
3841 ggcctggcat ggtggttat gcctgtaac ccagcatttt ggaaggccga ggtggcaaa  
3901 tcacctgagg tcaggaaattc aagaccagcc tggccaacag ggcaaaaccc cgtctctaaa  
3961 acaacaacaa caacaaaaaa atccaaaaag ttagctgggc ctggtgggcg cacctgtcat  
4021 tccagctact cgggaggctg aggcaggaga tttgcttgaa cccaggaggc acacgttgcg  
4081 gtaagctgag attataccac tgcactccag cctgggtgat aagagcggga cctctgtcca  
4141 gaggaaaaaa aaaaaagtgg agcagtggct gtctcatgtt cctctctctc tgcccttct  
4201 tgctcagtgt gaatcctttt cctgcttttc agccccgggt gatgaggttc agatttctat  
4261 cctgtcaagt aaggtggtgg agtctggaga ggacattgt ctgcaatgt ctgtgaatga  
4321 aggatctggt cccatcacct ataagtttta cagagaaaaa gagggcaaac ccttctatca  
4381 aatgacctca aatgccacc aggcattttg gaccaagcag aaggctaaca aggaacagga  
4441 gggagagtat tactgcacag ccttcaacac agcccaagtg gctccagtg tccccagag  
4501 caaaatactg acagtcagag gtgagtcagg gtctccatag caagctgtgc tgtgggcccc  
4561 caagggcaag accagaaaaa accccccttg taagaggag tttgggggga gtctagctta  
4621 tgtgactgaa ggctaggaga gtaatgtcct ccaggtctct ggttgcaagt gatgaaaacc  
4681 cactcaaat aagtaaaaaa gagaatacga ttattataag gaattgggag aatgtcacat  
4741 cgttccaatt acaaatgtt ggcagactca ccattgagtc atcttgggtc aaacatccaa  
4801 ccacagacca cctgtagcca aggggattgg gtcacgcaga acagacatga ttggggaacc  
4861 acttatgtgg gtgtgggggc ggtttcctgg agaagaagag ggctgaaaac acatgccaaa  
4921 aaggagtcta ctccacttga gccctggagt tggagaccag cctgggcaac atggtgaaac  
4981 cctgtctcta caaaaagtac aaaaataggt tgggcgagc ggctcatacc tghtaatcca  
5041 gctactcggg aggtgagac atgagaatca cttgaaccca ggaggtagag gttgagtgga  
5101 gcagagcttg ctccactgca ctccagcctg ggcaacagag caagactctg cctcaaaaat  
5161 caaaccaaca aaaaatagct gtgtgtggtg gtgtgtcct gtagtcccag ctactcggga  
5221 ggctgaggtg gaaggattgc tcaagcccag gaagttgagg ctgcagtgag ctgtcatcag  
5281 cctctagcct ggggtgacaga gtgagaccct gttcaaaaag aaagaaaaag aaaagagtct

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5341 acccagcaaa gctggtttgt tccctccttg aggaccacag ctgacctcta tttgtagcag
5401 aaacaatcat ttctgcacca gctctgagtg cagaaccctt cagaggtaga tggatgctaa
5461 ggcaagctgc cagttacaag agctgtgaga atcagactga cttttgttgc ttaaggcctg
5521 atattatttc ttctgtgcag aggaagagcc tatatacaaa aaaaattttt tgttttgtt
5581 tgttttcagt cattcttgcc ccattggaaga aaggacttat tgcagtgggt atcatcggag
5641 tgatcattgc tctcttgatc attgcggcca aatgttattt tctgaggaaa gccaaagggtg
5701 agcatagttc ttctcttcca tactgactgg tcgtccttgc caggaaacca gccagggatg
5761 cgtgggtgctt ttctgacccc tggattcagc taggcaaaaa tgaaagctat tattttcctc
5821 attgggcaaa ccagaaaaga taaaatttgg gggaaattac atctttgtgt ggttagaaga
5881 agccatttct gtagatttgt ccacacctag tctgtaatg cgtgtagagt ggggtgcaag
5941 cgtcttgtag acacacaaac atgcgcataa caccacatg ttgcacacac acattg

```

## (2) INFORMATION FOR SEQ ID NO:2771:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2771

```

1 acctctttct tttctgtctt ttgaaaaaga gtgaatatat ttgccttctt tttctctctt
61 tttctgggta ttcaatcttc tgggaagtcc aaacgtagct gaaaagagtg ttccttcaca
121 gcttactagg agtaaaacaa aaagaaaaga aaagtgtttt ctatctatta ggttagtgca
181 aaagccattg gcgttttggc cattatagtg gtatggatgt gggtagtgta tactgacttt
241 ggtttttcgt tttctgtttt taaagccaag cagatgccag tggaaatgtc caggtgagtg
301 tatttgtaag aagggggcgg ctgctctgtg agcacggtgg acatgtctgg agggagattc
361 tggtcattag gaagttttca gtggctcttg gcaaaacttag aaaaatatag gccttccttg
421 ggtgtgagtt gtgtgtgtga gttgtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtatctc
481 cgtgggaagaa tgccaattgt cctttcatgg gaaggaatgg cttttattct gagatcatgt
541 ccttcctaca tgattatttg tgaaatctcc ctttctttat gaaattataa tggtagtaga
601 taatttttta aaatttgaca aaatagagtt ggcctttaa aaatggtttt actaccttta
661 ctgttggtga aatcccaaat caaaagtata gaaatgattg ctctgttcca gagagaaaca
721 gtagcgtggg ataagaattt cagggggcct ggtagtagcc tgtgaaggac tccggtattc
781 atgtgtgctt tggctgtatg ttatttaata ggaaagtt

```

## (2) INFORMATION FOR SEQ ID NO:2772:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2772

```

1 aaaaaaaaaa aaagtttttt tacataatcc ttggagctgc caaaaaatat ttgttttcca
61 aatgagagag taaagttttc cttaccttgg aaaactcttc ctggttttct catgatcttc
121 ccttggttac tttggtggtt tggggttaga acaataacaa caacaaatat atctatatat
181 tgttttctgt ttttatattt cattttaaag gccagcagta ccacttctga actccaacaa
241 cgagaaaatg tcagatccca atatggaagc taacagtcac tacggtaaaag tcatgttctc
301 ctgccattta taattccccc caacttgcta catacttctt taccctcttc agaagcagaa
361 tatgtaagtg gtgggattac agttggaaga gaaaccttgg cttcaacagg gtacttcatc
421 tcatcagcca ctgggcatg taatatacgg aaacgtaaaa ggaagggtaa catattttat
481 tctaactttg ccaccttcca aactccccgt agaagaaaga tggagaataa tcataatgcc
541 ttcaaagact tgaacattg ctccagcgta atattataa tctccatttt caagacagag
601 acagatatgt aatgaaacat tggtaaacat cttctcagat ggaattatta caagcacaag
661 acagttttac ttcaaatttg gcacaaaggg aaagcaattt caatattctc tcagtaaagg
721 cataaataaa gtgttccaac taagaaaata tctattcata aggctcatca gtagcttcag
781 ggtcagctca gctgaatgag taggcagtc taggagtct taatcccagg ttagtaagaa
841 aattgctcaa gcatttcagc aggatgctac ttacttccca gaggggggta ttattacatc
901 acaaaaagtc ctgtcccaga ccaaatttgg ggacactctt cctctt

```

## (2) INFORMATION FOR SEQ ID NO:2773:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2773

```

1 atagccacga ctcaaatata ttgatcttag aatctaaaag acttaggtct gggcgcggtg
61 gctcagcct gtaatctcaa cactttggga ggccgaggta ggtggatcac ttgaggtcag
121 cagttcaaaa accacctggc caacatgggt taaccctgtt tctactaaaa atacaaaaaa
181 ttagctgggc atggtggtag atgtttataa tcccagctac tcaggcagggc tgaggcagga
241 gaataccctt gaacctggga ggtggaggtt gcatgacctg a
1 tggacctcaa catgcacacc agtccgagca acaagagcga aactccatct caaaaaagaa

```

```

61 agaaagaaag aaactatatt caggccaggc atggtagttc atgcctataa cccagctctt
121 ttgggaggct gaggtgggag gatcattgag cccaggagtt ggagaccagc ctgtgcaaca
181 aagcgagaca tggagaatgt ggaacgaggg acccaggacc cagagacagt gctgggtgtc
241 actacactga ataaatcagg cttgactttg ttaggggtac tgaattttta aaagggtttt
301 agaaaactag aatttccctt gtcactcacc ctaattgtta tttttcaact aggtcacaat
361 gacgatgtca gaaaccatgc aatgaaacca ataatgata ataaaggtaa ttatctaatt
421 acatgttttt attagaacca acttttacat taaaaaaaag actcatagga aaagaaaact
481 aaaacttgaa ggactgtgga taatttccca cctctcttaa tgacctgta cccagccgat
541 gtgtcaatga aggtagctag ctgctttcac cagagatgct atctagtgc ctcagtggga
601 agtacctaaa tcaaagtagg gaagaactgg gttatactca aaaaa

```

## (2) INFORMATION FOR SEQ ID NO:2774:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2774

```

1 acaacaactc tgtggtttct ttaggcagag cctctgaact cagacgtgca gtacacggaa
61 gttcaagtgt cctcagctga gtctcaciaa ggtaagtgcc actcagtgta gtccccaggc
121 attcgctttg gcttgggttt aaaccccagt ggtggcgggg gtgctgtgtt cagtgagaag
181 agtctgtgca ccctcagtcg ctccaaagga agtgattagc agacctaccg gcttgctaag
241 actggaagga gcaaggcccc tggcctggcc tgtctctgag ctgtaaaatt tcaataattt
301 aaaagaaaaa aagaaaaggc caggcactgt ggctcacacc tgtaatccta gcactttggg
361 aggccaaagg ggggtggatca cctgagatca

```

## (2) INFORMATION FOR SEQ ID NO:2775:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2775

```

1 tatattttat atattaatat ataaatataa atacatatat aatatataat atatgttttc
61 tttgtgtata atatatattt tataatatatt tatatttttt ttttatatat
121 tttatatata atatttttat atttatatta tttatatatt ttttatttta tatatatata
181 tatatttttt tttttctttg ttgagacgga gtctactctc tgcccaggct ggggtgcagt
241 tgcgagatct

```

## (2) INFORMATION FOR SEQ ID NO:2776:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2776

```

1 tgcaaacctc tgcctccggg ttaaagcagc attctcctcc ctcagcctcc cgagtagctg
61 ggattacagg catgtcaccg ccacagccgg gtaatttatt tttttttttt ttgtattttt
121 aagtagagat gggatttcac catgttgagg agcgtgaact cgaactctcg acttcaaaag
181 atccaccccc ctcagcctcc caaagtgtcg ggattacagg tgtgag

```

## (2) INFORMATION FOR SEQ ID NO:2777:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2777

```

1 gaattcaatt tgagttttcc agaccctgcc tcctccttgg cagctaagga gcagtgtggg
61 aagtcaggcc tgagcctcag gtgttccctc tctgccttcc tgtgggtgga gagccaggta
121 ttaccaggta cgaagggggg ctttgtgggt acaaggctca gtgggtagta catttgacct
181 ggtcttgacc aagccagttc cctgctctca agacttctc ctcctatgga ggagggtgtg
241 ggaaccacat ccagctctga ccctagtggc aggcgaccaa gtgggtcactt ggggtggagg
301 aggggcagga aggaactcag taaatcctgg tttgctgcat gtttgctctg agactaattg
361 ctgggaaaac cccatgacgt ttgaagccat ctccttctct gttatcacag agaaaaacag
421 aagccaaaat aaagccccc cgggaaacat cctgacagc agagacaaaag agcctgcccag
481 cctggtttac tcattagcaa gcagctgtc cctggagtgg gtggggagga gaggtagtga
541 tgagctgcaa ctctgcctgc ccacccatca cttaactggg cagatttggg ggcagctgca
601 actctagaag ctccaccaag aagcagaacc ccccaggccc aaacaccaag ccctctccct
661 ccatttattc ctcacctgcc ccagccccc cttgtggcct ggggtgggag gtgagctggc

```

721 cgtgaccacc ccaccatgcy cctggtatat ggtgtttgat agcatttgtr gcagtgctg  
781 cgtgttttgt gcacctgtct gcctcacagc ctggagctcc tgaaagctgg ggaccaggcc  
841 cgatcacctt tcctcttcca cagtgcgggg ttacactag gtgtctagga tttctgtgag  
901 tgagtgtatt ggccaggcct gacatcaagc agagggtgtc ttggggatgt ggaggatccc  
961 ccaatagggt tggggatccc tacagcttcc cttgagggcc ccacatctgg tgccacagaa  
1021 agagagtgag ggggtgtggt gcatctctgc tgtccagca gtgtggtgac ctggtagctc  
1081 agccactcta ctgagttcca aatcctgttt ggggtgccctg ggggaagtca gtgtaaggcc  
1141 ctagtca

## (2) INFORMATION FOR SEQ ID NO:2778:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2778

1 aaggaggaa atccacttga ccatggcaca ggaaccccc ttaccaate tgggccttcc  
61 ctttccccca tctgtaaaag gagaacagt cccacacgac atcagcctct tttcctacag  
121 tgagccttcc tggccctttg tgcagtagac aggagctggg aagtggccag gttccatcct  
181 gtttccctcag ggttggtggg tatgtatgtg tgtgcacacc ctgtgtgcat gagtgtgtgc  
241 acaccagat tgcattgttg tacatacagt gtgtatacaa tgtgtgtaga cacatcctat  
301 acactgtatg agggatataca tagcatgtat acacattgtg tgcattgtgt taaggtaaac  
361 tatgtgtgtg gtgtattttt gtatacacat cctgtgcccc taccacagtg taaggtaaac  
421 agatggcagg aagggcgccc ttgagtctcc tccaggtata cgccacaccc tgggtcagtc  
481 atcatgtgtc catattgaga gggctagacc cagaggatct cagccctgtc tgcattatag  
541 ggcccctgag gagatcctaa aaaaccagca ccagggaccc cccagacca atccaaccag  
601 aagctgcagt gaggcccagg agccagcagt gaaaacagcc agcccagctg tctatctctg  
661 taagagttct cagtcccagc tattcctagg gtcactgaca acccccaggc tctaaccag  
721 acctcaggat cttgttctgg atcccgggt ctgggctctc aggtgattgg gaggccatag  
781 cccaaccctg cgttgaggga cctggcagaa tgtctggaca agggtcacgg tggcagggga  
841 agaggagtgg gggcagcaag ctggaggctg caggcccttg ctggggggct ctccatccgt  
901 gggcccctca ggtccagggg ttcctctggt gcatgtggcc ctgctccaca atggcctgct  
961 gacctcctat tcccagactg ggagtacgc tcttagacc aagacctct tcttctctt  
1021 cttttttttt tttgggaggt ggtgtgtcac tgtgtgccc aggttgagg gtagtgccg  
1081 aatcttggct cactgcaacc tctgcatcct gggttcaagc gattctctgc ccttagctct  
1141 cgagtaactg ggatcacagg gacgcaccac catgcccgtt taattttttg gaatttttag  
1201 tagagacggg gtttcggcat gttggccaga atggtctcaa cctcctgacc tcaagtgatc  
1261 ttgccccctc aacctcccaa agtgctggga ttacaggtat gagccacctt gccagccag  
1321 gatcttctaa catcagaaat gacaaggtct ctgggtgctt ctggacctgg tctgtgtggg  
1381 gtgcagtggt ggggtacagc cttgcctgca gacccctaga ccttttctta tgactgcagt  
1441 ggactgacct cgttcccaga ggcagctact aacttatgct tggctctttt tccagatcta  
1501 ggaaagaagg acacagagac agtgtagcgt gaagtccgga aagctgtccc tgggtagtga  
1561 ggggtctccag tgcccagacc tgggggatgc cccctataat cactgatggg ggcttgggag  
1621 tgggcagaga aaagaagaag caaagaaggg caaaaaaggg gtggcacctc ttacaccagc  
1681 cgtgtgggct tctctctccc caccacctt aaaaagtcac ctcgggtcac atttactatt  
1741 catgtagtca acgagcgctt cttgaatgct tactgacccc agccgggtgac ccttacctgc  
1801 tccccacaca ggccctggtg gctgggggtc ccaagggtct tggacgtcga gtgttttggc  
1861 ttggagaccc ccagtagctt cagccttctt tcttgttttc ttttttctct ttttttttgg  
1921 gggatagcga gtctcgctct gtcactcagg ctggagtga gtgggtgca ctcgactcac  
1981 tgcaacctcc acttcccaga ttttaagtgt tctctgcct cagcctccca agtagatggg  
2041 attacaggcg cctgtcacca cactcagcta attttttttt tttatatttg ggagacagag  
2101 tttcgtctct gatgcccagg ctggggtgca atggag

## (2) INFORMATION FOR SEQ ID NO:2779:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2779

1 tgcgtggatt accaagtgtg accccccgcc ccagcagctt cagcttttct gacaagaaga  
61 ctgacttttg gagtgggtgt gggtttgagg atctactcta tttccttttg ttcggctgac  
121 cccacttgc tcccgtgac gaccactgc ttactcatga aagggtctcc cccagagctg  
181 agcacagagc ttaagcagac ccggaactgg gggagctcaa caagtccttt ttttcgggtg  
241 ggggtataaa taactgtatt caattcaggt gaaatgaaat acacaatgac aacttttaaa  
301 ttctgaaggt aagtcagcaa tccgaaagac gtaaacattg tgggggaaat agtgactgtg  
361 tgagtatctc gctttgtaca gcagacctct atttaagtgg gttcttggaa agggatcat  
421 taaaatggc caggacattt ctgcaagggt tgcctactca gcctaggcgt ggtggtcat  
481 taagcactca gtaagtgtt tatttattta cccaaataa ataaataaat ataaaggat  
541 gactcctccg agtacagtcg ccaaaccagc agcagcaatc tcggggccag cccagaccca  
601 caaaactagt ctctggaatc tgaacttagc cagcttcaga tgtttctgat gctgccaata  
661 tttgagaagc actgtttgtg ttttgttttg tttttttgtg tgaaacagag tctcactctg  
721 tcaccagac tggagtacag cagtgcacac tcagctgact gcaactccgt gcaacacccc  
781 ccagccccta aggccttaagc gatcctccca agtagctaga accacagaca cacaccacca

841 tgcccagcta agtttttcta tttttggtag agatgaggtt ttaccatgtt gccagactg  
 901 gtgttgtaatt cctgagctca agcaatccac ccccttcggc ctcccaaagt gctgggatta  
 961 caagcgtgag ccactgtgcc agggcaaaaag cactgtttta gaagaacat ccaattctct  
 1021 gaggaccctg ctttttatct gaaatagcga tcacttctta attcactttt aaaagttggt  
 1081 atatctacaa gaagaataga aactcaaccc ttgtggaact tgaccctgaa taatttttga  
 1141 aaaaccaatt ctctggggaa ttttagctc aaatacctca ttt

## (2) INFORMATION FOR SEQ ID NO:2780:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2780

1 aaaaaaaaaa aaaaaaagaa gaagtagttt ctgcttttag tcagataaac aagctctggg  
 61 gagacttctt tctacatctg aaccagctca aaacaatcct tatgccaaag gggcatattt  
 121 tgtggtggca tattctgatt tccttcatct gctttagggc agctggctgt tcaagtgggt  
 181 tctctcgggg tctccaggtt ggttctaga

## (2) INFORMATION FOR SEQ ID NO:2781:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2781

1 cttcttttct ttcctttctt tttttttttt ttgagacagg gtcttcgctc tgtcaccag  
 61 gctggagtg cagtggcgca tcgcagctca ctgcaacctc cagctccggg gttcaagtga  
 121 ttcttctgcc tcagcctcct gagtagctgg gaccacagct actgccacca cccccgggta  
 181 attttttttg tatttttagt agagacggtg ttccaccata ttggtcaggc tgatctcgaa  
 241 ctccagacct caggtgatcc acctgccttg gcctcccaaa gtgctgggat aacaggtgtg  
 301 agacaccacg cccggccaga tcatat

## (2) INFORMATION FOR SEQ ID NO:2782:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2782

1 gatcctatct acgggaaaca tgaagagtaa tattctactg tggcctgggt gaccctgggg  
 61 aagtcataga gctctcaag accttggtca cttctctgt gagatgaggt atgggctgga  
 121 ggcaggtcag tggctctcgg gctttattaa aacatcaata gtttgccgca cccactccc  
 181 tgtgaatttc ccattcacta ggtctggagc ggtgccgaaa acgtgcattt ctaacaggtg  
 241 tcacacgcga gctgctcgcc gacacgctgg ggcccgggct ttgagaacca ctcttgatgc  
 301 agcatgttcc tttctgattg tgccacgcta aggtctgct tcttgttgga aggagtaggg  
 361 tctttctcac cctccagaaa tcctggaggg atctttcagc attggtgggc aggtaaaacc  
 421 cagaaacact gtgcttatta gaggggaaggt tgtattgagt gacccccaat aaaacagggg  
 481 gccaggggcc gcgcgcagtg gctcacgcct gtaatcccag caatttggga ggctaaggcg  
 541 ggcgatcat gaggtcagga gatcgagacc atctgggcta acacggtgga aaccccatct  
 601 ctactaaaaa tacaaaaaat tagctggacg tggt

## (2) INFORMATION FOR SEQ ID NO:2783:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2783

1 agataagcaa tagggcatgg gcaggcctgc ctccaaggag cagccccagg gccgaggaga  
 61 gagagctggc gctggcccag gggacttgag tttgatggga aagcttgcag acagtggggg  
 121 agctgcctgg tctttccagt cttggctttt ggctctaagc acagcttttt tttttttttt  
 181 ttttaattgt gtatcatgag gcgccttcca ctacagctcc tccccacgtt aggggatgga  
 241 cacagcactg gcagggatcc tgtgtgtctc agtttcccta ttgactctct gtggcctaga  
 301 gatgtatggt agaattccac actatgcttt ttttccaccg tgtttttttt tttttttttt  
 361 tttgagacag ggtctctctc tgtcaccacg gctggagtgc agtggcgcaa tcttggtcca  
 421 ctgcaacctc cacctcccca ggcaggcccc tctgactcag ctgggactac aggcattgcac  
 481 caccagcacc cagcaaaata tttttatatt ttagtagaga tggggtttcg tcacattggc  
 541 caggctggtc ttgaactcca gagctcaagc aatccgccc cctcagcctc ccaaagtgtc  
 601 gggattacaa tgcccagccc accttttttt ttacttttta caattttatt cttaaaattg

661 tggtaaaaca catatcacat aaaatttacc attttaactc taagtatcca gctcagtggc  
 721 actaagacta cacttttggg tgtcatagcg tggatgaacag agaagagaat gctactgctg  
 781 ctctgtgaga gagggcagg gataccgcta aacatgacgac aatgcacagg acagtccctt  
 841 cccaccacaa aaacaccacc cagcccaaaa tttcaacagg gccaccatgg agaaaccctg  
 901 gccagaggaa ttcacctctt gcaactcttc caacaggaga gctggttttc ctctccagta  
 961 ccagcttggt gctgcccctt gtcttgggag ggtgacttaa gggcacatcc cacttgatta  
 1021 ctgtgggctc tggatgggtg ctgagtcttg gtctggggaa cag

## (2) INFORMATION FOR SEQ ID NO:2784:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2784

1 aaattaccca ggcattggtg tgtgcgctg tagtcccacc aacttgggag gctgaggcag  
 61 gagaattcct tgaatctggg aggcggaggg tgcagttagc cgagatagtg ccagctgagg  
 121 caggagaatt ccctggaggg agaggttacg gtgagccaag atggcgccac cacactccag  
 181 cctgagtgc aaagcgagac tctgtctcaa aaaaaaaaaa ataaagaaaa ttttaaatga  
 241 agtgccaggg actttatgcg catgtcatgt ggagctagct acagggtccc ggggaagctg  
 301 tcttgcaaaa aggagccata aacctctaag ggcactgccg gctgatgtct cctggctctc  
 361 gcctcctccc tcttttctcg acctgctcct gacctgtga tgttgttggg gcagttgaac  
 421 tgggttattt gcgttgcctc ctgccatgac atcctttgtt ttgtagatgc cgtggaaagc  
 481 agatactctg taagtacaca ttcatatac attatatata aaagtactcc actgaacagt  
 541 gaaatatttc cagactcacc cagcctgca ttcacacgaa ttcttcccgc ctccctagcc  
 601 tgttcagacc agaagccctg ggcttctctg actagccttg gccagttctg atttcgaata  
 661 tctctcctg caatttccat cattacatct cagcccacac gtgaagggat tgggactctg  
 721 ggtgcttag cgccaaacaa gcaagcaca catttcgttt aacgccaaag tctaggtctt  
 781 ggaagtggag cagatctagg gtgtatgctt ggaggagtgg agcagctgac agctcattgc  
 841 aatttagccg atactaatta cccctacac accaggccat cagctgcagg aggacacca  
 901 agcttcttga cctcagttca ccttctgatg agggaaatcag acatgtgatc acttatcata  
 961 aagccaagtg agctatgcca gagcctatgg gaacacagaa cagagacctg gctagtggcc  
 1021 tcttcccaa ggaatcattt ggaatggccc atgaagaatg aatggagtga tcatgccagc  
 1081 attgaggagg aaagatcagc agagacacaa ggtgaggga tgaccagttt caagcagttg  
 1141 gggatgggaa agaagagtgt gacagtgaac agtgacggga gaaagataag tcagggttta  
 1201 aatccaaagg atttacatcc cttgttaaga agcttcattc ttaggaaat ggagtttaga  
 1261 atctgcattt ggcagatggg aggttttatg aaagacacag aggccacgt tcaacttttg  
 1321 caaagacgtg tcttccaatc ccaacctttt tgtgagctac ccagcaatgc aggtttaa  
 1381 tgggcagcta atatctgaag aaatgaggca ttgcccgc ataaactctt taggtctggg  
 1441 aagaactttc agcaaagatt tcaggtagct cttccagtg gccctggctt cctttgtttt  
 1501 gcccatgtca ggaactctgt aaaacagagc tc

## (2) INFORMATION FOR SEQ ID NO:2785:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2785

1 gagctccagc tttccagctg tcttttgggt gagcctgtct tctcaagct caagcttctt  
 61 tatctataaa gtggagatgg tgatgacaat gatgataaga gcaacctatt aggattttaa  
 121 ggatgaaatg agcaactgca accaccatat aaaagctgca agctgcaaac caccatataa  
 181 aagctggttg atctcaagct cttttcatca cttgggcaat agtaggtgtg gatgggggac  
 241 ttaacttgat ttggccatga aatgacctg ccacatatgg agaagttagc agttgcttac  
 301 ccaaggcata ggattcaacc aaggccaggc tttgacttag gaatcagaga cccacattaa  
 361 catttgactt cccgcttctt agccatgtca ccattggcaa atttcttggc ctctcaagac  
 421 ctctgcttcc taatctgtaa actgggaatc ataaactccc tcaacttggtt gttgcaaggg  
 481 ttgaatgagc ac

## (2) INFORMATION FOR SEQ ID NO:2786:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2786

1 ctatcaatct ccagagcttt ttctttttta gtgtgagcga gtttattaga gaagtaaaga  
 61 gacccaagag tgcctactcc atagacagag cagccactgt gacactgtac ccattaaaca  
 121 ctaactctcc attgcccctc cagcaacccc tagcaccac tgctacttt ctgtctctat  
 181 gtggttgctt atttgaggga catcacataa gtggagtcat atatttgtcc ttctatgtct  
 241 cccttatttc atttagcata acgttttcaa ggggttccgt tgttgtaaat atatcagaat

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301 ttcatctctt ttttaaggtg gaatcatatc attttaaaac atttcagttg gaccatctaa
361 gttcagtcct tcattttcaa caattaaaaa acagccctca accgggtgca tctcacgtta
421 gctagagaca gaactggagc tagaagtcag atctcttacc aaagttgcct ttcttctctt
481 tggggtaagt ggggcaccct tgggacgctg tgctgggctg acatgggtgc ttgatgaagt
541 tacttggttg actgatgtga ttgatgtcca acatgtatgc agggacagag gctatggtcc
601 ctacagagca ggcattggaga gaaggagaaa tacatacggg caggagccag gagaggagg
661 gtgtagttag cagagaccgc gccactgcac tccagcctga gtgacagagt gagaatccat
721 ctaaaaaatt gcttactaaa gaagtgggtc cctgaggtct taagacgttc ctggcaatgt
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1921 agatggtgac atcagcaaat attattctta attgaaaact tgaatgtgt atgtttctta
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## (2) INFORMATION FOR SEQ ID NO:2787:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2787

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121 cctgcagtct tcactctcag gatgcagccg aggtggggcc aagggggccac gatgtggctt
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## (2) INFORMATION FOR SEQ ID NO:2788:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2788

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181 tttctgctctg ttcaagcctt gaggttcaag aaaactcttt cacaatcaac agtgttgaca  
241 tgaagagcct gccggactgg acggtgcaaa atgggaagaa cctgacctg cagtgtctcg  
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1381 tgggcagcta atatctgaag aaatgaggca tttgccgcat aaacttctt taggtctggg  
1441 aagaactttc agcaagatt tcaggtagct cttccagtgg ccctggctt ctttgtttt  
1501 gccatgtca ggactctgtt aaacagagc tc  
1 gagctccagc tttccagctg tcttttgggt gagcctgtct tctcaagct caagcttctc  
61 tatctataaa gtggagatgg tgatgacaat gatgataaga gcaacctatt aggtatttaa  
121 ggatgaaatg agcaactgca accaccatat aaaagctgca agctgcaaac caccatataa  
181 aagctggttg atctcaagct ctttcatca cttgggcaat agtaggtgtg gatgggggac  
241 ttaacttgat ttggccatga aatgacctg ccacatagtg agaattgagc agttgcttac  
301 ccaaggcata ggattcaacc aaggccaggc tttgacttag gaatcagaga cccacattaa  
361 catttgactt cccgcttctt agccatgtca ccatgggcaa atttcttggc ctctcaagac  
421 ctctgcttcc taactgttaa actgggaatc ataaactccc tcaacttggtt gttgcaaggg  
481 ttgaatgagc ac  
1 ctatcaatct ccagagcttt tcttttttaa gtgtgagcga gtttattaga gaagtaaaga  
61 gacccaagag tgcctactcc atagacagag cagccactgt gacactgtac ccattaaaca  
121 ctaactctcc attgcccctc cagcaacccc tagcaccac tgtctacttt ctgtctctat  
181 gtggttgtct atttgagga catcacataa gtggagtcat atatttgcct tttcatgtct  
241 ccttattttc atttagcata acgttttcaa gggtttctgt tgttggtaat atatcgaat  
301 ttcatctct ttttaaggta gaatcatatc attttaaaac atttcagttg gaccatctaa  
361 gtccagtcct tcattttcaa caattaaaaa acagccctca accgggtgca tctcacgtta  
421 gctagagaca gaactggagc tagaagtcag atctcttacc aaagtgtgct tcttctctt  
481 gtgggtaagt ggggcaccct tgggacgctg tgcgtggcgt acatgggtgc ttgatgaagt



541 tacttggtgg actgatgtga ttgatgtcca acatgtatgc agggacagag gctatggtcc  
601 ctacagagca ggcattggaga gaaggagaaa tacatacggg caggagccag gagagggagg  
661 gtgtagttag cagagaccgc gccactgcac tccagcctga gtgacagagt gagaatccat  
721 ctaaaaaatt gcttactaaa gaagtggctc cctgaggtct taagacgttc ctggcaatgt  
781 cttgagtggg tgggagagag cctccagtca ttgagctgtg gaatttcaga ggtgagaacc  
841 acacctaacc cccaattact ttcccctgtt tgccctcagt acacagctgc aggaaccctg  
901 gtgggtgttg tattaagtaa atttgacctt tattctttgc agatctgtga aatgttgtct  
961 tctgaggggc cacgtgtatc tgtagtgtcg aggactcctt ggggcctctg aagtcacaga  
1021 gagaacctgc aggtggggg accagtgtgt gacagccctg ctttgcattt tctttgagaa  
1081 gtgctgtcat tttgcatttc tctccaccag gggaatcttc aatcttgaga ggtgtgatca  
1141 taacttgctt tgtttcttgt cgctacagag aacggaaggc tcccttgatg gaacttagac  
1201 agcaaggcca gatgcacatc cctggaagga catccatgtt ccgagaagaa cagatgatcc  
1261 ctgtatttca agacctctgt gcacttattt atgaacctgc cctgtctcca cagaacacag  
1321 caattcctca ggctaagctg ccggttctta aatccatcct gctaagttaa tgttgggtag  
1381 aaagagatac agaggggctg ttgaatttcc cacataccct ccttccacca agttggaaca  
1441 tccttggaag ttgggaagag cacaagagga gatccagggc aaggccattg ggatattctg  
1501 aaacttgaat attttgtttt gtgcagagat aaagaccttt tccatgcacc ctcatacaca  
1561 gaaaccaatt ttctttttta tactcaatca ttcttagcgc atggcctggt tagaggctgg  
1621 tttttctctt ttctctttgg tcttcaaaag gcttgtagtt ttgggtagtc ctgttctttt  
1681 ggaaatacac agtcttgacc agacagcctc cccctgtccc ctctatgacc tcgcccctca  
1741 caaatgggaa aaccagacta cttgggagca ccgctgtgta aataccaacc tgaagacacg  
1801 gttcattcag gcaacgcaca aaacagaaaa tgaaggtgga acaagcacat atgttcttca  
1861 actgtttttg tctacactct ttctcttttc ctctacatgc tgaaggctga aagacaggaa  
1921 agatgggtgcc atcagcaaat attattctta attgaaaact tgaaaatgtgt atgtttctta  
1981 ctaattttta aaaatgtatt ccttgccagg gcaggcaagg tcgtcacgac tgtaatccca  
2041 gcacttcagg aggtctgagt gggcgagtc  
1 gaattccggg agaagtgacc agagcaattt ctgcttttca cagggcgggt ttctcaacgg  
61 tgacttggtg gcagtgcctt ctgctgagcg agtcatggcc cgaaggcaga actaactgtg  
121 cctgcagtct tcaactctcag gatgcagccg aggtggggcc aaggggccac gatgtggctt  
181 ggagtccctg tgaccttctt gctctgttca agccttgagg gtcaagaaaa ctctttcaca  
241 atcaacagtg ttgacatgaa gagcctgccc gactggacgg tgcaaaatgg gaagaacctg  
301 accctgcagt gcttcgcgga tgtcagcacc acctctcacg tcaagcctca gcaccagatg  
361 ctgttctata aggatgacgt gctgttttac aacatctcct ccatgaagag cacagagagt  
421 tattttatct ctgaagtccg gatctatgac tcagggacat ataaatgtac tgtgattgtg  
481 aacaacaaag agaaaaccac tgcaagatca cagctgttgg tggaggagt gcccagtcct  
541 aggtgtgacac tggacaagaa agagggcctc caaggtggga tctgtagggt caactgttct  
601 gtcccagagg aaaaggcccc aatacacttc acaattgaaa aacttgaact aaatgaaaaa  
661 atggtcaagc tgaagagaga gaagaattct cgagaccaga attttgtgat actggaattc  
721 ccggttgagg aacaggaccg cgttttatcc ttccgatgtc aagctaggat catttctggg  
781 atccatatgc agacctcaga atctaccaag agtgaactgg tcaccgtgac ggaatccttc  
841 tctacacca agttccacat cagccccacc ggaatgatca tggaggagc tcagctccac  
901 attaatgtca ccattcaagt gactcacctg gcccaggagt ttccagaaat cataattcag  
961 aaggacaagg cgattgtggc ccacaacaga catggcaaca aggtgtgta ctacgtcag  
1021 gccatggtgg agcacagtgg caactacacg tgcaaaagg agtccagccg catatccaa  
1081 gtcagcagca tctgtgtcaa cataacagaa ctattttcca agcccgaact ggaatcttcc  
1141 ttcacacatc tggaccaagg tgaagactg aacctgtcct gctccatccc aggagcacct  
1201 ccagccaact tcaccatcca gaaggaagat acgattgtgt cacagactca agatttcacc  
1261 aagatagcct caaagtccga cagtgggacg tatatctgca ctgcaggat tgacaaagtg  
1321 gtcaagaaaa gcaacacagt ccagatagtc gtatgtgaaa tgcctctcca gccaggatt  
1381 tcttatgatg cccagtgtga ggtcataaaa ggacagacca tcgaagtccg ttgcaatcg  
1441 atcagtggaa ctttgcttat ttcttacc aaatttataa caagttaaagt tttggagaat  
1501 agtaccaaga actcaaatga tcctgcggtt ttcaaagaca accccactga agacgtcgaa  
1561 taccagtgtg ttgcagataa ttgccattcc catgcaaaa tgtaagtga ggttctgagg  
1621 gtgaagggtg tagccccggt ggtgaggtc cagatttcta tctgtcaag taagggtgtg  
1681 gagtctggag aggacattgt gctgcaatgt gctgtgaatg aaggatctgg tcccatcacc  
1741 tataagtttt acagagaaaa agagggcaaa ccttctatc aaatgacct aaatgccacc  
1801 caggcathtt ggaccaagca gaaggctagc aaggaacagg agggagagta ttactgcaca  
1861 gccttcaaca gagccaacca cgcctcagc gtccccagaa gcaaaatac gacagtca  
1921 gtcattcttg ccccatggaa gaaaggactt attgcagtgg ttatcatcg agtgatcatt  
1981 gctctcttga tcattgcggc caaatgttat tttctgagga aagccaaggc caagcagatg  
2041 ccagtggaaa tgtccaggcc agcagtacca cttctgaact ccaacaacga gaaaatgtca  
2101 gatcccaata tggaaagctaa cagtcatcag ggtcacaatg acgatgtcag aaacctgca  
2161 atgaaaccaa taaatgataa taaagagcct ctgaactcag acgtgcagta cacggaagtt  
2221 caagtgtcct cagctgagtc tcacaaagat ctaggaaaga aggacacaga gacagtgtac  
2281 agtgaagtcc ggaagactgt cctgatgcc gtggaaagca gatacttag aacggaaggc  
2341 tcccttgatg gaacttagac agcaaggcca gatgcacatc cctggaagga catccatgtt  
2401 ccgagaagaa cagataatcc ctgtatttca agacctctgt gcacttattt atgaacctgc  
2461 cctgtctcca cagaacacag caattcctca ggctaagctg ccggttctta aatccatcct  
2521 gctaagttaa tgttgggtag aaagagatac agagggg

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2789

```
1  tggtcacatc agtttctttt ctcaccttga ctgcaagatg aaactccttg tgctagctgt
61  gctgctcaca gtggccgccc cgcagacggg catcagccct cgggccgtgt ggcagttccg
121 caaaatgata aagtgcgtga tcccggggag tgaccccttc ttggaataca acaactacgg
181 ctgctactgt ggcttggggg gctcaggcac ccccggtgat gaactggaca agtgctgcca
241 gacacatgac aactgctatg accaggccaa gaagctggac agctgtaaat ttctgtgga
301 caaccctgac acccacacct attcatactc gtgctctggc tcggcaatca cctgtagcag
361 caaaaacaaa gagtgtgagg ccttcatttg caactgcgac cgcaacgctg ccatctgctt
421 ttcaaaagct ccatataaca aggcacacaa gaacctggac accaagaagt attgtcagag
481 ttgaatatca cctctcaaaa gcatcacctc tatctgcctc atctcacact gtactctcca
541 ataaagcacc ttgttgaag aa
```

## (2) INFORMATION FOR SEQ ID NO:2790:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2790

```
1  ctgcagaggc tcaatcactg ttcatgtcag ccttgacctc cctggctcac gagatcctcc
61  catctcagcc tctgagttg ctgggacac aggtgcaatc caccaccaca cctgggttaac
121 attttttttt ttagagatga ggtctctcta tgttgcccag gctgcacttc cttcttgtct
181 cccttatccc agcgtccgac tgaactgacg gctttgcttt cccaaccag cccgtgaagc
241 ttggctgagt acaaagtggg gggatgagg gtcaagattg taagatctga aaactccaga
301 aacctccctt ttggttaaca gttgctaagg acaaatgcat aacatatttt ccagtgatcc
361 catgctggca aatcgtgagg gtcatctctg caacagacag attcaaggcc agccccaac
421 tcagccaaga gcaaagcaaa cactccagcc ttatctgggc agggtttgtt ggagactgac
481 tataagacta tacctgagac tggtcacatc agttcttttc tcaccttgac tgcaagatga
541 aactccttgt gctagctgtg ctgctcacag gtaggcaagt ctccccggct ccaccgcct
601 ttctctccca agtgagctaa gatctcactc ctctggaatg ggggccacac acagcaaaaca
661 gggatggcca gccccgcagt ctcaattcga ggttcccagt gggcttaagg gctcctctat
721 ttgggttccc tcaaggctgg cactttttca acctgcaagt ctgaactcag attgctgag
781 ctaagaaagc ttgcctttat tttctttttt ccagacaggg tcttgctcta taaccaggc
841 tggagttcag tggcatgac atagctcacc acagcttcca actcgtgggc tcaagtatc
901 ctcccacctt actcaactaa gtatgttagc caatctccca tttattttat tttattttaa
961 tttttatttt tattttactt tattttattt ttgagacggg gctcactctg tcgccaggct
1021 ggagtgccgt gggctgatct cagatcacta caacctccat ctccctggtc aaataattct
1081 cttgcctcag cctctcaagt agctggactt gtatgtctca agtagctggc acacaccacc
1141 atggccagct aattttttgt gtgttttttt tggtagagac aggttttccac catgttggcc
1201 aggetgggtg acctcccttt tagattctcc tcatctgctc ctattcttcc ctttctaaa
1261 tgcagtatcc agtttcctta cttatacact ttattattat tcttattatt attgagacag
1321 agtcttgctt tgtgccaag gctggagtac agtggtgcga tctcggctca ctgcaagctc
1381 cacctgctgg gttcacgcca ttctcccgcc tcagcctccc cagtagctgg gactaaagcg
1441 cctgccacca cgccccgcta atttttttgt atttttaata aagacggggg ttcactgtgt
1501 tagccaggat ggtctcgatc tcatgacctt gtgatccgcc tgcctcggcc tcccaaatgc
1561 tggattacag gcatgagcca ccgtgccggg ccttatcaca tttattattt attgtttttc
1621 tctccacta ggtgtgaagc tccatgaggt tagagattat tattattatt attattatta
1681 ttattattat tattattatt attatatctg ttactgctg tatctctagc tccatggaca
1741 gagcctggca catagtaagt gctcaataaa tttcactgg ataaacagtg cagatagttt
1801 aaaactatct gacctaggga ggctgaggca ggagaatggc gtgaacccgg gaagcagagt
1861 ttgcagttag ctgaaatcgt gtcactgcac tccaacctgg gcaacagagc aagactccat
1921 ctcaaaaaaa aaaaaaaaaa tatcaggcct agctgggtgg cacatgcctg taatcctagc
1981 tgaggcggtg gggctccaga agaagaagaa gaagaaaaag aagaagatat atatatatat
2041 acacacacac aaagatataa actttatata tataaagttt tcattaaaaa aaaaaaaaaa
2101 ctctaccacac tttcacttta ccaggttcct gggctccaacg gtcttcagag gaggcagctg
2161 gcaggggtca gggaggcagc gtgggaccgg agggagcagg aaggcagtggt gtccccgggg
2221 tgctggcaga ccgatttgaa ctctggctat gtcttcttgc agtggccgcc gccgacagcg
2281 gcatcagccc tcgggccgtg tggcagttcc gcaaaatgat caagtgcgtg atccccggga
2341 gtgacctctt cttggaatac aacaactacg gctgctactg tggcttgggg ggctcaggca
2401 cccccgtgga tgaactggac aagtaagtga tccgctgca ggaaaattgg agtgctgccc
2461 gggggcgggg tggggcacca cgccaaggat ctacagaggc atacaaaggg gacttgcata
2521 tctgctaagg ataactattt ttcacctctt gtcaaataaa catatatgtt ccaagaggac
2581 cctgtagcga acgcaccccg ttagagatgg aaacattgac cgacgtgcaa aacagtgggc
2641 gatgctgccc tccagtggca gaatgtagca acattaaaca tcacagcacc tatccacgtg
```

```

2701 tcatttttcta gcagtggttg tcactgcccc ttctggaata caggatttta ctgtattctt
2761 gcaaccatgt taaaaatcgc ttccaggcca ggccggttg ctcagcctg taatcccagc
2821 actttgggag gccgagggcg gcgcatcact tgaggtcagg agttcgagac cagcctggcc
2881 aacatggtga aaccctgtct ctactaaaaa atacaaaaat tagccggaca tgggtggcga
2941 cgctgtgaac ccagctact tgggagactg agttggaggt ttcagtagcc aaggtcgtgt
3001 cactgctgtc cagcctgggt aacagagcaa ctctgtctca aaaaaaaa atgctttcaa
3061 taaatatatg ataaaaggac ttatatTTTT tcaagccata ggatcatttc tcctgaagca
3121 tcttggcgaa gtcaccccca cctgttctct agagtgggca ggtgagggtc gacctattgc
3181 tctgcaacta ctcttatctc agctgtccct cccactttcc aggtgtgtgc agacacatga
3241 caactgctac gaccaggcca agaagctgga cagctgtaaa tttctgtgg acaaccgta
3301 caccacacac tattcatact cgtgctctgg ctccggcaatc acctgtagca gtaggtttat
3361 cccttccttg accta

```

## (2) INFORMATION FOR SEQ ID NO:2791:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2791

```

1 gccactccc accgccagct ggaaccctgg ggactacgac gtccctcaaa ccttgcttct
61 aggagataaa aagaacatcc agtcatggat aaaaatgagc tggttcagaa ggccaaactg
121 gccgagcagg ctgagcgata tgatgacatg gcagcctgca tgaagtctgt aactgagcaa
181 ggagctgaat tatccaatga ggagaggaat cttctctcag ttgcttataa aaatgttgta
241 ggagcccgtg ggtcatcttg gaggtgctgc tcaagtattg aacaaaagac ggaaggtgct
301 gagaaaaaac agcagatggc tcgagaatac agagagaaaa ttgagacgga gctaagagat
361 atctgcaatg atgtactgtc tcttttgtaa aagttcttga tccccaatgc ttcacaagca
421 gagagcaaa gttcttattt gaaaatgaaa ggagattact accgttactt ggctgaggtt
481 gccgtggtg atgacaagaa agggattgtc gatcagtcac aacaagcata ccaagaagct
541 tttgaaatca gcaaaaagga aatgcaacca acacatccta tcagactggg tctggccctt
601 aacttctctg tgttctatta tgagattctg aactccccag agaaagcctg ctctcttgca
661 aagacagctt ttgatgaagc cattgctgaa cttgatatac taagtgaaga gtcatacaaa
721 gacagcacgc taataatgca attactgaga gacaacttga catttggtgac atcggatacc
781 caaggagacg aagctgaagc aggagaagga ggggaaaatt aaccggcctt ccaacttttg
841 tctgcctcat tctaaaattt acacagtaga ccatttgta tccatgtctg cccacaaata
901 gttttttgtt tacgatttat gacaggttta tgttacttct atttgaattt ctatatttcc
961 catgtggttt ttatgtttta tattagggga gtagagccag ttaacattta gggagttatc
1021 tgttttcate ttgaggtggc caatatgggg atgtggaatt tttatacaag ttataagtgt
1081 ttgcatagt acttttggtg catttggtgc tcaaaagggc cagtgtaaaa ctgtctccat
1141 gtctaagcaa agaaaactgc ctacatactg gtttgtcctg gcggggaata aaagggatca
1201 ttggttccag tcacaggtgt agtaattgtg ggtactttta ggtttggagc acttacaagg
1261 ctgtggtaga atcatacccc atggatacca catattaaac catgtatata tgtggaatac
1321 tcaatgtgta cacctttgac tacagctgca gaagtgttcc tttagacaaa gttgtgacct
1381 attttactct ggataagggc agaaacggtt cacattccat tatttgtaaa gttacctgct
1441 gttagctttc attatttttg ctacactcat tttatttgta tttaaatgtt ttaggcaacc
1501 taagaacaaa tgtaaaagta aagatgcagg aaaaatgaat tgcctggat tctattctc
1561 atgtatatca agcacagcag taaaacaaaa acccatgtat ttaacttttt tttagattt
1621 ttgcttttgt gatttttttt tttttttttt gatacttgcc taacatgcat gtgctgtaaa
1681 aatagttaac agggaaataa cttgagatga tggctagctt tgtttaatgt cttatgaaat
1741 tttcatgaac aatccaagca taattgttaa gaacacgtgt attaaattca tgtaagtgga
1801 ataaaagttt tatgaatgga cttttcaact actttctcta cagcttttca tgtaaattag
1861 tcttggttct gaaacttctc taaaggaaat tgtacattct ttgaaattta ttccttattc
1921 cctcttgga gctaattggc tcttaccag tttaaacaca aaatttatca taacaaaaat
1981 actactaata taactactgt ttccatgtcc catgatcccc tctctctctc cccaccctga
2041 aaaaatgag ttcctatttt ttctgggaga gggggggatt gattagaaaa aaatgtagt
2101 tgttccattt aaaatttttg catatggcat tttctaactt aggaagccac aatgttcttg
2161 gcccatcatg acattgggta gcattaaact taagttttgt gcttccaaat cacttttttg
2221 tttttaagaa tttcttgata ctcttatagc ctgccttcaa ttttgatcct ttattctttc
2281 tatttgctag gtgcacaaga ttaccttctt gttttagcct tctgtcttgt caccaacct
2341 tcttacttgg tggccatgta cttggaaaaa ggccgcatga tctttctggc tccactcagt
2401 gtctaaggca cctgtcttcc tttgttggtc tccacagac tatttccctc atctatttta
2461 ctgcagcaaa tctctcctta gttgatgaga ctgtgtttat ctccctttta aacctacct
2521 atcctgaatg gtctgtcatt gtctgccttt aaaatccttc ctctttcttc ctctctatt
2581 ctctaaataa tgatggggct aagttatacc caaagctcac tttacaaaat atttctctag
2641 tactttgcag aaaacaccaa acaaaaatgc cattttaaaa aaggtgtatt tttcttttta
2701 gaatgtaagc tcctcaagag cagggacaat gttttctgta tgttctattg tgcctagtag
2761 actgtaaatg ctcaataaat attgatgatg ggaggcagtg agtcttgatg ataaggtgta
2821 gaaactgaaa tccc

```

## (2) INFORMATION FOR SEQ ID NO:2792:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: \_ base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2792

```
1  tggtcattctc agtttctttt ctacacctga ctgcaagatg aaactccttg tgctagctgt
61  gctgctcaca gtggccgccc cgcacagcgg catcagccct cgggcccgtg ggcagttccg
121  caaaatgata agtgctgta tcccggggag tgaccccttc ttggaatata acaactacgg
181  ctgctactgt ggcttggggg gctcaggcac ccccggtgat gaactggaca agtgctgcca
241  gacacatgac aactgctatg accaggccaa gaagctggac agctgtaaat ttctgctgga
301  caaccctgac acccacacct attcatactc gtgctctggc tcggcaatca cctgtagcag
361  caaaaacaaa gagtgtgagg ccttcatttg caactgcgac cgcaacgctg ccatctgctt
421  ttcaaaagct ccatataaca aggcacacaa gaacctggac accaagaagt attgtcagag
481  ttgaatatca cctctcaaaa gcatcacctc tatctgcctc atctcacact gtactctcca
541  ataaagcacc ttgttgaaag aa
1  ctgcagaggc tcaatcactg ttcatgtcag ccttgacctc cctggctcac gagatcctcc
61  catctcagcc tcctgagttg ctgggatcac aggtgcaatc caccaccaca cctggttaac
121  attttttttt tttagatgta ggtctctcta tgttgcccag gctgcacttc cttctgtctt
181  cctttatccc agcgtccgac tgaactgacg gctttgcttt ccccaaccag cccgtgaagc
241  tgggctgagt acaaagtggg gggtatgagg gtcaagattg taagatctga aaactccaga
301  aaccatccct ttggttaaca gttgctaagg acaaatgcat aacataatct ccagtgtacc
361  catgctggca aatcgtgagg gtcattcctg caacagacag attcaaggcc agccccaaac
421  tcagccaaga gcaaagcaaa cactccagcc ttatctgggc agggttgtgt ggagactgac
481  tataagacta tacctgagac tggctcatctc agttcttttc tcaccttgac tgcaagatga
541  aactccttgt gctagctgtg ctgctcacag gtaggcaagt ctccccggct ccaccgcctt
601  ttctctccca agtgagctaa gatctcactc ctctggaatg ggggccacac acagcaaaaa
661  gggatggcca gcccgcagt ctcaattcga ggttcccagt gggcttaagg gctcctctat
721  tgggggtccc tcaagctggt cactttttca acctgcaagt ctgaactcag attgcctgag
781  ctaagaaaagc ttgcctttat tttctttttt ccagacaggg tctgtctcta taaccaggc
841  tggagttcag tggcatgac atagctcacc acagcttcca actcgtgggc tcaagtgtac
901  ctccccactt actcaactaa gtatgtaggc caatctccca tttattttat tttattttaa
961  tttttttttt tttttactt tttttattt ttgagacggg gctcactctg tcgccaggct
1021  ggagtgcggt gggctgatct cagatcacta caacctccat ctctgggttc aaataattct
1081  cttgcctcag cctctcaagt agctggactt gtatctctca agtagctggc acacaccacc
1141  atgccagctc aattttttgt gtgttttttt tggtagagac aggttttcac catgttgccc
1201  aggctgggtg acctcccttt tagattctcc tcactcctgt ctattcttcc cctttctaaa
1261  tgcagtatcc agtttcttta cttatacact ttattattat tcttattatt attgagacag
1321  agtcttgctt tgtgcccagg gctggagtac agtgggtcga tctcggtcca ctgcaagctc
1381  cactgctggg gttcacgcca ttctcccggc tcagcctccc cagtagctgg gactaaagcg
1441  cctgccacca cgcccgtcta atttttttgt atttttaata aagacggggg ttcatcgtgt
1501  tagccaggat ggtctcgatc tcattgacct gtgatccgcc tgcctcggcc tccccaatgc
1561  tggattacag gcatgagcca ccgtgcccgg ccttatcaca tttattattt attgtttttc
1621  tctccacta ggttgtaagc tccatgaggt tagagattat tattattatt attattatta
1681  ttattattat tattattatt attatatctg ttactgctg tatctctagc tcttaggaca
1741  gagcctggca catagtaagt gctcaataaa tttactctgg ataaacagtg cagatagttt
1801  aaaactatct gacctaggga ggctgaggca ggagaatggc gtgaaccggg gaagcagagt
1861  ttgcatgtag ctgaaatcgt gtcactgcac tccaacctgg gcaacagagc aagactccat
1921  ctcaaaaaaa aaaaaaaaac tatcaggcct agctgggtgg cacatgcctg taatcttagc
1981  tgaggcggtg ggttcccaga agaagaagaa gaagaaaaag aagaagatat atatatatat
2041  acacacacac aaagatataa actttatata tataaagttt tcattaaaaa aaaaaaaaac
2101  ctctaccac tttcacttta ccaggttcct ggggtccacg gtcttcagag gaggcagctg
2161  gcaggggtca gggaggcagc gtgggaccgg agggagcagg aaggcagtgt gtccccgggg
2221  tgctggcaga ccgatttgaa ctctggttat gtcttcttgc agtggccggc gccgacagcg
2281  gcatcagccc tcgggcccgt tggcagttcc gcaaaatgat caagtgcgtg atccccggga
2341  gtgacccctt cttggaatac aacaactacg gctgctactg tggcttgggg ggctcaggca
2401  ccccggtgga tgaactggac aagtaagtga tccgctgca ggaaaattgg agtgctggcc
2461  gggggcgggg tggggcacca cgccaaggat ctcacgaggc atacaaaggg gacttgcata
2521  tctgctaagg ataacatatt ttcacctctt gtcaataaaa catatatgtt ccaagaggac
2581  cctgtagcga acgcaccccg ttagagatgg aaacattgac cgacgtgcaa aacagtgggc
2641  gatgctgccc tccagtggca gaatgtagca acattaaaca tcacagcacc tatccacgtg
2701  tcattttcta gcagtgggtg tcaactgccc ttctggaata caggatttta ctgtattctt
2761  gcaaccatgt taaaaatcgc tttcaggcca ggcgcgggtg ctcatgctg taatcccagc
2821  actttgggag gccgagggcg gcggtcact tgaggtcagg agttcgagac cagcctggcc
2881  aacatgggtg aaccctgtct ctactaaaaa atacaaaaat tagccggaga tgggtggcag
2941  cgctgtaac ccgactact tgggagactg agttggagggt ttcatgagcc aaggctggtg
3001  cactgtgtgc cagcctgggt aacagagcaa ctctgtctca aaaaaaaaaa atgttttcaa
3061  taaatatatg ataaaaggac ttatattttt tcaagccata ggatcatttc tctgaagca
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3121 tcttggcgaa gtcattccca cctgttctctg agagtgggca ggtgagggct gacctattgc
3181 tctgcaacta ctcctatctc agctgtccct cccactttcc aggtgctgcc agacacatga
3241 caactgctac gaccaggcca agaagctgga cagctgtaaa tttctgctgg acaacccgta
3301 caccacacac tattcatact cgtgctctgg ctcggcaatc acctgtagca gtagggttat
3361 cccctccttg accta
1 gccactccc accgcagct ggaaccctgg ggactacgac gtccctcaaa ccttgttct
61 aggagataaa aagaacatcc agtcatggat aaaaatgagc tgggtcagaa ggccaaactg
121 gccgagcagg ctgagcgata tgatgacatg gcagcctgca tgaagtctgt aactgagcaa
181 ggagctgaat tatccaatga ggagaggaat cttctctcag ttgcttataa aaatgttgta
241 ggagcccgta ggtcatcttg gaggtctgtc tcaagtattg aacaaaagac ggaaggtgct
301 gagaaaaaac agcagatggc tcgagaatac agagagaaaa ttgagacgga gctaagagat
361 atctgcaatg atgtactgtc tcttttgaa aagttcttga tccccaatgc ttcacaagca
421 gagagcaaaag tcttctattt gaaaatgaaa ggagattact accgttactt ggctgaggtt
481 gccgctgggt atgacaagaa agggattgtc gatcagtcac aacaagcata ccaagaagct
541 tttgaaatca gcaaaaagga aatgcaacca acacatccta tcagactggg tctggccctt
601 aacttctctg tgttctatta tgagattctg aactccccag agaaagcctg ctctcttgca
661 aagacagctt ttgatgaagc cattgctgaa cttgatacat taagtgaaga gtcatacaaa
721 gacagcacgc taataatgca attactgaga gacaacttga cattgtggac atcggatacc
781 caaggagacg aagctgaagc aggagaagga ggggaaaatt aaccggcctt ccaacttttg
841 tctgcctcat tctaaaattt acacagtaga ccatttgtca tccatgctgt cccacaaata
901 gttttttgtt tacgatttat gacaggttta tgttacttct atttgaattt ctatatttcc
961 catgtggttt ttatgtttaa tattagggga gttaggccag ttaacattta gggagtattc
1021 tgttttctc ttgaggtggc caatatgggg atgtggaatt tttatacaag ttataagtgt
1081 ttggcatagt acttttggta cattgtggct tcaaaagggc cagtgtaaaa ctgcttccat
1141 gtctaagcaa agaaaactgc ctacatactg gtttgcctg gcggggaata aaagggatca
1201 ttggttccag tcacaggtgt agtaattgtg ggtactttaa ggtttggagc acttacaagg
1261 ctgtggtaga atcatacccc atggatacca catattaaac catgtatatc tgtggaatac
1321 tcaatgtgta cactttgac tacagctgca gaagtgttcc tttagacaaa gttgtgacct
1381 attttactct ggataagggc agaaacgggt cacattccat tatttgaata gttactgtct
1441 gttagctttc attatttttg ctacactcat tttatttgta tttaaatgtt ttaggcaacc
1501 taagaacaaa tgtaaaagta aagatgcagg aaaaatgaat tgcttggtat tcattacttc
1561 atgtatatca agcacagcag taaaacaaaa acccatgtat ttaacttttt ttaggatttt
1621 ttgcttttgt gatttttttt tttttttttt gatacttggc taacatgcat gtgctgtaaa
1681 aatagttaac agggaaataa cttgagatga tggctagctt tgtttaatgt cttatgaaat
1741 tttcatgaac aatccaagca taattgttaa gaacacgtgt attaaattca tgtaagtgga
1801 ataaaagttt tatgaatgga cttttcaact actttctcta cagcttttca tgtaaatag
1861 tcttggttct gaaacttctc taaaggaaat tgtacattct ttgaaattta ttccttattc
1921 cctcttgcca gctaattggc tcttaccag tttaaacaca aaatttatca taacaaaaat
1981 actactaata taactactgt ttccatgtcc catgatcccc tctcttctc cccaccctga
2041 aaaaaatgag ttccattttt ttctgggaga gggggggatt gattagaaaa aaatgtagtg
2101 tgttccattt aaaatttttg catatggcat tttctaactt aggaagccac aatgttcttg
2161 gcccatcatg acattgggta gcattaactg taagttttgt gcttccaaat cacttttttg
2221 tttttaagaa tttcttgata ctcttatagc ctgccttcaa ttttgatcct ttattcttct
2281 tatttgtcag gtgcacaaga ttaccttctt gttttagcct tctgtcttgt caccacat
2341 tcttacttgg tggccatgta cttggaaaaa ggccgcatga tctttctggc tccactcagt
2401 gtctaaggca cctgcttcc tttgcttgca tcccacagac tatttccctc atcctattta
2461 ctgcagcaaa tctctcctta gttgatgaga ctgtgtttat ctccctttta aacctacct
2521 atcctgaatg gtctgtcatt gtctgccttt aaaatcctc ctcttcttct ctcccttatt
2581 ctctaaataa tgatggggct aagttatacc caaagctcac tttacaaaat atttctcag
2641 tactttgcag aaaacaccaa acaaaaatgc cattttaaaa aaggtgtatt ttttcttita
2701 gaatgtaagc tcctcaagag cagggaacaat gtttctgta tgttctattg tgcctagtac
2761 actgtaaatg ctcaataaat attgatgatg ggaggcagtg agtcttgatg ataagggtga
2821 gaaactgaaa tccc

```

## (2) INFORMATION FOR SEQ ID NO:2793:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2793

```

1 gctgtgcaac ctgcgcgcca tgcgcaacct ctatgcatg caccggcgccg tgcagcgcca
61 cccgcgctcc tgcaccaggg actgtgccga gccgcgcgcg gacgggaggg aagcgtcccc
121 tcagcccctg gagagctgg atcacctcct gctgctggcg ctgatgaccg tgctcttcac
181 tatgtgttct ctgcccgtaa ttatcgcgc ttactatgga gcatttaagg atgtcaagga
241 gaaaaacagg acctctgaag aagcagaaga cctccgagcc ttgcgatttc tatctgtgat
301 ttcaattgtg gacccttggg tttttatcat tttcagatct ccagtatttc ggatattttt
361 tcacaagatt ttcattagac ctcttaggta caggagccgg tgcagcaatt ccactaacat
421 ggaatccagt ctgtgacagt gtttttctact ctgtggttaa ctgaggaata tgtcacattt

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481 tcagccaaag aacca

## (2) INFORMATION FOR SEQ ID NO:2794:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2794

1 gaattctggc tattttctc ctgccgttcc gactcggcac cagagtctgt ctctactgag  
61 aacgcagcgc gtcagggccg agctcttcac tggcctgctc cgcgctcttc aatgccagcg  
121 ccaggcgtc accctgcaga gcgtcccgcc tctcaaagag ggggtgtgacc cgcgagttaa  
181 gataggaggt tctgtccgtg gggaacaccc cgcgcctc ggagctttt ctgtggcgca  
241 gcttctcgc ccgagccgcg cgcggagctg ccgggggctc cttagcacc gggcgccggg  
301 gccctcgccc ttccgcagcc ttcactccag ccctctgctc ccgcacgcca tgaagtgcgc  
361 gttctaccgc tgccagaaca ccacctctgt ggaaaaaggc aactcggcgg tgatggcgcg  
421 ggtgctcttc agcaccggcc tcttgggcaa cctgctggcc ctgggggtgc tggcgcgctc  
481 ggggctgggg tgggtctgcg ggcgtccact gcgcccgtg cctcgggtct tctacatgct  
541 ggtgtgtggc ctgacgggtc ccgacttgct ggcaagtgc ctctaagcc cgggtgtgct  
601 ggtgcctac gctcagaacc ggagtctgcg ggtgcttgcg ccgcattgg acaactcgtt  
661 gtgcaagcc ttgccttct tcatgtcctt ctttgggctc tctcgcacac tgcaactcct  
721 ggccatggca ctggagtgtt ggtctccct agggcaccct ttcttctacc gacggcacat  
781 caccctgcgc ctggggcgac tgggtggccc ggtgggtgag gccttctccc tggctttctg  
841 cgcgtacct ttcatgggct tcgggaagtt cgtgcagtac tgcccgggca cctggtgctt  
901 tatccagatg gtccacgagg agggctcgct gtcggtgctg gggtaactct tgctctactc  
961 cagcctcatg gcgctgctgg tctcgcac cgtgctgtgc aacctcggcg ccattgcgcaa  
1021 cctctatgcg atgcaccggc ggctgcagcg gcacccgcgc tctgcacca gggactgtgc  
1081 cgagccgcgc gcggacggga gggaagcgtc ccctcagccc ctggaggagc tggatcacct  
1141 cctgctgctg gcgctgatga ccgtgctctt cactatgtgt tctctgcccg taattgtgag  
1201 tccccgggccc ccgagg

## (2) INFORMATION FOR SEQ ID NO:2795:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2795

1 gggccgcgt cggcgcgctg ggtgcgggaa gggggctctg gatttcggtc cctccccctt  
61 ttcctctgag tctcggaaac ctccagctct cagaccctct tctcccagg taaaggccgg  
121 gagaggaggg cgcattctct ttccaggcac ccaccatgg gcaatgctc caatgactcc  
181 cagtctgagg actgcgagac gcgacagtgg ctccccccag gcgaaagccc agccatcagc  
241 tccgtcatgt tctcggccgg ggtgctgggg aacctcatag cactggcgct gctggcgcg  
301 cgtcggcggg gggacgtggg gtgcagcgcc ggccgcagga gctccctctc ctgttccac  
361 gtctgggtga ccgagctggt gttcaccgac ctgctcggga cctgcctcat gacccagtg  
421 gtactggctt cgtacgcgcg gaaccagacc ctggtggcac tggcgcccga gagccgcgcg  
481 tgcacctact tcgctttcgc catgaccttc ttcagcctgg ccacgatgt catgtcttc  
541 gccatggccc tggagcgcta cctctcgatc gggcaccctt acttctacca gcgcgcgctc  
601 tcggcctcgc ggggcctggc cgtgctgcct gtcattctat cagtctccct gctctctgc  
661 tcgctgccgc tgctggacta tgggcagtag gtccagtagt gccccgggac ctggtgcttc  
721 atccggcacg ggcggaccgc ttacctgcag ctgtacgcca cctgctgct gcttctcatt  
781 gtctcgggtc tcgcctgcaa cttcagtgct attctcaacc tcattccgat gcaccgcga  
841 agccggagaa gccgctgcgg accttccctg ggcagtggcc ggggcggccc cggggccgcg  
901 aggagagggg aaagggtgtc catggcgagg gagacggacc acctcattct cctggctatc  
961 atgaccatca ccttcgccgt ctgctccttg cctttcacga tttttgcata tatgaatgaa  
1021 acctcttccc gaaaggaaaa atgggacctc caagctctta ggtttttatc aattaattca  
1081 ataattgacc cttgggtctt tgccatcctt aggcctcctg ttctgagact aatgcgttca  
1141 gtcctctggt gtcggatttc attaagaaca caagatgcaa cacaacttc ctgttctaca  
1201 cagtcagatg ccagtaaaca ggctgacctt tgaggctcagt agtttaaaag ttcttagtta  
1261 tatagcatct ggaagatcat ttgaaaattg ttccctggag aaatgaaaac agtgtgtaaa  
1321 caaaatgaag ctgccctaatt aaaaaggagt atacaaacat ttaagctgtg gtcaaggcta  
1381 cagatgtgct gacaaggcac ttcatgtaaa gtgtcagaag gagctacaaa acctaccctc  
1441 aatgagcatg gtacttggcc tttggaggaa caatcggctg cattgaagat ccagctgcct  
1501 attgatttaa gctttcctgt tgaatgacaa agtatgtggt tttgttaatt gtttgaaacc  
1561 ccaaacagtg actgtacttt ctattttaat ctgtactata ccgttatata catatagtgt  
1621 acagccagac cagattaaac ttcatatgta atctctagga agtcaatatg tggaaagcaac  
1681 caagcctgct gtcttgtgat cacttagcga accctttatt tgaacaatga agttgaaat  
1741 cataggcacc ttttactgtg atgtttgtgt atgtgggagt actctcatca ctacagtatt  
1801 actcttacaa gagtggactc agtgggttaa catcagtttt gtttactcat cctccaggaa

1861 ctgcagggtca agttgtcagg ttattttatt tataatgtcc atatgctaag agtgatcaag  
 1921 aagacttttag gaatggttct ctcaacaaga aataatagaa atgtctcaag gcagttaatt  
 1981 ctcatataata ctcttattat cctatttctg ggggaggatg tacgtggcca tgtatgaagc  
 2041 caaatatttag gcttaaaaac tgaaaaatct gggttcattct tcagatatac tggaaacctt  
 2101 ttaaagttga tattggggcc atgagtaaaa tagattttat aagatgactg tgtgtacca  
 2161 aaattcatct gtctatattt tatttagggg aacatgggtt gactcatctt atatgggaaa  
 2221 ccatgtagca gtgagtcata tcttaataata tttctaaatg tttggcatgt aaatgtaaac  
 2281 tcagcatcaa aatatttcag tgaatttgca ctgtttaatc atagtactg tgtaactca  
 2341 tctgaaatgt tacaaaaata aactataaaa ca

## (2) INFORMATION FOR SEQ ID NO:2796:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2796

1 agagaggaag gcgtggctcc ctccgggcc agtgagccct ggcgcgcgcg cggccgcggg  
 61 ccagcagcg gaggtagggc gcggctgcgc cccgcacat ggggggcagc ccagccccag  
 121 ccgcggtaaa cgcgcacctc gcgcgcgcgc cgcgcgcgct ctgccccctc ccgctgcggc  
 181 tctctggacg ccatccctc ctcacctga agccaacatg aaggagaccg ggggtacgg  
 241 aggggatgcc ccctctgca cccgcctcaa cactcctac acaggcatgt gggcgccga  
 301 gcgttcgcgc gaggcgcggc gcaacctcac gcgcctcca gggctctggc aggattgcgc  
 361 atcgggtgtc gtggccttcc cgatcacat gctgtcact ggtttcgtg gcaacgcact  
 421 ggcgatgtg ctctgtgtgc gcagctaccg gcgcgggag agcaagcgca agaagtcctt  
 481 cctgctgtgc atcggctggc tggcgctcac cgacctggtc gggcagcttc tcaccacccc  
 541 ggtcgtcatc gtcgtgtacc tgtccaagca gcgttgggag cacatcgacc cgtcggggcg  
 601 gctctgcacc ttttcgggc tgaccatgac tgttttcggg ctctcctcgt tgttcacgc  
 661 cagcgccatg gccgtcgagc gggcgctggc catcagggcg ccgactggt atgcgagcca  
 721 catgaagacg cgtgccaccc gcgctgtgct gctcggcgtg tggctggccg tgcctgcctt  
 781 cgccctgctg ccggtgctgg gcgtgggcca gtacaccgtc cagtggcccg ggacgtggtg  
 841 cttcatcagc accgggcgag ggggcaacgg gactagctct tcgcataact ggggcaacct  
 901 tttcttcgcc tctgcctttg ccttcctggg gctcttggcg ctgacagtca ccttttctg  
 961 caacctggcc accattaagg ccctggtgtc ccgctgccg gccaaaggcca cggcatctca  
 1021 gtccagtgcc cagtggggcc gcatcacgac cgagacggcc attcagctta tggggatcat  
 1081 gtgcgtgctg tcggtctgct ggtctccgct cctgataatg atgttgaata tgatcttcaa  
 1141 tcagacatca gttgagcact gcaagacaca cacggagaag cagaaagaat gcaacttctt  
 1201 cttaatatgt gttcgccctg cttcactgaa ccagatcttg gatccttggg ttacctgct  
 1261 gtaagaaag atccttcttc gaaagttttg ccaggtagca aatgctgtct ccagctgtc  
 1321 taatgatgga cagaaaggcg agcctatctc attatctaata gaaataatac agacagaagc  
 1381 atgaaagaaa aacttaact tgcattgtga cagcttctgg taacaaatat cgctaaacct  
 1441 tactgtgaat ttaggcattc ctggcatgcc actgtttatg cattgaagtg gaatttttgg  
 1501 tataaagcta aatggtctta gaagcataga aaatccctat gtgccaaaag tagtgaacaa  
 1561 caaacaaggg aaaatatatt aataacagtc tagtggtttt gttgagtctg ccattcgtag  
 1621 ctgaatatgt gattaattat gtgatgaaaa ctttttttat aaatgatctt ggtctattgg  
 1681 gg

## (2) INFORMATION FOR SEQ ID NO:2797:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2797

1 cccggggccag tgagccctgg cgcgcgcgcg gccgcggtcc cagcagcgga gtagggcggc  
 61 ggctgcgcgc cgcacatggt ggggcagccc agccccagcc gcggtaaaac ccgacctccg  
 121 ccgcccgcgc gcgcgcgtct gccccctccc gctgcggctc tctggacgcc atccccctct  
 181 cacctcgaag ccaacatgaa ggagaccgga ggtacggag gggatgcccc cttctgcacc  
 241 cgctcaacc actcctacac agcatgtgg gcgcgcgagc gttccgcccga ggcgcggggc  
 301 aacctcacgc gccctcagg gtctggcgag gattgcggat cgggtgtcgt ggccttcccg  
 361 atcacatgc tgcctactgg tttcgtgggc aacgcactgg ccatgctgct cgtgtcgcgc  
 421 agctaccggc gccgggagag caagcgcaag aagtccttcc tgcgtgcat cggctggctg  
 481 gcgctcaccg acctggctcg gcagcttctc accaccccg tctcatcgt cgtgtacctg  
 541 tccaagcagc gttgggagca catcgaccgc tcggggcggc tctgcacctt tttcgggctg  
 601 accatgactg ttttcgggct ctctcgtttg ttcacgcgca gcgccatgac cgtcagcgcc  
 661 gcgctggcca tcaggcgccc gcaactggtat gcgagccaca tgaagacgc tgccacccgc  
 721 gctgtgctgc tcggcggtg gctggccgtg ctgccttcg cctgctgccc ggtgctgggc  
 781 gtgggcccag acaccgtcca gtggccggg acgtggtgct tcacagcac cgggcgaggg  
 841 ggcaacggga ctactcttc gcataactgg ggcaaccttt tcttcgcctc tgcctttgcc

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901 ttccggggc tcttggcgct gacagtcacc ttttctcgca acctggccac cattaaggcc
961 ctggtgtccc gctgccgggc caaggccacg gcatctcagt ccagtgccca gtggggccgc
1021 atcacgaccg agacggccat tcagcttatg gggatcatgt gcgtgctgtc ggtctgctgg
1081 tctccgctcc tgataatgat gttgaaaatg atcttcaatc agacatcagt tgagcactgc
1141 aagacacaca cggagaagca gaaagaatgc aacttcttct taatagctgt tcgcctggct
1201 tcaactgaacc agatcctgga tccttggggt tacctgctgt taagaaagat ccttcttcga
1261 aagttttgcc agatcaggta ccacacaaac aactatgcat ccagctccac ctcttacctc
1321 tgccagtgtt cctcaacctt gatgtggagc gaccatttgg aaagataatg aaagaacgga
1381 gttggacatt ttattgcaat tctgcttcc ctgaatttgc atatttcttc ccacctgaga
1441 aggataatta tatattttaa tttggattat ttcttcattt ttatcttttt attttaatga
1501 ttgttttgc agtaataccc atggagatca actttattat tataatccat gcctctgaat
1561 attagattgg tttcttggat gggattttga atatgcattt aagaagtgg gaagaatttc
1621 acagatgatg attggaggaa aagtgatgaa aagaaagacc tgtgttccag gagttttctc
1681 caacttcaaa cctttacgtg aatcttaacc aaagtggaca tctttacatt tcatgatagc
1741 ttgcttttgc aatatgagtt tgaaaaatca gtataagctt atgatggta aaagtcaaca
1801 tattgagagt gataattcaa ttaataggat atgaacttaa cgatataaaa gcaaatgagg
1861 gcaggagggg

```

## (2) INFORMATION FOR SEQ ID NO:2798:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2798

```

1 agagaggaag gcgtggctcc ctccggggcc agtgagccct ggcgcgcgcg cgccgcgcgt
61 cccagcagcg gagtagggcg gcggtgctgc cccgcacccat ggggggcagc ccagccccag
121 ccgcggtaaa cgccgacctc cgccgcgcgc cgccgcgcgt ctgccccctc ccgctgcggc
181 tctctggacg ccatccccctc ctccctcga agccaacatg aaggagaccc ggggctacgg
241 aggggatgcc cccttctgca ccgcctcaa ccactcctac acaggcatgt gggcgcccga
301 gcgttccgcc gaggcgcggg gcaacctcac gcgccctcca ggtctggcg aggattgcgg
361 atcgggtgtc gtggccttcc cgatcaccat gctgctcact ggttctgtgg gcaacgcact
421 ggccatgctg ctgctgtcgc gcagctaccg gcgcgcggag agcaagcgca agaagtcctt
481 cctgctgtgc atcggtggc tggcgtcac cgacctggtc ggcagcttc tcaccacctc
541 ggtcgtcatc gtcgtgtacc tgtccaagca gcgttgggag cacatcgacc cgtcggggcg
601 gctctgcacc ttttccgggc tgaccatgac tgttttcggg ctctctcgt tgttcacgc
661 cagcgccatg gccgtcgagc gggcgctggc catcaggggc ccgcaactgt atgcgagcca
721 catgaagacg cgtgccaccc gcgtgtgtct gctcggcggt tggtggccg tgcctgcctt
781 cgccctgtg ccggtgtgtg gcgtgggcca gtacaccgtc cagtggcccg ggacgtggtg
841 cttcatcagc accgggcgag ggggcaacgg gactagctct tcgcataact ggggcaacct
901 tttcttcgcc tctgcctttg cttcctggg gctcttggcg ctgacagtc ccttttcctg
961 caacctggcc accattaagg ccctggtgtc ccgctgccg gccaaaggcca cggcatctca
1021 gtccagtgcc cagtggggcc gcatcacgac cgagacggcc attcagctta tggggatcat
1081 gtgcgtgtg tcggtctgct ggtctccgct cctgataatg atgttgaaaa tgatcttcaa
1141 tcagacatca gttgagcact gcaagacaca cacggagaag cagaaagaat gcaacttctt
1201 cttaataget gttcgccctg cttcactgaa ccagatcttg gatccttggg ttacctgct
1261 gtttaagaa atccttcttc gaaagtttgc ccaggtagca aatgctgtct ccagctgtc
1321 taatgatgga cagaaagggc agcctatctc attatcta atgaaataat agacagaagc
1381 atgaaagaaa acacttaact tgcattgtgc cagcttcttg taacaaatat cgctaaacct
1441 tactgtgaat ttaggcattc ctggcatgcc actgtttatg cattgaagt gaatttttgg
1501 tataaagcta aatggtctta gaagcataga aaatccctat gtgccaaaag tagtgaaca
1561 caaacaagg aaaaatatatt aataacagtc tagtgttttt gttgagctg ccattcgtag
1621 ctgaatatgt gattaattat gtgatgaaaa ctttttttat aaatgatctt ggtctattgg
1681 gg

```

## (2) INFORMATION FOR SEQ ID NO:2799:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2799

```

1 agagaggaag gcgtggctcc ctccggggcc agtgagccct ggcgcgcgcg cgccgcgcgt
61 cccagcagcg gagtagggcg gcggtgctgc cccgcacccat ggggggcagc ccagccccag
121 ccgcggtaaa cgccgacctc cgccgcgcgc cgccgcgcgt ctgccccctc ccgctgcggc
181 tctctggacg ccatccccctc ctccctcga agccaacatg aaggagaccc ggggctacgg
241 aggggatgcc cccttctgca ccgcctcaa ccactcctac acaggcatgt gggcgcccga
301 gcgttccgcc gaggcgcggg gcaacctcac gcgccctcca ggtctggcg aggattgcgg
361 atcgggtgtc gtggccttcc cgatcaccat gctgctcact ggttctgtgg gcaacgcact

```



```

421 ggccatgctg ctcgtgtcgc gcagctaccg gcgccgggag agcaagcgca agaagtcttt
481 cctgctgtgc atcggttggc tggcgctcac cgacctggc gggcagcttc tcaccacccc
541 ggtcgtcatc gtcgtgtacc tgtccaagca gcgttgggag cacatcgacc cgtcggggcg
601 gctctgcacc tttttcgggc tgaccatgac tgttttcggg ctctcctcgt tgttcacgc
661 cagegccatg gccgtcgagc gggcgctggc catcaggggc ccgcactggt atgcgagcca
721 catgaagacg cgtgccaccc gcgctgtgct gctcggcggt tggctggccg tgcctgcctt
781 cgccctgctg ccggtgctgg gcgtgggcca gtacaccgtc cagtggcccg ggacgtgggtg
841 cttcatcagc accggcgagc ggggcaacgg gactagctct tcgcataact ggggcaacct
901 tttcttcgcc tctgcctttg ccttcctggg gctcttggcg ctgacagtca ccttttctg
961 caacctggcc accattaagg ccctgggtgc ccgctgccgg gccaaaggcca cggcatctca
1021 gtccagtgcc cagtggggcc gcatcacgac cgagacggcc attcagctta tggggatcat
1081 gtgcgtgctg tcggtctgct ggtctccgct cctgataatg atgttgaaaa tgatcttcaa
1141 tcagacatca gttgagcact gcaagacaca cacggagaag cagaaagaat gcaacttctt
1201 cttaatagct gttcgccctg cttcactgaa ccagatcttg gatccttggg tttacctgct
1261 gtttaagaaag atccttcttc gaaagttttg ccaggaggaa ttttggggaa attaaacctt
1321 gcctttctgc caggatcaca tcaactggaag ctccatgact ctctttttgt aaaagaaa

```

## (2) INFORMATION FOR SEQ ID NO:2800:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: \_ base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2800

```

1 gtgcgcggag gggacgagc gctggaccac agccggcgcc cgatcaggat ctccgcgctg
61 ggatcggttg aactgagggc agcggcgccg cgggcgccca tggcacaccg agcggctccg
121 tcttctgctc ctacagagac ccggtggcg gcttgggatg acaagatgtc tggactgcaa
181 tcttgacacg ttttgagagg gagatgactt gagtgggttg cttttatctc cacaacaatg
241 tccatgaaca attccaaaca gctagtgtct cctgcagctg cgcttctttc aaacacaacc
301 tgccagacgg aaaaccggct ttccgtatct ttttcagtaa tcttcatgac agtgggaaac
361 ttgtcaaaaa gccttgccat cgccattctc atgaaggcat atcagagatt tagacagaag
421 tccaaggcat cgtttctgct tttggccagc ggcctggtaa tcaactgatt ctttggccat
481 ctcatcaatg gagccatagc agtatttgta tatgcttctg ataaagaatg gatccgcttt
541 gaccaaatcaa atgtcctttg cagtattttt ggtatctgca tgggtgtttc tgggtctgtg
601 ccacttcttc taggcaggtg gatggccatt gagcgggtga ttggagtcac aaaaccaata
661 tttcattcta cgaaaattac atccaaacat gtgaaaatga tgttaagtgg tgtgtgcttg
721 tttgctgttt tcatagcttt gctgcccac cttggacatc gagactataa aattcaggcg
781 tcgaggacct ggtgtttcta caacacagaa gacatcaaag actgggaaga tagattttat
841 cttctacttt tttcttttct ggggctctta gcccttgggt tttcattggt gtgcaatgca
901 atcacaggaa ttacactttt aagagttaaa tttaaaagtc agcagcagat acaaggcaga
961 tctcatcatt tggaaatggt aatccagctc ctggcgataa tgtgtgtctc ctgtatttgt
1021 tggagcccat ttctggttac aatggccaac attggaataa atggaaatca ttctctggaa
1081 acctgtgaaa caacactttt tgctctccga atggcaacat ggaatcaaat cttagatcct
1141 tgggtatata ttcttctacg aaaggctgtc cttaagaatc tctataagct tgccagtcaa
1201 tgctgtggag tgcatgtcat cagcttacat atttgggagc ttagttccat taaaaattcc
1261 ttaaagggtg ctgctatttc tgagtcacca gttgcagaga aatcagcaag cacctagctt
1321 aataggacag taaatctgtg tggggctaga acaaaaatta agacatgttt ggcaatat
1381 cagtttagtta aataactgta gcctaactgg aaaattcagg cttcatcatg tagtttgaag
1441 atactattgt cagattcagg ttttgaaatt tgtcaataaa acaggataac tgtacatttt
1501 caacttgttt ttgccaatgg gaggtagaca caataaaata atgccatggg agtcacactg
1561 aaagcaattt tgagcttata tgtcttattt atgctttgag tgaatcatct gttgaggtct
1621 aatgcctcta cttggcctat ttgccagaga acatcttaac gcagcctgca tagtgaaatg
1681 gttattttga gatcaccgct ctgtagctaa cctttataaa ctaggctcag taaaataaag
1741 cactcttatt ttttgatctg gcctattttg cccctcattg ttagcctcctc attaacacat
1801 gcattgtcat gacaccaga atctatgatg gtttgttata acaacctctg catattccag
1861 gtctggcaga caggttgctt gacctgcaa tccatcttag aatgggcccc ttcttgtcac
1921 atttgacaaa taggactgcc tacatttatt attatgaagg tcgattgttg ttggaagtgt
1981 tttttcatgt catagattag caattttcaa ataattattt tttctctgaa aattttgtgt
2041 gtgattgcac aataaataat ttttagagaa acaaaggctc tttctcagca cattgatggg
2101 caactagaat tacagcagtt tcaaactcta ccattggataa tgcaaaacaaa ccgaagctac
2161 atgccaatga taggtgcaaa gaattattggc aaaagggtgt ttaccttgag ccattatttg
2221 tgtcagagaa caaaagaaac agaataataa tataaattca aagactatct gcagctagtg
2281 tgtttcttct ttacacacat atacacacag acatcagaaa attctgttga gagcaggttc
2341 attaaatttg taagatggca tattctaaag cctgtgtctc cagtactaag aggggaagac
2401 tggcaatttg ccaagcactt ggggattatt ataacaatta actaggagat caagagataa
2461 taatctctcc ccaattttc caataataat tgag

```

## (2) INFORMATION FOR SEQ ID NO:2801:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2801

```
1 ggcacagacg cacgggacag gagagcctgg gcaagactgg agagcccaga cctgggatgg
61 cggattcgtg caggaacctc acctacgtgc ggggctcggg ggggcccggc accagcaccc
121 tgatgttcgt ggccggtgtg gtgggcaacg ggctggccct gggcaccctg agcgacggc
181 gaccggcgcg ccctcgggcc ttccggtggt tggtaaccgg actggcggcc accgacctgc
241 tgggcaccag ctctctgagc ccggccgtgt tcgtggccta tgcgcgcaac agctccctgc
301 tgggcccggc ccgaggcggc cccgccctgt gcgatgcctt cgcttcgcc atgaccttct
361 tcggccctggc gtccatgctc atctctttg ccatggccgt ggagcgctgc ctggcgctga
421 gccacccccta cctctacgag cagctggagc ggcccgcgtg cggccgctg gcgctgccag
481 ccattctacg ctctctgctc ctctctgctg cgctggccct gctgggctg ggccaacacc
541 agcagtactg ccccggcagc tgggtgcttc tccgcatgag ctgggcccag ccggcgggcg
601 ccgcttcttc gctggcctac gccggcctgg tggccctgct ggtggctgcc atcttctct
661 gcaacggctc ggtcacctc agcctctgct gcatgtaccg ccagcagaag cgccaccagg
721 gctctctggg tccacggccg cgcaccggag aggacgaggt ggaccacctg atcctgctgg
781 ccctcatgac agtgggtcat gccgtgtgct ccctgctct cactatccgc tgcctcacc
841 aggtctgtcg ccctgacagc agcagtgaag tgggggacct ccttgccctc cgcttctacg
901 ccttcaaccc cactctggac ccctgggtct tcatcctttt ccgcaaggct gtcttcagc
961 gactcaagct ctgggtctgc tgcctgtgct tggggcctgc ccacggagac tcgcagacac
1021 ccttttccca gctcgcctcc gggaggaggg acccaagggc cccctctgct cctgtgggaa
1081 aggaggggag ctgctgctct ttgtcggctt ggggagaggg gcaggtggag cccttgctc
1141 ccacacagca gtccagcggc agcgccgtg gaacgtcgtc caaagcagaa gccagcgctg
1201 cctgctccct ctgctgacat ttcaagctga ccctgtgatc tctgccctgt ctccggcgga
1261 caggagccag aaaatcaggg acatggctga tggctgcgga tgctggaacc ttggccccc
1321 aactctgggg ccgatcagct gctgtttctc tgcggcaggg cagtcgctgc tggctctggg
1381 aagagagtga gggacagagg aaacgtttat cctggag
```

## (2) INFORMATION FOR SEQ ID NO:2802:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2802

```
1 gctgtgcaac ctggcgcca tgcgcaacct ctatgcgatg caccggcgcc tgcagcgcca
61 cccgcgctcc tgcaccaggg actgtgccga gccgcgcgcg gacgggaggg aagcgtcccc
121 tcagccctg gaggagctgg atcacctcct gctgctggcg ctgatgaccg tgccttccac
181 tatgtgttct ctgcccgtaa ttatcgcgc ttactatgga gcatttaagg atgtcaagga
241 gaaaaacagg acctctgaag aagcagaaga cctccgagcc ttgcgatttc tatctgtgat
301 ttcaattgtg gacccttggg tttttatcat ttccagatct ccagtatttc ggatattttt
361 tcacaagatt ttcattagac ctcttaggta caggagccgg tgcagcaatt ccactaacat
421 ggaatccagt ctgtgacagt gtttttcaat ctgtggttag ctgaggaata tgtcacattt
481 tcagtcaag aacca
1 gaattctggc tattttctc ctgcccgtcc gactcggcac cagagtctgt ctctactgag
61 aacgcagcgc gtcaggcgcc agctcttcac tggcctgctc cgcgctcttc aatgccagcg
121 ccaggcgctc accctgcaga gcgtcccgcc tctcaaagag ggggtgtgac cgcgagtta
181 gataggaggt tcctgcctg ggaacaccc cgcgcctc ggagctttt ctgtggcgca
241 gcttctccgc ccgagccgag cgcggagctg ccgggggctc cttagcacc gggcgccggg
301 gccctcgccc ttccgcagcc ttactccag ccctctgctc ccgcacgcca tgaagtgcg
361 gttctaccgc tgcagaaca ccacctctgt ggaagaggc aactcggcg tgatggcgcg
421 ggtgctcttc agcaccggcc tctgggcaa cctgctggcc ctggggctgc tggcgcgctc
481 ggggctggg tgggtctgc ggcgtccact gcgcccgtg ccctcggtct tctacatgct
541 ggtgtgtggc ctgacggtca ccgacttgc tggcaagtgc ctctaagcc cgggtgtgct
601 ggctgcctac gtcagaacc ggagtctgc ggtgcttgc cccgattgg acaactcgtt
661 gtgccaagcc ttcgcttct tcatgtcctt ctttgggctc tctcgacac tgcaactcct
721 ggccatggca ctggagtgt ggctctccct agggcaccct ttcttctacc gacggcacat
781 caccctgcgc ctgggcgcac tgggtggccc ggtggtgagc gccttctccc tggcttctg
841 cgcgctacct ttcatgggt tgggaagtt cgtgcagtac tggcccgga cctggtgctt
901 taccagatg gtccacgagg agggctcgct gtcggtgctg ggtactctg tgctctactc
961 cagctcatg gcgctgctg tctcgccac cgtgctgtgc aacctcggc ccatgcgcaa
1021 cctctatgag atgcaccggc ggctgcagcg gcacccgcgc tctgcacca gggactgtgc
1081 cgagccgcgc gcggacggga ggaagcgtc ccctcagccc ctggaggagc tggatcacct
1141 cctgctgctg gcgctgatga ccgtgctct cactatgtgt tctctgccc taattgtgag
1201 tccccggg ccgagg
1 gggccgccc ctggcgctg ggtgcgggaa gggggctctg gatttcggtc cctccccctt
61 ttctctgag tctcggaac ctccagctct cagaccctct tctcccagg taaaggccgg
```

121 gagaggaggg cgcattcttt ttccaggcac cccaccatgg gcaatgcctc caatgactcc  
 181 cagtctgagg actgcgagac ggcacagtgg ctccccccag gcgaaagccc agccatcagc  
 241 tccgtcatgt tctcgccggg ggtgctgggg aacctcatag cactggcgct gctggcgcg  
 301 cgctggcggg gggacgtggg gtgcagcgcc ggccgcagga gctccctctc cttgttccac  
 361 gtgctgggtga ccgagctggg gttaccgcag ctgctcggga cctgcctcat cagcccagtg  
 421 gtactggctt cgtacgcgcg gaaccagacc ctgggtggcag tggcgcccga gagccgcgcg  
 481 tgcacctact tcgctttcgc catgaccttc ttcagcctgg ccacgatgct catgctcttc  
 541 gccatggccc tggagcgcta cctctcgatc gggcaccctt acttttacca gcgcgcgctc  
 601 tcggcctccg ggggcctggc cgtgctgcct gtcattctat cagtctccct gctcttctgc  
 661 tcgctgcgcg tgcctggacta tgggcagtag gtccagtagt gcccggggac ctgggtgcttc  
 721 atccggcacg ggcggaccgc ttacctgcag ctgtacgcca ccctgctgct gcttctcatt  
 781 gtctcgggtgc tcgcctgcaa cttcagtgct attctcaacc tcatccgcat gcaccgcccga  
 841 agccggagaa gccgctgcgg accttccctg ggcagtgggc ggggcccggc cggggcccgc  
 901 aggagagggg aaagggtgtc catggcgga ggcagggacc acctcattct cctggctatc  
 961 atgaccatca ccttcgcccgt ctgctccttg cctttcacga tttttgata tatgaatgaa  
 1021 acctcttccc gaaaggaaaa atgggacctc caagctctta ggtttttatc aattaattca  
 1081 ataattgacc cttgggtctt tgccatcctt aggcctcctg ttctgagact aatgcgttca  
 1141 gtctctgtgt gtcggatttc attaagaaca caagatgcaa cacaacttct ctgttctaca  
 1201 cagtcatgat ccagtaaaaca ggctgacctt tgagggtcagt agtttaaaag ttcttagtta  
 1261 tatagcatct ggaagatcat tttgaaattg ttccctggag aaatgaaaac agtgtgtaaa  
 1321 caaaatgaag ctgccctaata aaaaaggagt atacaaacat ttaagctgtg gtcaaggcta  
 1381 catagtgtgt gacaaggcac ttcatgtaaa gtgtcagaag gagctacaaa acctaccctc  
 1441 aatgagcatg gtacttggcc tttggaggaa caatcggtg cattgaagat ccagctgcct  
 1501 attgatttaa gctttcctgt tgaatgacaa agtatgtggt tttgtaattt gtttgaacc  
 1561 ccaaacagtg actgtacttt ctattttaat cttgtacta ccgttatata catatagtgt  
 1621 acagccagac cagattaaac ttcatatgta atctctagga agtcaaatag tggagcaac  
 1681 caagcctgct gtcttgatgt cacttagcga accctttatt tgaacaatga agttgaaaat  
 1741 cataggcacc tttactgtgt atgtttgtgt atgtgggagt actctcatca ctacagtatt  
 1801 actcttaca gactggactc agtgggttaa catcagtttt gttactcat cctccaggaa  
 1861 ctgcaggcca agttgtcagg ttatttattt tataatgtcc atatgctaag agtgatcaag  
 1921 aagactttag gaatggttct ctcaacaaga aataatagaa atgtctcaag gcagttaatt  
 1981 ctcatataa ctcttattat cctatttctg ggggaggatg tacgtggcca tgtatgaagc  
 2041 caaatattag gcttaaaaaac tgaaaaatct ggttcattct tcagatatac tggaaacctt  
 2101 ttaaagttga tattggggcc atgagtaaaa tagattttat aagatgactg tgttgtaacca  
 2161 aaattcatct gtctatattt tatttagggg aacatggttt gactcatctt atatgggaaa  
 2221 ccagttagca gtgagtcata tcttaataata tttctaaatg tttggcatgt aaatgtaaac  
 2281 tcagcatcaa aatatttcag tgaatttgca ctgtttaatc atagttactg tgtaaacatc  
 2341 tctgaaatgt taaaaaata aactataaaa ca  
 1 agagaggaag gcgtggctcc ctccccggcc agtgagccct ggcgcgcgcg cggccgcggt  
 61 ccagcagcg gagtagggcg ggcgctgcgc cccgcaccat ggggggcagc ccagccccag  
 121 ccgcggtaaa cgcgcacctc cgcgcgcgcg cgcgcgcgct ctgccccctc ccgctgcggc  
 181 tctctggacg ccacccccct ctcacctcga agccaacatg aaggagaccc ggggctacgg  
 241 aggggatgcc cccttctgca cccgcctcaa ccactcctac acaggcatgt gggcgcccga  
 301 gcgttccgcc gaggcgcggg gcaacctcac gcgcctcca gggctctggc aggtatgcgg  
 361 atcggtgtcc gtggccttcc gcatcaccat gctgctcact ggtttcgtgg gcaacgcact  
 421 ggccatgctg ctctgtctgc gcagctaccg gcgcggggag agcaagcgca agaagtcctt  
 481 cctgctgtgc atcggtggc tggcgctcac cgacctggc gggcagcttc tcaccacccc  
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## (2) INFORMATION FOR SEQ ID NO:2803:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: \_ base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2803

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## (2) INFORMATION FOR SEQ ID NO:2804:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: \_ base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2804

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(2) INFORMATION FOR SEQ ID NO:2805:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: \_ base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2805

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## (2) INFORMATION FOR SEQ ID NO:2806:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2806

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2881 ccaatccact cttctcttc tatcattccc ctgcccacct ccttccagca ctgactggaa  
2941 gggaagtca ggctctgaga cagccccaa catgcctgca cctgcagcgc gcacacgcac  
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## (2) INFORMATION FOR SEQ ID NO:2807:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2807

1 tttattttta atttaacac ttaattttta atttttaaga tggagtctca ctctgttgcc  
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181 gataattttt tgtatttttt agtagagacg gggcttcacc atgttggcca ggtgtgtctt  
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8941 aaaagccagt tccagcgggg ctgtgcacac tgtcgttcag gtcgcatacct gtacaagtgg
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## (2) INFORMATION FOR SEQ ID NO:2808:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2808

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1 ggaaagaaaag aaagaaaaga aacctgtcc tcaccctact tcaggccctg tctctgcccc
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121 atgccttctc tgagatggtg aggaagctcc ttggtagtgt gaggaagac ggtgcagggt
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601 cagaagatct tcaatgacaa cagcctcagt atggaggcct tccagaccg tctgtgtccc
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## (2) INFORMATION FOR SEQ ID NO:2809:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2809

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121 tgggtggttca tgctgtaat ccagcactt tgggaggccg agacggatag atcacctgag
181 gtcaggagtt cgagaccagc ctggccaaca tggcaaaacc ccgtctctac taaaaacaaa
241 aaaatagcca ggatggtcgt ttgctgtctg aatcccagct actcggctga ggcaggaggt

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301 gaaccagga ggtaaaggct gcaggggaag atgaaaccat tgcaactccag cctgggcaag  
361 actctgtatc aaaaaaaaaa aaaaaaaggc taggtgtggt ggctcacacc tgtaatccca  
421 gcactttggg aggtgagggc gggcggatca caaggtcaag aaatcgagac catcctgacc  
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661 tctgtc

## (2) INFORMATION FOR SEQ ID NO:2810:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2810

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5221 tgaaggatc ccacaccac cgcccctatg tagggcaggg aagaaattgc aaaggacttg  
5281 ggggatagat gggaatggga gggcaaactg cagcatttgt taaattaatt aaagaaacaa  
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## (2) INFORMATION FOR SEQ ID NO:2811:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2811

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121 agagggagaa tgggataggg gagtgaaggg aagctggcgg tggatggggc aacagaaaag  
181 atgcagcagg cagggccctc tcatacactg gagggccaca tggccaggctc tggaccaga  
241 ctctcaccct ggctcccagg cagcattgga ggtgtggagc catacgtaga tgtcacagcc  
301 acttgagccc acttgggcac agtcagactc caaattcaga gtatttgggg gttagcatat  
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1441 tgccaccag cctccactcc caagctgccac ctac

## (2) INFORMATION FOR SEQ ID NO:2812:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2812

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(2) INFORMATION FOR SEQ ID NO:2813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2813

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## (2) INFORMATION FOR SEQ ID NO:2814:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2814

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## (2) INFORMATION FOR SEQ ID NO:2815:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2815

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2281 catgctacct gtgaaaatga agaggaaatg gacaatctaa agcacagcag agtgactgta  
2341 gcaatacctt taaaatatga ggttaagctg actgttcatg ggtttgtaaa cccaacttca  
2401 tttgtgtatg gatcaaatga tgaaaatgag cctgaaacgt gcattggtgga gaaaatgaac  
2461 ttaactttcc atgttatcaa cactggcaat agtatggctc ccaatgttag tgtggaata  
2521 atggtaccaaa attcttttag ccccaaaact gataagctgt tcaacatttt ggatgtccag  
2581 actactactg gagaatgccaa ctttgaataa tatcaaagag tgtgtgcatt agagcagcaa  
2641 aagagtgcga tgcagacctt gaaaggcata gtccggttct tgtccaagac tgataagagg  
2701 ctattgtact gcataaaagc tgatccacat tgtttaaatt tcttgtgtaa ttttgggaaa  
2761 atggaaagtg gaaaagaagc cagtgttcat atccaaactg aaggccggcc atccatttta  
2821 gaaatggatg agacttcagc actcaagttt gaaataagag caacagggtt tccagagcca  
2881 aatccaagag taattgaact aaacaaggat gagaatgttg cgcattgtct actggaagga  
2941 ctacatcatc aaagacccaa acgttatctt accatagtga ttatttcaag tagcttgcta  
3001 cttggactta ttgtacttct gttgatctca tatgttatgt ggaaggctgg cttctttaaa  
3061 agacaataca aatctatcct acaagaagaa aacagaagag acagttggag ttatatcaac  
3121 agtaaaagca atgatgatta aggacttctt tcaaattgag agaattgaaa acagactcag  
3181 gttgtagtaa agaaatttaa aagacactgt ttacaagaaa aaatgaattt tgtttggact  
3241 tcttttactc atgatcttgt gacatattat gtcttcatgc aaggggaaaa tctcagcaat  
3301 gattactctt tgagatagaa gaactgcaaa ggtaataata cagccaaaaga taatctctca  
3361 gcttttaaat gggtagagaa acactaaagc attcaattta ttcaagaaaa gtaagccctt  
3421 gaagatatct tgaaatgaaa gtataactga gttaaaattat actggagaag tcttagactt  
3481 gaaatactac ttaccatatg tgcttgcttc agtaaaatga accccactgg gtgggcagag  
3541 gttcatttca aatacatctt tgatacttgt tcaaaatatg ttctttaaaa atataatttt  
3601 ttagagagct gttcccaaat tttctaacga gtggaccatt atcactttaa agccctttat  
3661 ttataataca tttctacgg gctgtgttcc aacaaccatt ttttttcagc agactatgaa  
3721 tattatagta ttataggcca aactggcaaa cttcagactg aacatgtaca ctggtttgag  
3781 cttagtgaat tgacttccgg aatct

## (2) INFORMATION FOR SEQ ID NO:2816:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2816

## (2) INFORMATION FOR SEQ ID NO:2817:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2817

## (2) INFORMATION FOR SEQ ID NO:2818:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2818

## (2) INFORMATION FOR SEQ ID NO:2819:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \_ base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2819

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

1  cagctgtccc tccccactgc catttattcc ttccttcatt caaaccttat gtggctgcta
61  cttaccgtgt gttaagtgtt cacttttttt cttggaattc aaaaaagaa ggacagtatt
121 tggggcacag atcttttgggt gttctatata tttttttaa gtttcatttt acatttgtgt
181 gtgcgtgtgt gtgtgtgtgt gagacagtct tgctctgttg ccaggctgg agtcagtggt
241 cataatcatt ggctcactgt agcctcaaag tcctgggccc aagcgatctt cccacctcag
301 ccacccaaaa tgctgggggtt acaggtttat gccactctgt ctgacctgaa agttttgggt
361 ttactttccc ttctttctct ttgctgaagt cagagatgat ggcagcttcc agattctctg
421 gtgcctgtgc tgggctcgtg ctggctcatg tcttgggtcc aggattcatt ctggagactc
481 tcagggaagt ttcccatgac aaggaaatgt aggagagtgt gctggctttg cgtgctcctc
541 tgccaagccc tgcttctcct ggtgggacac actgaaccac agccagggca ttttgggtgt
601 tagttaaaaa aaaaaaaaaa aaaaaaagg aagaagaagg cactgtgtaa ttgtgccggg
661 gatcttcaga aattgtaatg atgaaagagt gcaagctctc acttcccctt cctgtacagg
721 gcaggttgtg cagctggagg cagagcagtc ctctctgggg agcctgaagc aaacatggat
781 caagaaactg taggcaatgt tgtcctgttg gccatcgta ccctcatcag cgtggtccag
841 aatggtaagg aaagcccttc actcagggaa gaacagaagg ggagattttc tttgatggtt
901 gtttggaagt caggcttaaa caattgtgtc tgtgtgtgct catgcacaaa cacttttacc
961 ttatctttat tttcttctt ttatttgaat gtataggggt gtgtgtattt ctgtgtaaat
1021 ttgggggttt cctcctctta gtctttcact tttgtggtga ttaccagtcc catttttaga
1081 gccagggctg caacttgaag gttttgct

```

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

1  tgcgttttgg gggttcctgg agtatcaatc atggatcaag aaactgtagg caatgttgtc
61  ctgttgccca tcgtcaccct catcagcgtg gtccagaatg gattctttgc ccataaagt
121 gagcacgaaa gcaggaccca gaatggagg agcttccaga ggaccggaac acttgccttt
181 gagcggtgtc acactgccaa ccagaactgt gtatgtgcgt accccacttt cctcgtgtg
241 ctctggtctg cggggctact ttgcagccaa gttcctgctg cgtttgtgtg actgatgtac
301 ttgtttgtgc ggcaaaagta ctttgtcggg tacctaggag agagaacgca gagcaccctt
361 ggctacatat ttgggaaacg catcatactc ttctgttcc tcatgtccgt tgctggcata
421 ttcaactatt acctcatctt ctttttcgga agtgactttg aaaactacat aaagacgatc
481 tccaccacca tctcccctct acttctcatt tcctaactct ctgctgaata tggggttggg

```

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2022 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
1 atgccctcct acacggtcac cgtggccact ggcagccagt ggctgcgcgg cactgacgac
61 tacatctacc tcagcctcgt gggctcggcg ggctgcagcg agaagcacct gctggacaag
121 ccccttctaca acgacttcga gcgtggcgcg gtggattcat acgacgtgac tgtggacgag
181 gaactggggcg agatccagct ggtcagaatc gagaagcgca agtactggct gaatgacgac
241 tggtagctga agtacatcac gctgaagacg cccacacggg actacatcga gttccctcgc
301 taccgctgga tcaccggcga tgtcgaggtt gtcctgaggg atggacgcgc aaagtgggcc
361 cgagatgacc aaattcacat tctcaagcaa caccgacgta aagaactgga aacacggcaa
421 aaacaatatc gatggatgga gtggaaccct ggcttcccct tgagcatcga tgccaaatgc
481 cacaaggatt taccctgta tatccagttt gatagtga aaaggatgga ctttgttctg
541 aattactcca aagcgatgga gaacctgttc atcaaccgct tcatgcacat gttccagtct
601 tcttggaatg acttcgccga ctttgagaaa atctttgtca agatcagcaa cactatttct
661 gagcgggtca tgaatcactg gcaggaagac ctgatgtttg gctaccagtt cctgaatggc
721 tgcaaccctg tgttgatccg gcgctgcaca gagctgcccg agaagctccc ggtgaccacg
781 gagatggtag agtgacgctt ggagcggcag ctgagcttgg agcaggaggt ccagcaaggg
841 aacattttca tcgtggactt tgagctgctg gatggcatcg atgccaacaa aacagacccc
901 tgcacactcc agttcctggc cgtcccatc tgcttctgtg ataagaacct ggccaacaag
961 attgtcccca ttgccatcca gctcaaccaa atcccgggag atgagaacct tattttcctc
1021 ccttcggatg caaaatcacg ctggcttttg gccaaaatct ggggtcgttc cagtgaactc
1081 cagctccacc agaccatcac ccactttctg cgaacacatc tgggtgtctga ggtttttggc
1141 attgcaatgt accgccagct gcctgctgtg caccctattt tcaagctgct ggtggcacac
1201 gtgagattca ccattgcaat caacaccaag gccgtgagc agctcatctg cgagtgtggc
1261 ctctttgaca aggccaacgc cacagggggc ggtgggcacg tgcagatggt gcagagggcc
1321 atgaaggacc tgacctatgc ctccctgtgc tttcccgagg ccatcaaggc ccggggcatg
1381 gagagcaaag aagacatccc ctactacttc taccgggacg acgggctcct ggtgtgggaa
1441 gccatcagga cgttcacggc cgaggtggtg gacatctact acgagggcga ccaggtggtg
1501 gaggaggacc cggagctgca ggacttcgtg aacgatgtct acgtgtacgg catgccccgc
1561 cgcaagtccct caggcttccc caagtccgtc aagagccggg agcagctgtc ggaagtacctg
1621 accgtggtga tcttcaccgc ctccgcccag cacgcccggg tcaacttcgg ccagtacgac
1681 tgggtctcct ggatcccaa tgcccccac accatgcgag ccccgccacc gactgccaa
1741 ggcgtggtga ccattgagca gatcgtggac acgctgcccg acccgggcgc ctctgtctg
1801 catctgggtg cagtgtgggc gctgagccag ttccaggaaa acgagctgtt cctgggcatg
1861 taccagaaag agcattttat cgagaagcct gtgaaggaa ccatggcccg attccgcaag
1921 aacctcgagg ccattgtcag cgtgattgct gagcgcaaca agaagaagca gctgccatat
1981 tactacttgt cccagaccg gattccgaac agtgtggcca tc
```

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2500 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
1 gggcccgcg ctcgtgtct ccgcccgcg cgccatgcc tcctacacgg tcaccgtggc
61 cactggcagc cagtggttcg ccggcactga cgactacatc tacctcagcc tcgtgggctc
121 ggccggctgc agcgagaagc acctgctgga caagcccttc tacaacgact tcgagcgtgg
181 cgcggtggat tcatacgacg tgactgtgga cgaggaaactg ggcgagatcc agctggtcag
241 aatcgagaag cgcaagtact ggctgaatga cgactggtac ctgaagtaca tcacgctgaa
301 gacgccccac ggggactaca tcgagttccc ctgctaccgc tggatcaccg gcgagtgcga
361 ggtgtcctg agggatggac gcgcaaagtt ggcccagat gaccaaattc acatttcaa
421 gcaacaccga ctgaaagaac tggaaacacg gcaaaaacaa tatcgatgga tggagtggaa
481 ccctggcttc cccttgagca tcgatgccaa atgccacaag gatttacctc gtgatatcca
541 gtttgatagt gaaaaaggag tggactttgt tctgaattac tccaaagcga tggagaacct
601 gttcatcaac cgcttcatgc acatgttcca gtcttcttgg aatgacttcg ccgactttga
661 gaaaatcttt gtcaagatca gcaacactat ttctgagcgg gtcatgaatc actggcagga
721 agacctgatg ttggctacc agttcctgaa tggctgcaac cctgtgttga tccggcgctg
781 cacagagctg cccgagaagc tcccgtgac cacggagatg ttagagtga ccctggagcg
841 gcagctcagc ttggagcagg aggtccagca agggaaacatt tcatcgtgg actttgagct
901 gctggatggc atcgatgcca acaaaacaga cccctgcaca ctccagttcc tggccgctcc
961 catctgcttg ctgtataaga acctggccaa caagattgtc cccattgcca tccagctcaa
1021 ccaaatcccc ggagatgaga accctatttt cctcccttcg gatgcaaaat acgactggct
1081 tttggccaaa atctgggtgc gttccagtga cttccacgtc caccagacca tcacccacct
1141 tctgcgaaca catctggtgt ctgaggtttt tggcattgca atgtaccgcc agctgcctgc
1201 tgtgcacccc attttcaagc tgctggtggc acacgtgaga ttcaccattg caatcaacac
```

1261 caaggcccggt gagcagctca tctgcgagtg tggcctcttt gacaaggcca acgccacagg  
1321 gggcggtggg cacgtgcaga tgggtgcagag ggccatgaag gacctgacct atgcctccct  
1381 gtgctttccc gaggccatca agggccgggg catggagagc aaagaagaca tcccctacta  
1441 cttctaccgg gacgacgggc tcctggtgtg ggaagccatc aggacgttca cggccgaggt  
1501 ggtagacatc tactacgagg gcgaccaggt ggtggaggag gacccggagc tgcaggactt  
1561 cgtgaacgat gtctacgtgt acggcatgcg gggccgcaag tcctcaggct tccccaagtc  
1621 ggtcaagagc cgggagcagc tgtcggagta cctgaccgtg gtgatcttca ccgcctccgc  
1681 ccagcacgcc gcggtcaact tcggccagta cgactggtgc tcctggatcc ccaatgcgcc  
1741 cccaaccatg cgagccccgc caccgactgc caagggcggtg gtgaccattg agcagatcgt  
1801 ggacacgctg cccgaccgcg gccgctcctg ctggcatctg ggtgcagtgt gggcgctgag  
1861 ccagttccag gaaaacgagc tgttcctggg catgtacca gaagagcatt ttatcgagaa  
1921 gcctgtgaag gaagccatgg cccgattccg caagaacctc gaggccattg tcagcgtgat  
1981 tgcgtgagcg aacaagaaga agcagctgcc atattactac ttgtccccag accggattcc  
2041 gaacagtgtg gccatctgag cacactgcca gtctcactgt ggggaaggcca gctgccccag  
2101 ccagatggac tccagcctgc ctggcaggtg tctggccagg cctcttgga ctcacatctc  
2161 ttctcccgag gccagtacct ttccatttat tctttgatct tcagggaact gcatagattg  
2221 atcaaagtgt aaacaccata gggacccatt ctacacagag caggactgca cagcgtcctg  
2281 tccacacca gctcagcatt tccacacca gcagcaacag caaatcacga ccaactgatag  
2341 atgtctattc ttgttgagga catgggatga ttattttctg ttctatttgt gcttagtcca  
2401 attccttgca catagtaggt acccaattca attactattg aatgaattaa gaattggtg  
2461 ccataaaaat aaatcagttc atttaaaaaa aaaaaaaaaa

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2484 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

1 gggcccggtg ctcgctgctc ccgcgcccg cgccatgcc tcctacacgg tcaccgtggc  
61 cactggcagc cagtggttcg ccggcactga cgactacatc tacctcagcc tcgtgggctc  
121 gggcggtgac agcgagaagc acctgctgga caagcccttc tacaacgact tcgagcgtgg  
181 cgcggtggat tcatacgacg tgactgtgga cgaggaactg ggcgagatcc agctgggtcag  
241 aatcgagaag cgcaagtact ggctgaatga cgactggtac ctgaagtaca tcacgtgaa  
301 gacgccccac ggggactaca tcgagttccc ctgctaccgc tggatcaccg gcgatgtcga  
361 ggttgtcctg agggatggac gcgcaaagtt ggcccgagat gaccaaattc acattctcaa  
421 gcaacaccga cgtaaagaac tggaaacacg gcaaaaacaa tatcgatgga tggagtggaa  
481 ccctggcttc cccttgagca tcgatgccaa atgccacaag gatttaccct gtgatattca  
541 gtttgatagt gaaaaaggag tggactttgt tctgaattac tccaaagcga tggagaacct  
601 gttcatcaac cgcttcagc acatgttcca gtcttcttgg aatgacttcg ccgactttga  
661 gaaaatcttt gtcaagatca gcaacactat ttctgagcgg gtcagtgaac actggcagga  
721 agacctgatg tttggctacc agttcctgaa tggctgcaac cctgtgttga tccggcgtg  
781 cacagagctg cccgagaagc tcccgggtgac cacggagatg gttagagtga gcctggagcg  
841 gcagctcagc ttggagcagg aggtccagca agggaacatt ttcatcgtgg actttgagct  
901 gctggatggc atcgatgcc acaaaacaga cccctgcaca ctccagttcc tggccgctcc  
961 catctgcttg ctgtataaga acctggccaa caagattgtc cccattgcca tccagctcaa  
1021 ccaaattccg ggagatgaga accctatttt cctcccttcg gatgcaaaat acgactggct  
1081 tttggccaaa atctgggtgc gttccagtga cttccacgtc caccagacca tcaccacct  
1141 tctgcgaaca catctggtgt ctgaggtttt tggcattgca atgtaccgc agctgcctgc  
1201 tgtgcacccc attttcaagc tgctggtggc acacgtgaga ttcaccattg caatcaacac  
1261 caaggcccggt gagcagctca tctgcgagtg tggcctcttt gacaaggcca acgccacagg  
1321 gggcggtggg cacgtgcaga tgggtgcagag ggccatgaag gacctgacct atgcctccct  
1381 gtgctttccc gaggccatca agggccgggg catggagagc aaagaagaca tcccctacta  
1441 cttctaccgg gacgacgggc tcctggtgtg ggaagccatc aggacgttca cggccgaggt  
1501 ggtagacatc tactacgagg gcgaccaggt ggtggaggag gacccggagc tgcaggactt  
1561 cgtgaacgat gtctacgtgt acggcatgcg gggccgcaag tcctcaggct tccccaagtc  
1621 ggtcaagagc cgggagcagc tgtcggagta cctgaccgtg gtgatcttca ccgcctccgc  
1681 ccagcacgcc gcggtcaact tcggccagta cgactggtgc tcctggatcc ccaatgcgcc  
1741 cccaaccatg cgagccccgc caccgactgc caagggcggtg gtgaccattg agcagatcgt  
1801 ggacacgctg cccgaccgcg gccgctcctg ctggcatctg ggtgcagtgt gggcgctgag  
1861 ccagttccag gaaaacgagc tgttcctggg catgtacca gaagagcatt ttatcgagaa  
1921 gcctgtgaag gaagccatgg cccgattccg caagaacctc gaggccattg tcagcgtgat  
1981 tgcgtgagcg aacaagaaga agcagctgcc atattactac ttgtccccag accggattcc  
2041 gaacagtgtg gccatctgag cacactgcca gtctcactgt ggggaaggcca gctgccccag  
2101 ccagatggac tccagcctgc ctggcaggtg tctggccagg cctcttgga gtcacatctc  
2161 ttctcccgag gccagtacct ttccatttat tctttgatct tcagggaact gcatagattg  
2221 atcaaagtgt aaacaccata gggacccatt ctacacagag caggactgca cagcgtcctg  
2281 tccacacca gctcagcatt tccacacca gcagcaacag caaatcacga ccaactgatag  
2341 atgtctattc ttgttgagga catgggatga ttattttctg ttctatttgt gcttagtcca

2401 atttcttgca catagtaggt acccaattca attactattg aatgaattaa gaattggttg  
2461 ccataaaaaat aatcagttc attt

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2497 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

1 gggcgccgag gctccccgcc gctcgtgct ccccgcccg cgccatgcc tctacacgg  
61 tcaccgtggc cactggcagc cagtgggtcg ccggcactga cgactacatc tacctcagcc  
121 tcgtgggctc ggcgggctgc agcgagaagc acctgctgga caagcccttc tacaacgact  
181 tcgagcgctg cgcggtggat tcatacgacg tgactgtgga cgaggaactg ggcgagatcc  
241 agctggctag aatcgagaag cgcaagtact ggctgaatga cgactggtag ctgaagtaca  
301 tcacgctgaa gacgccccac ggggactaca tcgagttccc ctgctaccgc tggatcaccg  
361 gcgagtgcga ggttgctctg agggatggac gcgcaaagtt ggcccagat gaccaaattc  
421 acattctcaa gcaacaccga cgtaaagaac tggaaacacg gcaaaaacaa tatcgatgga  
481 tggagtggaa ccctggcttc cccttgagca tcgatgcaa atgccacaag gatttaccct  
541 gtgatatcca gtttgatagt gaaaaaggag tggactttgt tctgaattac tccaaagcga  
601 tggagaacct gttcatcaac cgcttcatgc acatgttcca gtcttcttgg aatgacttcg  
661 ccgactttga gaaaatcttt gtcaagatca gcaacactat ttctgagcgg gtcatgaatc  
721 actggcagga agacctgatg tttggctacc agttcctgaa tggctgcaac cctgtgttga  
781 tccggcgctg cacagagctg cccgagaagc tcccggtgac cacggagatg gtagagtga  
841 gcctggagcg gcagctcagc ttggagcagg aggtccagca agggaaacatt ttcacgtgg  
901 actttgagct gctggatggc atcgatgcca acaaaacaga cccctgcaca cctcagttcc  
961 tggcgcgtcc catctgcttg ctgtataaga acctggccaa caagattgtc cccattgcca  
1021 tccagctcaa ccaaatcccg ggagatgaga accctatatt cctcccttcg gatgcaaat  
1081 acgactggct tttggccaaa atctgggtgc gttccagtga ctccacgct caccagacca  
1141 tcacccacct tctcgaaaca catctggtgt ctgaggtttt tggcattgca atgtaccgcc  
1201 agctgectgc tgtgcacccc attttcaagc tgctggtggc acacgtgaga ttcaccattg  
1261 caatcaacac caaggcccgt gagcagctca tctgcgagtg tggcctcttt gacaaggcca  
1321 acgccacagg ggcggtggg cagctgcaga tgggtcagag ggccatgaag gacctgacct  
1381 atgcctccct gtgctttccc gaggccatca aggcccgggg catggagagc aaagaagaca  
1441 tcccctacta cttctaccgg gacgacgggc tctggtgtg ggaagccatc aggacgttca  
1501 cggccgaggt ggtagacatc tactacgagg gcgaccaggt ggtggaggag gaccggagc  
1561 tgcaggactt cgtgaacgat gtctacgtgt acggcatgag gggccgcaag tctcaggct  
1621 tccccaaagc ggtcaagagc cgggagcagc tgcggagta cctgaccgtg gtgatcttca  
1681 ccgctccgc ccagcagcc gcggtcaact tcggccagta cgactggtgc tctggatcc  
1741 ccaatgcgcc ccaaccatg cgagccccgc caccgactgc caagggcgtg gtgaccattg  
1801 agcagatcgt ggacacgtg cccgaccgag gccgctcctg ctggcatctg ggtgcagtgt  
1861 gggcgctgag ccagttccag gaaaacgagc tgttcctggg catgtacca gaagagcatt  
1921 ttatcgagaa gcctgtgaag gaagccatgg cccgattccg caagaacctc gaggccattg  
1981 tcagcgtgat tgcgtgagcg aacaagaaga agcagctgcc atattactac ttgtccccag  
2041 accgatttcc gaacagtgt gccatctgag cacttgcca gtctcactgt gggaaggcca  
2101 gctgccccag ccagatggac tccagcctgc ctggcaggct gtctggccag gcctcttggc  
2161 agtcacatct cttctccga ggccagtacc ttccattta ttctttgatc ttcagggaac  
2221 tgcatagatt gtatcaaat gttaaaccca tagggacca ttctacacag agcaggactg  
2281 cacaggcgtc ctgtccacac ccagctcagc atttccacac caagcagcaa cagcaaatca  
2341 cgaccactga tagatgtcta ttctgttgg agacatggga tgattatttt ctgttctatt  
2401 tgtgcttagt ccaattcctt gcacatagta ggtaccat tcaattacta ttgaatgaat  
2461 taagaattgg ttgccataaa aataaatcag ttcattt

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10151 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

1 cagctgtccc tccccactgc catttatccc ttccttcatt caaaccttat gtggctgcta  
61 cttaccgtgt gtttaagtgt cacttttttt cttggaattc aaaaaagaa ggacagtatt  
121 tggggcacag atcttttggg gttctatata tttttttaaa gtttcatttt acatttgtgt  
181 gtgcgtgtgt gtgtgtgtgt gagacagtct tgctctgttg cccaggctgg agtgcagtgg  
241 cataatcatt ggctcactgt agcctcaaaag tccctggccc aagcgatctt cccacctcag  
301 ccacccaaaa tgctgggggt acaggtttat gccactctgt ctgacctgaa agttttgggt  
361 ttactttccc ttctttctct ttgctgaagt cagagatgat ggcagcttcc agattctctg  
421 gtgcctgtgc tgggctcgtg ctggtcatgg tcttgggtcc aggtattcatt ctggagactc  
481 tcagggaagt ttcccatgac aaggaaatgt aggagagtgt gctggctttg cgtgctcctc

541 tgccaagccc tgcttctcct ggtgggacac actgaaccac agccagggca ttttgggtgt  
601 tagttaaaaa aaaaaaaaaa aaaaaaaagg aagaagaagg cactgtgtaa ttgtgccggg  
661 gatcttcaga aattgtaatg atgaaagagt gcaagctctc acttcccctt cctgtacagg  
721 gcaggtttgtg cagctggagg cagagcagtc ctctctgggg agcctgaagc aaacatggat  
781 caagaaactg taggcaatgt tgcctgttg gccatcgtca ccctcatcag cgtgggtccag  
841 aatggtaagg aaagcccttc actcagggaa gaacagaagg ggagatttt tttgatgggt  
901 ttgtggaaagt caggcttaaa caattgtgtc tgtgtgtgcy catgcacaaa cacttttacc  
961 ttatctttat tttcttctt ttatttgaat gtataggggt gtgtgtattt ctgtgtaaat  
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1 tgcgttttgg gggttcctgg agtatcaatc atggtatcaag aaactgtagg caatgttgtc  
61 ctgttgccca tgcctaccct catcagcgtg gtccagaatg gattctttgc ccataaagt  
121 gagcacgaaa gcaggaccca gaatgggagg agcttccaga ggaccggaac acttgccttt  
181 gagcgggtct acactgccaa ccagaactgt gtatagtcgt cccactttt cctcgtgtg  
241 ctctgggtctg cggggctact ttgcagccaa gttcctgctg cgtttgtgg actgatgtac  
301 ttgtttgtgc ggcaaaagta ctttgtcgtg tacctaggag agagaacgca gagcacccct  
361 ggctacatat ttgggaaacg catcactctc ttctgttcc tcatgtccgt tgtgtgcata  
421 ttcaactatt acctcatctt ctttttcgga agtgactttg aaaactacat aaagacgatc  
481 tccaccacca tctcccctct acttctcatt tcctaactct ctgtgaata tgggggtgg  
1 atgcctctct acacggtcac cgtggccact ggcagccagt ggttcgccc cactgacgac  
61 tacatctacc tcagcctcgt gggctcggcg ggctgcagcg agaagcacct gctggacaag  
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301 taccgctgga tcaccggcga tgtcaggtt gtctgaggg atggacgccc aaagtggcc  
361 cgagatgacc aaattcacat tctcaagcaa caccgacgta aagaactgga aacacggcaa  
421 aaacaatctc gatggatgga gtggaaccct ggcttcccct tgagcatcga tgccaaatgc  
481 cacaaggatt taccctgtga tatcagttt gatagtgaag aaggagtga ctttgttctg  
541 aattactcca aagcgatgga gaacctgttc atcaaccgct tcatgcacat gttccagctt  
601 tcttggaaatg acttcgccc ctttgagaaa atctttgtca agatcacgaa cactatttct  
661 gagcgggtca tgaatcactg gcaggaagac ctgatgtttg gctaccagtt cctgaatggc  
721 tgcaaccctg tgtgatccg gcgctgcaca gagctgccc agaagctccc ggtgaccacg  
781 gagatggtag agtgcagcct ggagcggcag ctgagcttg agcaggaggt ccagcaaggg  
841 aacattttca tcgtggactt tgagctgtg gatggcatcg atgccaacaa aacagacccc  
901 tgcacactcc agttcctggc cgtcccctc tgcctgtgtg ataagaacct ggccaacaag  
961 attgtcccca ttgccatcca gctcaaccaa atcccggag atgagaacct tattttctc  
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1081 cactgccacc agaccatcac ccacttctg cgaacacatc tgggtgtctg ggtttttggc  
1141 attgcaatgt accgccagct gctgtgtgt caccctatt tcaagctgct ggtggcacac  
1201 gtgagattca ccattgcaat caacaccaag gcccggtgag agctcatctg cgagtgtggc  
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1321 atgaaggacc tgacctatgc ctccctgtgc ttcccgagg ccataaggc ccggggcatg  
1381 gagagcaaa aagacatccc ctactactt taccgggacg acgggtcctt ggtgtgggaa  
1441 gccatcagga cgttcacggc cgaggtggtg gacatctact acgagggcga ccaggtggtg  
1501 gaggagacc cggagctgca ggacttcgtg aacgatgtct acgtgtacg catgcggggc  
1561 cgcaagtctc caggcttccc caagtcggtc aagagccggg agcagctgtc ggagtacctg  
1621 accgtggtga tcttcaccgc ctccgccag cagccgcgg tcaacttcgg ccagtacgac  
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1741 ggcgtggtga ccattgagca gatcgtggac acgctgccc acccgggccg ctctgtctg  
1801 catctgggtg cagtgtggg gctgagccag ttccaggaaa acgagctgtt cctgggcatg  
1861 taccagaaag agcattttat cgagaagcct gtgaaggaa ccatggccc attccgcaag  
1921 aacctcgagg ccattgtcag cgtgattgct gagcgcaaca agaagaagca gctgccatat  
1981 tactacttgt cccagaccg gattccgaac agtgtggcca tc  
1 gggcccgcg ctgctgtct cgcggccc cgcctatccc tctacacgg tcaccgtggc  
61 cactggcagc cagtgttct cgcgactga cgactacatc tacctcagcc tctggggctc  
121 ggcgggtctg agcgagaagc acctgctgga caagccctt tacaacgact tcgagcgtgg  
181 cgcgggtgat tcatacgacg tgactgtgga cgaggaactg ggcgagatcc agctggtcag  
241 aatcgagaag cgcaagtact ggctgaatga cgactgttac ctgaagtaca tcacgtgaa  
301 gagccccac ggggactaca tcgagttccc ctgctaccgc tggatccag gcgatgtcga  
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421 gcaacaccga ctgaaagaac tggaacacg gcaaaaaaaa tatcgatgga tggagtggaa  
481 ccctggcttc cccttgagca tcgatgccaa atgccacaag gatttacct gtgatattca  
541 gtttgatagt gaaaaaggag tggactttgt tctgaattac tccaaagcga tggagaacct  
601 gttcatcaac cgcttcatgc acatgttcca gtcttcttgg aatgacttcg ccgactttga  
661 gaaaatcttt gtcaagatca gcaacactat ttctgagcgg gtcataatc actggcagga  
721 agacctgatg ttggctacc agttcctgaa tggctgaac cctgtgttga tccggcgtg  
781 cacagagctg cccgagaagc tcccgtgac cagcgagatg gtatagtgca ccctggagcg  
841 gcagctcagc ttggagcagg aggtccagca agggaacatt ttcactgtg actttgagct

901 gctgctggc atc gatgcca acaaaacaga cccctgcaca cccagttcc tggccgctcc  
961 catctgcttg ctgtataaga acctggccaa caagattgtc cccattgcca tccagctcaa  
1021 ccaaattccc ggagatgaga accctatttt cctcccttcg gatgcaaaat acgactggct  
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1141 tctgcgaaca catctgggtg ctgaggtttt tggcattgca atgtaccgcc agctgcctgc  
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1261 caaggcccgt gagcagctca tctgcgagtg tggcctcttt gacaaggcca acgccacagg  
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2461 ccataaaaaat aaatcagttc attt  
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301 tcacgctgaa gacgccccac ggggactaca tcgagttccc ctgctaccgc tggatcacccg  
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601 tggagaacct gttcatcaac cgcttcatgc acatgttcca gtcttcttgg aatgacttcg  
661 ccgactttga gaaaatcttt gtcaagatca gcaacactat ttctgagcgg gtcataatc  
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2221 tgcatagatt gtatcaaatg gtaaacacca tagggaccca ttctacacag agcaggactg  
2281 cacaggcgtc ctgtccacac ccagctcagc atttccacac caagcagcaa cagcaaatca  
2341 cgaccactga tagatgtcta ttctgttgg agacatggga tgattatttt ctgttctatt  
2401 tgtgcttagt ccaattcctt gcacatagta ggtacccaat tcaattacta ttgaatgaat  
2461 taagaattgg ttgccataaa aataaatcag ttcattt

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2383 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

1 ggcacgaggg tggtgagcc atgatgctgc tgccagaacc cctgcagagg gcctggttcc  
61 aggagactca gattcctctg tgaaaaagcc cttggagagg cgccccagca gggctgcact  
121 tggctcctgt gaggaagggg ctcagggtct gggccctcc gctggggccg ggctgggagc  
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241 agcctgcctg tcgtctgtgg ccattgccatc atgggctcct cgggtgtacat cacgggtggag  
301 ctggccattg ctgtgctggc catcctgggc aatgtgctgg tgtgctgggc cgtgtggctc  
361 aacagcaacc tgcagaacgt caccaactac tttgtggtgt cactggcgcc ggccgacatc  
421 gcagtgggtg tgctcgccat cccctttgcc atcaccatca gcaccgggt ctgcgtgcc  
481 tgccacggct gcctcttcat tgctgcttc gtctgtgtcc tcacgcagag ctccatcttc  
541 agtctcctg ccctgcctat tgaccgtac attgccatcc gcacccgct ccggtacaat  
601 ggcttgggtg ccggcacgag ggctaaggcc atcattgcca tctgctgggt gctgtcgttt  
661 gccatcgccc tgactcccat gctagggtgg aacaactgcy gtcagccaaa ggagggcaag  
721 aaccactccc agggctgcgg ggagggccaa gtggcctgtc tctttgagga tgtgttccc  
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961 tcaactggca tcattgtggg gctctttgcc ctctgctggc tgcccctaca catcatcaac  
1021 tgcttcaatt tcttctgccc cgactgcagc cagccccctc tctggctcat gtacctggcc

1081 atcgctctt cccacaccaa ttcggttggt aatcccttca tctacgccta ccgtatccgc  
1141 gagttccgcc agaccttccg caagatcatt cgcagccacg tcttgaggca gcaagaacct  
1201 ttcaaggcag ctggcaccag tgcccgggtc ttggcagctc atggcagtga cggagagcag  
1261 gtcagcctcc gtctcaacgg ccaccgcgca ggagtgtggg ccaacggcag tgctccccac  
1321 cctgagcggg ggcccaatgg ctatgccctg gggctgtgta gtggagggag tgcccaagag  
1381 tcccagggga acacgggcct ccagacgtg gagctcctta gccatgagct caagggagtg  
1441 tggccagagc cccctggcct agatgacccc ctggcccagg atggagcagg agtgtcctga  
1501 tgattcatgg agtttgcccc ttctaagggt aaggagatct ttatctttct ggttggttg  
1561 accagtcacg ttgggagaag agagagagtg ccaggagacc ctgagggcag ccggttccta  
1621 ctttgactg agagaaggga gcccagggt ggagcagcat gaggcccagc aagaagggt  
1681 tgggttctga ggaagcagat gttcatgct gtgagcctt gcaccaggtg ggggccacag  
1741 caccagcagc atctttgtg ggaggggccc agccctccac tgcaagaagca tctggaagca  
1801 ccacctgtgc tccacagagc agcttgggca cagcagactg gcctggcctt gagactgggg  
1861 agtggctcca acagcctcct gccaccaca caccactctc cctagactct cctagggttc  
1921 aggagctgct gggcccagag gtgacatttg acttttttcc aggaaaaaat taagtgtgag  
1981 gaaacctttt ttattttatt accttttact ctctggctgc tgggtctgcc gtcggtcctg  
2041 ctgctaacct ggcaccagag cctctgccgg ggagcctcag gcagtcctct cctgctgtca  
2101 cagctgccat ccacttctca gtcccagggt catctcttgg agtgacaaag ctgggatcaa  
2161 ggacagggag ttgtaacaga gcagtgccag agcatgggcc caggtcccag gggagaggtt  
2221 ggggctggca ggccactggc atgtgctgag tagcgagag ctacccagtg agaggccttg  
2281 tctaactgcc ttctcttcta aagggaatgt ttttttctga gataaataa aaacgagcca  
2341 catcgtgttt taagcttgct caaatgaaaa aaaaaaaaaa aaa

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2988 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

1 catcaccttt ttttaagtag taagaataaa gccactgtat gattctctta atagctatac  
61 attaatcctg tttttagtg tgactgggcc agccttccgg gaactggagt ctgtctcttt  
121 cagtgccttt ttgttttttg ttggtttttt cgagacgggg tcgatcacgg ctcaccacag  
181 ccttaacctc cagggctcca gcaatcctcc caccctcagc tctgagtag ctgggaccac  
241 aggtgtgtgc caccatctcc agcagtttgt ttattttatt tttctttttt tttttttggt  
301 agaaatgggc ttttcgcccc tgttgcccaa gctggtcttg cacttctggg ctgaagcaat  
361 cctctcgctt tggcctccca gagccttggg attacagaat catgggtgag agctggcatg  
421 gcccctagag gtcatttggg gtccagctgc ctcaccgtat caatgaggaa actgaggccc  
481 agaaaaagaa agcatttttg ccagagctcc ctcagaaaaa aacagaccac atctgacctt  
541 tggccctgag tccagagtgg gaggcaccgt gacaacaatg cgcagagcag ggaatgcagg  
601 gagccatgga tagtgctggg gtgcctcagg aacctgaag ctgggctgag ccattgatgt  
661 gctgccagaa cccctgcaga gggcctggtt tcaggagact cagagtcctc tgtgaaaaag  
721 cccttgagga gcgccccagc agggctgcac ttggctcctg tgagggaagg gctcagggtt  
781 ctgggcccct ccgctggggc cgggctggga gccaggcggg cggctgggct gcagcaatgg  
841 accgtgagct ggcccagccc gcgtccgtgc tgagcctgcc tgcgtctgt ggcattgcca  
901 tcatgggctc ctgggtgtac atcacggtg agctggccat tgctgtgctg gccatcctgg  
961 gcaatgtgct ggtgtgctgg gccgtgtggc tcaacagcaa cctgcagaac gtcaccaact  
1021 actttgtggt gtcactggcg gcggccgaca tcgcagtggg tgtgctcgcc atcccccttg  
1081 ccatcaccat cagcaccggg ttctgcgtgc cctgccacgg ctgectcttc attgctgct  
1141 tcgtcctggt cctcacgcag agctccatct tcagtctcct ggccatcgcc attgaccgct  
1201 acattgccat ccgcatcccg ctccggtaca atggcttggg gaccggcacg agggctaagg  
1261 gcatcattgc catctgctgg gtgctgtcgt ttgccatcgg cctgactccc atgctaggtt  
1321 ggaacaactg cggctagcca aaggagggca agaaccactc ccagggtgct ggggagggcc  
1381 aagtggcctg tctctttgag gatgtggtcc ccatgaacta catggtgtac ttcaacttct  
1441 ttgctgtgtg gctggtgccc ctgctgctca tgctgggtgt ctatttgagg atcttctctg  
1501 cggcgcgacg acagctgaag cagatggaga gccagcctct gccgggggag cgggcacggt  
1561 ccacactgca gaaggagggt catgtgcca agtcactggc catcattgtg gggctctttg  
1621 ccctctgctg gctgccccta cacatcatca actgcttcac tttcttctgc cccgactgca  
1681 gccacgcccc tctctggctc atgtacctgg ccactgctct ctcccacacc aattcgggtg  
1741 tgaatccctt catctacgcc taccgtatcc gcgagttccg ccagaccttc cgcaagatca  
1801 ttgcagacca cgtcctgagg cagcaagaac ctttcaaggc agctggcacc agtgcccggg  
1861 tcttggcagc tcatggcagt gacggagagc aggtcagcct ccgtctcaac ggccaccgct  
1921 caggagtgtg ggccaacggc agtgctcccc accctgagcg gaggcccaat ggctatggcc  
1981 tgggctgggt gagtggagg agtgcccaag agtcccagg gaacacggcg ctcccagagc  
2041 tggagctcct tagccatgag ctcaaggagg tgtgcccaga gcccctggc ctccagagc  
2101 ccctggccca ggatggagca ggagtgtcct gatgattcat ggagtttgcc ctttctaag  
2161 ggaaggagat ctttatcttt ctggttggct tgaccagtca cgttgggaga agagagagag  
2221 tgccaggaga ccctgagggt agccggttcc tactttggac tgagagaagg gagccccagg  
2281 ctggagcagc atgaggccca gcaagaaggg cttgggttct gaggaaagcag atgttctatg



2341 ctgtgagggc ttgcaccagg tggggggccac agcaccagca gcagcatctt tctgggcagg  
2401 cccagccctc cactgcagaa gcatctggaa gcaccacctt gtctccacag agcagcttgg  
2461 gcacagcaga ctggcctggc cctgagactg gggagtggct ccaacagcct cctgccaccc  
2521 acacaccact ctccctagac tctcctaggg ttcaggagct gctggggcca gaggtgacat  
2581 ttgacttttt tccaggaaaa atgtaagtgt gaggaaaccc cttttatattt attacctttc  
2641 actctctggc tgctgggtct gccgtcggtc ctgctgctaa cctgggcagca gaggctctgc  
2701 ccggggagcc tcaggcagtc ctctcctgct gtcacagctg ccattccactt ctacgtccca  
2761 gggccatctc ttggagtgc aaagctggga tcaaggacag ggagtgttaa cagagcagtg  
2821 ccagagcatg gggccaggtc ccaggggaga ggttggggct ggcaggccac tggcatgtgc  
2881 tgagttagcg agagctaccc agtgagaggc cttgtctaac tgcctttcct tctaaaggga  
2941 atgttttttt ctgagataaa ataaaaacga gccacatcgt gttttaag

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2157 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

1 ggcacgagcc cagaaacaaa gacttcacgg acaaaagtccc ttggaaccag agagaagccg  
61 ggatggaaac tccaaacacc acagaggact atgacacgac cacagagttt gactatgggg  
121 atgcaactcc gtgccagaag gtgaacgaga gggcctttgg ggcccaactg ctgccccctc  
181 tgtactcctt ggtatttgtc attggcctgg ttggaacat cctggtggtc ctggctcctg  
241 tgcaatacaa gaggctaaaa aacatgacca gcatctacct cctgaacctg gccatttctg  
301 acctgctctt cctgttcacg ctctccttct ggatcgacta caagtgaag gatgactggg  
361 tttttggtga tgccatgtgt aagatcctct ctgggtttta ttacacaggc ttgtacagcg  
421 agatcttttt catcatcctg ctgacgattg acaggtaacct ggccatcgtc cagccctgtg  
481 ttgccttgcg ggcacggacc gtcacttttg gtgtcatcac cagcatcatc atttggggccc  
541 tggccatctt ggcttccatg ccaggcttat acttttccaa gacccaatgg gaattcactc  
601 accacacctg cagccttcac tttcctcagc aaagcctacg agagtggaa ctgtttcagg  
661 ctctgaaact gaacctcttt gggctgggtat tgcctttgtt ggtcatgac atctgctaca  
721 cagggattat aaagattctg ctaagacgac caaatgagaa gaaatccaaa gctgtccggt  
781 tgaattttgt catcatgac atcttttttc tcttttgac cccctacagg ttgactatac  
841 ttattttctg tttccaagac ttctgttca cccatgagt tgagcagagc agacatttgg  
901 acctggctgt gcaagtgcg gaggtgatcg cctacacgca ctgctgtgtc aaccacgtga  
961 tctacgcctt cgttgggtgag aggttccgga agtacctgcg gcagttgttc cacaggcgtg  
1021 tggctgtgca cctggttaaa tggctccct tctctccgt ggacaggctg gagagggtca  
1081 gctccacatc tccctccaca ggggagcatg aactctctgc tgggttctga ctacagccat  
1141 aggaggccaa cccaaaataa gcaggcgtga cctgccaggc aactgagcc agcagcctgg  
1201 ctctccagc caggttctga ctcttggcac agcatggagt cacagccact tgggatagag  
1261 agggaatgta atgggtgcct ggggttctg aggtctctgg ggcttcagtc tttccatga  
1321 acttctcccc tggtagaaag aagatgaatg agcaaaacca aatattccag agactgggac  
1381 taagtgtacc agagaagggc ttggactcaa gcaagatttc agatttgtga ccattagcat  
1441 ttgtcaacaa agtcaccacac ttccactat tgcctgcaca aaccaattaa acccagtagt  
1501 ggtgactgtg ggtccattc aaagtgcgct cctaagccat gggagacact gatgtatgag  
1561 gaatttctgt tcttccatca cctccccccc cccgccaccc tccactgccc aagaacttgg  
1621 aaatagtgtat ttccacagtg actccactct gactccaga gccaatcagt agccagcatc  
1681 tgccctccct tcaactccac cgcaggattt gggctcttgg aatcctggg aacatagaac  
1741 tcatgacgga agagttgaga cctaacgaga aatagaaatg ggggaactac tgctggcagt  
1801 ggaactaaga aagcccttag gaagaatttt tatatccact aaaatcaaac aattcaggga  
1861 gtgggctaag cacgggccat atgaataaca tgggtgtgctt cttaaaatag ccataaaggg  
1921 gagggactca tcatctccat ttacccttct tttctgacta tttttcagaa tctctctct  
1981 tttcaagttg ggtgatattg tggtagattc taatggcttt attgcagcga ttaataacag  
2041 gcaaaaggaa gcagggttgg tttcccttct ttttgttct catctaagcc ttctggtttt  
2101 atgggtcaga gttccgactg ccactcttga cttgtcagca aaaaaaaaaa aaaaaa

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 949 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

1 agaagctttt gctcctggga ttaggttgat gggcctctaa tgtcaccagt gaaatgggat  
61 attagatatt ttccagctag gatacgacag ctcccaataa aaccaaatta ctaagccttt  
121 tctgcaagca aggagccgtc tggaacataa ggactttaac cttgggtagg agacaggcaa  
181 gcagaagtct tcaattgtgt cacaattttc actgaggact caagtgcctt aagaaagtaa  
241 ttgtgattgt cagagccttg ttcttctttt tctttctcca gccgcagct tcacctactc  
301 aggagagtgc ctacgcaatc tgacttgaca gcttctagaa agaaattaga gcaacagggg

361 tcttcagcagg gtggtcttgg gccaaacact gaaagcaggc aggcctaccc tttcctcttc  
421 tgcccccttc aactttttcc tgatgttctt acccacatcc ctcaccacac cacacccttt  
481 cattcatcct tgtccagac ttattaagta tatacagata agcaatccag ggaacttgca  
541 ttcatttagga gaaaccaga aattcaaaag caataatgat ctaatcccag aggagtagaa  
601 aacaggaagt gggcagctgc cagctttctt gctttgctgg agtattctgg aatttgatgg  
661 gttgaggggt ctggacacaa tgcccaagc cccttccttg ttgtgctggg ttcctatttc  
721 tgctctcggc actgacttag cagctgctca agagctcact atgttggtt ggattacact  
781 ggtctcacc acatctccgg cagtttggg gcaaacctcc tgagcagcct tgggtgatga  
841 aacctttcat ggtagcagga gaatgggact gtgaattctc aatcccctgt ccccaacct  
901 tccttcctct ctcagggcct taaagtctag gaggaggaag cacagcagc

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3734 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

1 ctgtcttgc tggagtattc tggtaatttg atgggttgag ggttctggac acaatgcccc  
61 aagccccctc ctgttgctgc tgggttccca tttctgctct cggcactgac ttagcagctg  
121 ctcaagagct cactatgttg gcttgatta cacggctctca cccacatctc cggcagtttg  
181 tgggcaaacc tcctgagcag ccttgggtga tgaaaccttt catggtagca ggagaatggg  
241 actgtgaatt ctcaatcccc tgtccccacc ccttccttcc tctctcaggg ccttaaagtc  
301 taggaggagg aagcacagca gcaactgact gggcagcctt tcaggaaaga tgcagccact  
361 cctgtctctg ctggcctttc tcctaccacac tggggctgag gcaggtagt gaccatcccc  
421 accctcagag gcctgacctc atcccataga ttcttgagcc aaattgcctt ggtatatcct  
481 aattctgtac tgttagcaa gttatttga tttgtgttcc ctcactata aaatgagaat  
541 aatattaata ccgatcttgc agagtgtcca tgagagttaa ataagttaga gtatttaaat  
601 gtcttgaat tgccgcaca ctataagtgc tataaaaaca tgctttgtgt aaataatttg  
661 gcagcatgtg tcagacccta ctaggaggt aagaatacag caataacagt accatcagct  
721 catgtctaga tttttaaaca ccagtcccac gtggtcttga attggactca gagggtctg  
781 ggaagctcca tgaggataaa agtataaggg aacttcagga acaatcctgt acttacagca  
841 aagcattctc ctcaatacct gaggctgaag ctggccttgc ctggaacaag ggttgttctc  
901 cctcttttgg agaggaggag ggaggtgagg cctaggatgg ggaaggggc tcctttcaag  
961 acagcagtg ttcctgtaga accctggagc cccctcccaa tctgctgccc catagactcc  
1021 aagcctcagc accatctcct ccctctctg caccctctct cctgcccgtc ccatcttcca  
1081 gcctttcttg agccaccaat ctggtacca cattgcaggt tcagcaagca tagagctaag  
1141 tgccaaatgc ttccttcag gggagatcat cggaggccgg gagagcaggc cccactcccg  
1201 ccctacatg gcgtatcttc agatccagag tcagcaggt cagagcagat gtggagggtt  
1261 cctggtgcga gaagactttg tgctgacagc agctcattgc tggggaaggt gagagctaa  
1321 ggaacttctt ggccagccag gaacacagcc ctgaggagct cttcgttggg agagccatct  
1381 gaaagaagag ttgtagcaat gaaagggtga aagaaagacc aagttagtct ttgaggagg  
1441 gaacaggcca gtgtaaatga ggaggaaagg aggataagat caaaaagagc aagaggaaga  
1501 gatggaagac acatattggg gctcaaaata taaactcagg ctatttatca acttaatctg  
1561 gggagtaaa cctgaaggca agtaccaccc tgtcatccct agctcagagc tgtgagaaa  
1621 gaggatacag ctgagcccca gggccctccc atcccctcga ttctggttag ctgcagctct  
1681 gccctccccg tgctgtctgc ctaccctgca gagctgggtg accatagctc ctgcagccca  
1741 gacctacctc ttgcttttgc agcaatata atgtcacctt gggcgccac aatatccaga  
1801 gacgggaaaa ccccagcaa cacatcactg cgcgcagagc catccgccac cctcaatata  
1861 atcagcggac catccagaat cacatcactg tattgcaggt accacctacc tggccctctg  
1921 gctccttctt agtgtgtccg gggacaatgg aggaggaagt gagggcaagg ctccggggtg  
1981 gcggggaggg catgggatgt gtactgcacc agcgaccccc gagccttggc tggaggcccc  
2041 agctgagcgg gaacgcctac attcttcttc cagctgagca gaagagtcag acggaatcga  
2101 aacgtgaacc cagtggctct gcctagagcc caggagggac tgagaccggg gacgctgtgc  
2161 actgtggccg gctggggcag ggtcagcatg aggaggggaa cagatacact ccgagaggtg  
2221 cagctgagag tgagaggga taggcagtgc ctccgcatct tcggttccca cgacccccga  
2281 aggcagattt gtgtgggga ccggcgggaa cggaaggctg ccttcaaggt aaggcatggg  
2341 cattggccaa cacaccggg gagagagggg cccgtgcaga gccagcaggt gcgaacagat  
2401 tccatcccca cagcctcagc ctggcagcca gaccagggtg ggctggggat tgttttcccc  
2461 atcaacctgg tctctggggg aataggagga agaccacaaa cacatacata ggcaacattc  
2521 tcctggagaa gggagaggta ccttgactca gattgggctg gagacagtaa ttaaggcaga  
2581 gctgaagtcc agcgaccgaa aagatccaga ggcttggtc ctgtaccoca ccgatcttcc  
2641 atctcacaca caccagcaa ttgaaggggc ccacccaccc ctgccttccc tgagagccccg  
2701 gagctcaggg aagcaggagc agggaggcct gtctcagtct ccttctctct ctctacctac  
2761 agggggattc cggaggcccc ctgctgtgta acaattgtgc ccacggcctc gtctcctatg  
2821 gaaagtcgtc aggggttctt ccagaagtct tcaccagggt ctcaagtttc ctgccctgga  
2881 taaggacaac aatgagaagc ttcaaaactgc tggatcagat ggagaccccc ctgtgactga  
2941 ctcttcttct cggggacaca ggccagctcc acagtgttgc cagagcctta ataaacgtcc  
3001 acagagtata aataaccaat tcctcatttg ttcattaaac gtcattcagt acttagtttg

3061 tttggattgc tacaacaaaa tagcacaaat tgggtggcctt ataaataaca aatttatttc  
3121 tcacaggtct agaggctaag aagtctaaga tcaagtcact agcagattca gtgtctaatt  
3181 agggccatt ttctggttca cagacaacca tcctctccct gtgtccacat atggcaaaaag  
3241 gggcaaggga attctctgat gtctctttta caaggacact agtctcattc aaagagctca  
3301 gcttttacga cctaatacaca tcccaaaggc cccacctaata gccatcadga cattggggat  
3361 taggtctggg aaacataggg aaagagtgtc tctacacaaa aattttaaaa ttagccaggc  
3421 atggtggcat gtgtctatat tcccagctac ttgggaggct aaagtggag gattagttaga  
3481 acccacgagg ttgaggcttc agtgaacat gcaactccagc ctgagcgaca gagcaagaca  
3541 ccattccaag aaagaaaaaa aaaaagactg gcaggccaaa aagacagaac tgaaattcca  
3601 aaaaaaaga cctacttttag tgtatgaaaa aggtggcatc tcaaatcact gggaaacaat  
3661 ggaatttttg aataaatagc attagaacca acctagatag atatttggag gggatggaag  
3721 gtataattgg atcc

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4683 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

1 agaagctttt gctcctggga ttaggttgat gggcctctaa tgcaccagt gaaatgggat  
61 attagatatt ttccagctag gatacgacag ctccaataa aaccaaatta ctaagccttt  
121 tctgcaagca aggagccgtc tggaacataa ggactttaac ctgggtagg agacaggcaa  
181 gcagaagtct tcaattgtgt cacaattttc actgaggact caagtgcact aagaaagtaa  
241 ttgtgattgt cagagccttg ttctctctt tcttctcca gccgcacgt tcacctactc  
301 aggagagtgc ctacgcaatc tgacttgaca gcttctagaa agaaattaga gcaacagggg  
361 tctcagcagg gtggtcttgg gccaaacact gaaagcaggc aggcttacct ttctctctc  
421 tgcccccttc aactttttcc tgatgttctt acccacatcc ctccaccac cacacccttt  
481 cattcatcct tgtccagac ttattaagta tatacagata agcaatccag ggaacttgca  
541 ttcattagga gaaacccaga aattcaaaag caataatgat ctaatcccag aggagtagaa  
601 aacaggaagt gggcagctgc cagctttctt gctttgctgg agtattctgg aatttgatgg  
661 ttgaggggtt ctggacacaa tgcccacgc cccttcctg ttgtgctggg ttctatttc  
721 tgtctcggc actgacttag cagctgctca agagctcact atgttgctt ggattacact  
781 ggtctcacc acatctccg cagtttggg gcaaacctcc tgagcagcct tgggtgatga  
841 aacctttcat ggtagcagga gaatgggact gtgaattctc aatcccctgt ccccccctc  
901 tccttctct ctcagggcct taaagtctag gaggaggaag cacagcagc  
1 cttgctttgc tggagtattc tggtaatttg atgggttgag gtttctggac acaatgccc  
61 aagccccctt cttgttggc tgggttctta tttctgctc cggcactgac ttagcagctg  
121 ctcaagagct cactatgttg gcttgatta cacggtctca cccacatctc cggcagtttg  
181 tgggcaaac tcctgagcag ccttgggtga tgaaacctt catggttaga gagaataggg  
241 actgtgaatt ctcaatcccc tgcctccacc ccttctctc tctctcagg ccttaaagtc  
301 taggaggagg aagcacagca gcaactgact gggcagcctt tcaggaaaga tgcagccact  
361 cctgcttctg ctggccttcc tcctaccac tggggtgag gcaggtgagt gaccatcccc  
421 accctcagag gcctgacctc atcccataga ttcttgagcc aaattgcctt ggtatctct  
481 aattctgtac tgttgagcaa gttatttgaa tttgtgttc ctcatctata aaatgagaat  
541 aatattaata ccgatcttgc agagtggcca tgagagttaa ataagttaga gtatttaaat  
601 gtcttggaa tgcccgaca ctataagtgc tataaaaaa tgctttgtgt aaataatttg  
661 gcagcatgtg tcagacccta cctaggaggt aagaatacag caataacagt accatcagct  
721 catgtctaga tttttaaaca ccagtcccac gtggtcttga attggactca gagggctctg  
781 ggaagctcca tgaggataaa agtataaggg aacttcagga acaatcctgt acttacagca  
841 aagcattctc ctcaatacct gaggtgaag ctggccttgc ctggaacaag ggtgttctc  
901 cctcttttgg agaggaggag ggaggtgagg cctaggatgg ggaaggggc tcctttcaag  
961 acagcagtg ttctgtaga accctggagc cccctccaa tctgtgccc catagactcc  
1021 aagcctcagc accatctct cctctcctg caccctctc cctgcccct ccactctcca  
1081 gcctttctg agccaccaat ctggtacctc cattgcaggt tcagcaagca tagagctaag  
1141 tgccaaatgc ttcttccag gggagatcat cggaggccgg gagagcaggc cccactccc  
1201 cccctacatg gcgtatcttc agatccagag tccagcaggt cagagcagat gtggagggtt  
1261 cctggtgcga gaagactttg tgcagacagc agctcattgc tggggaagg gagagctaa  
1321 ggaacttct ggccagccag gaacacagcc ctgaggagct cttcgggtga agagccatct  
1381 gaaagaagag ttgtagcaat gaaagggtga aagaaagacc aagttagtct ttgcgggagg  
1441 gaacaggcca gtgtaaatga ggaggaaagg aggataagat caaaaagagc aagaggaaga  
1501 gatggaagac acatattggg gctcaaaata taaactcagg ctattatca acttaattctg  
1561 ggaagtaaa cctgaaggca agtaccaccc tgtcatccct agctcagagc tgcgtagaaa  
1621 gaggatacag ctgagcccca gggccctccc atccctcga ttctggttag ctgcagtctt  
1681 gccctcccc tgctgtctgc ctacctgca gagctggtgg accatagctc ctgcagccca  
1741 gacctacctc ttgcttttgc agcaatataa atgtcaccct gggcgccac aatatccaga  
1801 gacgggaaaa caccagcaa cacatcactg cgcgcagagc catccgccac cctcaatata  
1861 atcagcggac catccagaat gacatcatgt tattgcaggt accacctacc tggccctctg  
1921 gctccttctc agtgtgtccg gggacaatgg aggaggaagt gagggcaagg ctccggggtg

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1981 gcggggaggg catgggatgt gtactgcacc agcgaccccc gagccttggc tggaggcccc
2041 agctgagcgg gaacgcctac attcttcctc cagctgagca gaagagtcag acggaatcga
2101 aacgtgaacc cagtggctct gcctagagcc caggagggac tgagaccggg gacgctgtgc
2161 actgtggccg gctggggcag ggtagcatg aggaggggaa cagatacact ccgagagggtg
2221 cagctgagag tgcagaggga taggcagtgc ctccgcatct tcggttccta cgacccccga
2281 aggcagattt gtgtggggga ccggcgggaa cggaaggctg ccttcaaggt aaggcatggg
2341 cattggccaa cacaccccg gaggagggg cccgtgcaga gccaggcagt gcgaacagat
2401 tccatcccca cagcctcagc ctggcagcca gaccagggtg ggctggggat tgttttcccc
2461 atcaacctgg tctctggggg aataggagga agaccacaa cacatacata ggcaacattc
2521 tcctggagaa gggagaggta ccttgactca gattgggctg gagacagtaa ttaaggcaga
2581 gctgaagtcc agcgaccgaa aagatccaga ggcttggctc ctgtacccca ccatctctcc
2641 atctcacaca caccagcaa ttgaaggggc ccacccaccc ctgccttccc tgagagcccg
2701 gagctcaggg aagcaggagc agggaggcct gtctcagtct ccttctctct ctctacctac
2761 agggggattc cggaggcccc ctgctgtgta acaatgtggc ccacggcatc gtctcctatg
2821 gaaagtctgc aggggttctt ccagaagtct tcaccagggt etcaagtttc ctgccctgga
2881 taaggacaac aatgagaagc ttcaaaactgc tggatcagat ggagaccccc ctgtgactga
2941 ctcttcttct cggggacaca ggccagctcc acagtgttg cagagcctta ataaactgcc
3001 acagagtata aataaccaat tcctcatttg ttcattaaac gtcattcagt acttagtttg
3061 tttggattgc tacaacaaaa tagcacaat tgggtggctt ataaataaca aatttatttc
3121 tcacaggtct agaggctaag aagtctaaga tcaagtcact agcagattca gtgtctaatt
3181 agggccattt ttctggttca cagacaacca tcctctccct gtgtccacat atggcaaaag
3241 gggcaaggga attctctgat gtctctttta caagggacct agtctcattc aaagagctca
3301 gcttttacga cctaatacaca tcccaaaggc cccacctaat gccatcacga cattggggat
3361 taggtctggg aaacataggg aaagagtgtc tctacacaaa aattttaaaa ttagccaggc
3421 atgggtgcat gtgtctatag tcccagctac ttgggaggct aaagtgaag gattagtga
3481 acccacaggg ttgaggcttc agtgaaccat gcaactccagc ctgagcgaca gagcaagaca
3541 ccattccaag aaagaaaaaa aaaaagactg gcaggccaaa aagacagaac tgaaattcca
3601 aaaaaaaga cctactttag tgtatgaaaa aggtggcatc tcaaatcact gggaacaat
3661 ggaatttttg aataaatagc attagaacca acctagatag atatttgag gggatggag
3721 gtataattgg atcc

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## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2156 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

1 ggcacgagcc cagaaacaaa gacttcacgg acaaagtccc ttggaaccag agagaagccg
61 ggatggaaac tccaaacacc acagaggact atgacacgac cacagagttt gactatgggg
121 atgcaactcc gtgccagaag gtgaacgaga gggcctttgg ggcccaactg ctgccccctc
181 tgtactcctt ggtatttgtc attggcctgg ttggaacat cctggtggtc ctggctcctt
241 tgcaatacaa gaggtctaaa aacatgacca gcatctacct cctgaacctg gccatttctg
301 acctgctctt cctgttcacg ctcccttctt ggatcgacta caagttgaag gatgactggg
361 tttttgggtg tgccatgtgt aagatcctct ctgggtttta ttacacaggc ttgtacagcg
421 agatcttttt catcatcctg ctgacgattg acaggtacct ggccatcgtc cagcgcgtgt
481 ttgccttgcg ggcacggacc gtcacttttg gtgtcatcac cagcatcact atttggggcc
541 tggccatctt ggcttccatg ccaggcttat acttttccaa gacccaatgg gaattcactc
601 accacacctg cagccttcac tttcctcacg aaagcctacg agagtgaag ctgtttcagg
661 ctctgaaact gaacctcttt gggctggtat tgcctttgtt ggtcatgatc atctgtaca
721 cagggtattt aaagattctg ctaagacgac caaatgagaa gaaatccaaa gctgtccggt
781 tgatttttgt catcatgatc atcttttttc tcttttggac cccctacaat ttgactatac
841 ttatttctgt tttccaagac ttctgttca cccatgagtg tgagcagagc agacatttgg
901 acctggctgt gcaagtgcg gaggtgatcg cctacacgca ctgctgtgtc aaccagtgga
961 tctacgcctt cgttggtag aggttccgga agtacctgag gcagttgttc cacaggcggt
1021 tggctgtgca cctggttaaa tggctccctt tcctctccgt ggacaggctg gagagggtca
1081 gctccacatc tccctccaca ggggagcatg aactctctgc tgggttctga ctacagccat
1141 aggaggccaa ccaaaaataa gcaggcgtga cctgccaggc aactgagcc agcagcctgg
1201 ctctccagc caggttctga ctcttggcac agcatggagt cacagccact tgggatatag
1261 agggaaatga atgggtggcct ggggcttctg aggttcttgg ggcttcagtc ttttccatga
1321 acttctcccc tggtagaaag aagatgaatg agcaaaacca aatattccag agactggggc
1381 taagtgtacc agagaagggc ttggactcaa gcaagatttc agatttgtga ccattagcat
1441 ttgtcaacaa agtcaccacac ttcactat tgcttgcaaa aaccaattaa acccagtagt
1501 ggtgactgtg ggctccattc aaagtgcagt cctaagccat gggagacact gatgtatgag
1561 gaatttctgt tcttccatca cctccccccc cccgccaccc tccactgccc aagaacttgg
1621 aaatagtgat ttccacagtg actccactct gactcccaga gccaatcagt agccagcatc
1681 tgcctccctt tactccccc cgcaggattt gggctcttgg aatcctgggg aacatagaac
1741 tcatgacgga agagttgaga cctaacgaga aatagaaatg ggggaactac tgctggcagt

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1801 ggaactaaga aagcccttag gaagaatttt tatatccact aaaatcaaac aattcagggg  
1861 gtgggctaag cacgggcat atgaataaca tgggtgtgctt cttaaaatag ccataaaggg  
1921 gagggactca tcatttccat ttacccttct tttctgacta tttttcagaa tctctcttct  
1981 tttcaagttg ggtgatatgt tggtagattc taatggcttt attgcagcga ttaataacag  
2041 gcaaaaggaa gcagggttg tttcccttct tttgttctt catctaagcc tcttggtttt  
2101 atgggtcaga gttccgactg ccatcttgga cttgtcagca aaaaaaaaaa aaaaaa

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2955 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

1 gagagccccc ccccgagac tgaagtttt ggagattcag gggtcggggg aaagggttca  
61 ggaataggta attgagtttc caagggatag tgttacaagt ggtatgggag gccccctatt  
121 tctgatatga atagagaata ttttctttgt tcattatgat agaaccctg gataaagag  
181 ggaataataa tgttgggagt ccccgaggag agaggagaga atccaacagg gtgatttgct  
241 gatatttgta cgaggaggga aagaattttt caaagacaaa gttggagtga ggagtttttg  
301 tagagggaac caggtggggt acaagagag agacacactg agccggtggg aagggaagaa  
361 ttaagagggg tgttccccc cactgtatat taagaaagaa aaacaatggg gacaggacgg  
421 cagaagttag agtttcttaa ccaggatgag agggggattt cacggttaact aatgagtgat  
481 ttcagacctt attccactat cccagggcaa tcagatatta atcatgtaca agttgaaatc  
541 atgctgttcc tttgaggtaa gacttacata atcctattta gcataacagg cccccagatc  
601 cagaaagggg agggttccgc ccctacact gaaggggatc agggatatga aagtggctca  
661 tggttgacca tcacgtttta caggaaatgg caatcaggag gggtaggtcc aattgtgacc  
721 aacagaccaa acttccatta atgcttgagg ttcttggggc aaagccagtc tgtgaggttt  
781 gatggggatg gacttggtga gcagagagca gggggacaac gaatcccaga agctgagggg  
841 aatgggggtc caaagagccg ctgctgcctc tgggagcacc catgtcagtt agtttttccg  
901 tacgggactc agggttccag attattcgtt tttaaatcct tccattcaca atctttaaga  
961 agaagaaaaa aaagaagtct gccgctgacc acaagagctc tatgccctgc ccccatccca  
1021 catacacaca tcccacactt caattgtctc aaacattctg ggaacatctc actgccaccc  
1081 acctcaccca actcagcttc acctgcccc aattccctta aggtctgagc cccagggccca  
1141 agactcaaga ggctcagagt gagcagagaa aatcctcgca gttacttgg cttccaggaa  
1201 gtggccactg gtgggcgttg tggccattca tgagcaccaa accacacaaa aagaacttg  
1261 tccctttctt gtcattttga aagactgtga aactggagcc aattctccat catcacacag  
1321 gaagctgagt acttccctact tggtcaggat cttgaaactt gaattcataa aaccagaaaa  
1381 gccccagaaa caaagacttc acggacaaaag tcccttgga cagagtaag tgtcacttgt  
1441 ctattctgtc ttatctgtta ctgtggaggg cagtgttggt caaagacatg catgcagcta  
1501 ggggtccttc aaaggtaggg ggaattcttt gagtaggctg ggcaaatgtc taagtagccc  
1561 atggatgcat ctccaaggca attaatactg tagcaatact gagaatgggt gatttataaa  
1621 gctgggtgct cagatgaaat ataggctttt ttgctaaaaa ggaagcttac ttgaaggatt  
1681 ggcttttggt tactgattaa gaaagtcagt cagtactaag ggacaaaagg tgttttctgt  
1741 gaaaacctat tcaataagaa attacttggc ggggcgcagt ggctcacggc tgtaatccca  
1801 gcactttggg agaccgaggc aggtggatca tgaggtcaag agatggagac aatcctggcc  
1861 atatggtgaa accctgtctc tactaaaaa aaaaattagc cgggcagggt gccgcagcct  
1921 gttagtccca gctactcaag aggtgaggc aggagaatca ctcgaatccg ggaggtggag  
1981 gttgcagtga gctgagattg caccacaaca ctccagcctg gcgacagagc aagagtctgt  
2041 ctgaaaaaaa aaaattgctt gccaaattcc ccaagttaa ggaacacaa acatgggtga  
2101 tgaagaaatt atagcaagag ggaatatta gctagaaaaa tcttggcaga tgcaaggatg  
2161 atttgatact gaacctatct cttaagaaga ctagaaccaa ggatcctcaa aattggcact  
2221 gctatctttg gaagagaggt aggttttcac tcacccaaag gcaaggagct ggccagggtga  
2281 tcttgggggg catctgttct gctctactaa caaagacaca ggtcaggatt ttgttctgaa  
2341 gatagagggg catggtggct ccgtataggt atctacttca taggtggcct tgggtgggtcc  
2401 cagatttcaa agaagagatg gaaactccca aaagtgtgca caacctggca ccaggctatg  
2461 tgccactcac tgatccttta gtccccgcac cgagcagtggt gacagtgtgt gactgttcag  
2521 aatgtggggc ctgggcagtg atgtgtggt aaatgttcaa caactgactc ttctgaagaa  
2581 aagatccctg ctttataaca tttgttgatt ttcattggtat aaatgcccc actgtgtgta  
2641 gtttcaagct accaactatg tgaatgtgga gtggggaaga gatgcacgca attggcattt  
2701 ataaaccagt ataagccagc cagcgcacca taggcctggg tgtctttcac catcacagac  
2761 tgctctactc tgctcagaga ctccaccaat cccaggctgg aagacactag cagtggaaag  
2821 tccaggatcc agggctatac tgaccactgt gccagtggcc ttgaggcaga ctctgcagta  
2881 gacaacanc agggctggcc nattagatga caacatgncc ttggtccctc tcggggcccaa  
2941 cccagacacc tctctg

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1495 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
1 atggaactc caaacaccac agaggactat gacacgacca cagagtttga ctatggggat
61 gcaactccgt gccagaaggt gaacgagagg gcctttgggg cccaactgct gccccctctg
121 tactccttgg tatttgtcat tggcctggtt ggaaacatcc tgggtgtcct ggtccttgtg
181 caatacaaga ggctaaaaaa catgaccagc atctacctcc tgaacctggc cttttctgac
241 ctgctcttcc tgttcacgct tcccttctgg atcgactaca agttgaagga tgactgggtt
301 tttggtgatg ccatgtgtaa gatcctctct ggggtttatt acacaggcct gtacagcgag
361 atctttttca tcatcctgct gacgattgac aggtacctgg ccatcgcca cgcctgttt
421 gccttgccgg cacggaccgt cacttttggg gtcacacca gcatcatcat ttgggcctg
481 gccatcttgg ctccatgcc aggtttatac tttccaaga cccaatggga attcactcac
541 cacacctgca gccttcactt tctcacgaa agcctacgag agtggaaagt gtttcaggct
601 ctgaaactga acctctttgg gctggtattg cctttgttgg tcatgatcat ctgctacaca
661 gggattataa agattctgct aagacgacca aatgagaaga aatccaaagc tgtccgtttg
721 atttttgtca tcatgatcat ctttttctc ttttgaccc cctacaattt gactatactt
781 atttctgttt tccaagactt cctgttcacc catgagtgtg agcagagcag acatttggac
841 ctggctgtgc aagtgcgga ggtgatcgcc tacacgcact gctgtgtcaa cccagtgate
901 tacgccttgc ttggtgagag gttccggaag tacctgcggc agttgttcca caggcgtgtg
961 gctgtgcacc tggttaaatg gctccccttc ctctcctggt acaggctgga gagggtcagc
1021 tccacatctc cctccacagg ggagcatgaa ctctctgctg ggttctgact cagaccatag
1081 gaggccaaac caaaataagc aggcgtgacc tggcaggcac actgaccagc agcctggctc
1141 tcccagccag gttctgactc ttggcacagc atggagtccg cctcttggat agagaggaat
1201 gtaatggtgg cctggggctt ctgaggcttc tgggcttgag tcttttccat gaacttctcc
1261 cctggtagaa aagaagatga atgagcaaaa ccaaattatc cagagactgg gactaagtgt
1321 accagagaag ggcttggact caagcaagat ttcagatttg tgaccattag catttgtcaa
1381 caaagtcacc cacttccac tattgcttgc acaaaccaat taaaccagat agtggtgact
1441 gtgggctcca ttcaaagtga gctcctaagc catgggagac actgatgtat gagga
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(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6606 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
1 ggcacgagcc cagaaacaaa gacttcacgg acaagtcctc ttggaaccag agagaagccg
61 ggatggaaac tccaaacacc acagaggact atgacacgac cacagagttt gactatgggg
121 atgcaactcc gtgccagaag gtgaacgaga gggcctttgg ggcccaactg ctgccccctc
181 tgtactcctt ggtatttgtc attggcctgg ttggaacatc cctgggtgct ctggtccttg
241 tgcaatacaa gaggtcaaaa aacatgacca gcatctacct cctgaacctg gccatttctg
301 acctgctctt cctgttcacg cttcccttct ggatcgacta caagttagaag gatgactggg
361 tttttggtga tgccatgtgt aagatcctct ctgggtttta ttacacaggc ttgtacagcg
421 agatcttttt catcatcctg ctgacgattg acaggctact ggccatcgtc cagcgcgtgt
481 ttgccttgcg ggcacggacc gtcacttttg gtgtcatcac cagcatcatc atttgggccc
541 tggccatctt ggcttccatg ccaggcttat acttttccaa gacccaatgg gaattcactc
601 accacacctg cagccttcac ttctctcag aaagcctaag agagtggagg ctgtttcagg
661 ctctgaaact gaacctcttt gggtgtggtt tgccattgtt ggtcatgac atctgtaca
721 cagggtattat aaagattctg ctaagacgac caaatgagaa gaaatccaaa gctgtccgtt
781 tgatttttgt catcatgac atcttttttc tcttttggac cccctacaat ttgactatac
841 ttatttctgt tttccaagac ttctgttca cccatgagtg tgagcagagc agacatttgg
901 acctggctgt gcaagtgcag gaggtgatcg cctacacgca ctgctgtgtc aaccagtgga
961 tctacgcctt cgttgggtgag aggttccgga agtacctgag gcagtgttgc cacaggcgtg
1021 tggctgtgca cctggttaaa tggctcccct tctctcctg ggacaggctg gagagggtca
1081 gctccacatc tccctccaca ggggagcatg aactctctgc tgggttctga ctcagacctat
1141 agggaggcaa cccaaaataa gcaggcgtga cctgccaggc acactgagcc agcagcctgg
1201 ctctcccagc cagggttctga ctcttggcac agcatggagt cacagccact tgggatatag
1261 aggggaatga atggtggcct ggggcttctg aggttcttgg ggcttcagtc ttttccatga
1321 acttctcccc tggtagaaag aagatgaatg agcaaaacca aatattccag agactgggac
1381 taagtgtacc agagaagggc ttggactcaa gcaagatttc agatttgtga ccattagcat
1441 ttgtcaacaa agtcacccac ttcccactat tgcttgaca aaccaattaa acccagtagt
1501 ggtgactgtg ggctccattc aaagtgaagt cctaagccat gggagacact gatgtatgag
1561 gaatttctgt tcttccatca cctccccccc cccgccccc tcccactgcc aagaacttgg
1621 aaatagtgtt ttccacagt actccactct gagtcccaga gccaatcagt agccagcatc
1681 tgctccctt tcactccac cgcaggattt gggctcttgg aatcctgggg aacatagaac
1741 tcatgacgga agagttgaga cctaacgaga aatagaaatg ggggaactac tgctggcagt
1801 ggaactaaga aagcccttag gaagaatttt tatatccact aaaatcaaac aattcaggga
1861 gtgggctaag cacgggccat atgaataaca tgggtgtgctt cttaaaatag ccataaaggg
1921 gagggactca tcatttccat ttacccttct tttctgacta ttttcagaa tctctcttct
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1981 tttcaagttg ggtgatatgt tggtagatgc taatggcttt attgcagcga ttaataacag  
2041 gcaaaaggaa gcagggttgg tttcccttct ttttgttctt catctaagcc ttctggtttt  
2101 atgggtcaga gttccgactg ccattcttga cttgtcagca aaaaaaaaaa aaaaaa  
1 gagagccccc cccccgagac tgaaagtttt ggagattcag gggtcggggg aaagggttca  
61 ggaaatggtta attgagtttc caagggatag tgttacaagt ggtatgggag gccccctatt  
121 tctgatagta atagagaata ttttctttgt tcattatgat agaaccctgt ggataaagag  
181 ggaaaaataaa tgttgggagt cccccagggt agaggagaga atccaacagg gtgatttgct  
241 gatatttgta cgaggaggga aagaattttt caaagacaaa gttggagtga ggagtttttg  
301 tagagggaac cagggtgggt acaagagag agacacactg agccggtggg aaggggaagaa  
361 ttaagagggtg tgttcccca cactgtatat taagaaagaa aaacaatggg gacaggacgg  
421 cagaagttag agtttcttaa ccaggatgag agggggattt cacggttaact aatgagtgat  
481 ttcagacctt attccactat cccagggtcaa tcagatatta atcatgtaca agttgaaatc  
541 atcgctgtcc tttgaggtaa gacttacata atcctattta gcataacagg cccccagatc  
601 cagaaagggtg aggggttcgc ccttatcact gaaggggagc agggatagga aagtggctca  
661 tgggtgacca tcacgtttta caggaatggg caatcaggag gggtaggtcc aattgtgacc  
721 aacagaccaa acttccatta atgcttgctg tcttgtggc aaagccagtc tgtgaggttt  
781 gatggggatg gacttggtga gcagagagca gggggacaac gaatccaga agctgagggg  
841 aatgggggtt caaagagccg ctgctgcttc tgggagcacc catgtcagtt agtttttccg  
901 tacgggactc aggggtccag attattcgtt tttaaatcct tccattcaca atctttaaga  
961 agaagaaaaa aaagaagtct gccgtgacc acaagagctc tatgcccctg ccccatccca  
1021 catacacaca tcccacactt caattgctcc aaacattctg ggaacattgc actgccacc  
1081 acctcaccca actcagcttc acctgcccc aattccctta agctgagct cccaggcca  
1141 agactcaaga ggctcagagt gacgagagaa aatcctcgca gttacttggt cttccaggaa  
1201 gtggccactg gtggcggtt tggccattca tgagcaccaa accacacaaa aagaactttg  
1261 tccctttctt gtcattttga aagactgtga aactggagcc aattctccat catcacacag  
1321 gaagctgagt acttccactt tggtcaggat cttgaaactt gaattcataa aaccagaaa  
1381 gccccagaaa caaagacttc acggacaaa tcccttgga ccagagtaag tgtcacttgt  
1441 ctttctgtc ttatctgtta ctgtggagg cagtgttgtt caaagacatg catgcagcta  
1501 ggggtcctc aaaggtaggg ggaattcttt gagtaggctg ggcaaatgtc taagtagccc  
1561 atggatgcat ctccaaggca attaatactg tagcaatact gagaatgggt gatttataaa  
1621 gctgggtgct cagatgaaat ataggctttt ttgctaaaaa ggaagcttac ttgaaggatt  
1681 ggcttttggg tactgattaa gaaagtcagt cagtactaag ggacaaaagg tgttttctgt  
1741 ggaaacctat tcaataagaa attacttggc ggggcgcagt ggctcacggc tgtaatccca  
1801 gcactttggg agaccgaggg aggtggatca tgaggtcaag agatggagac aatcctggcc  
1861 atatggtgaa accctgtctc tactaaaaat aaaaattagc cgggcaggtg gccgcagcct  
1921 gttagtccca gctactcaag aggtgagggc aggagaatca ctgcaatccg ggaggtggag  
1981 gttgcagtga gctgagattg caccacaaca ctccagcctg gcgacagagc aagagtctgt  
2041 ctgaaaaaaa aaaattgctt gccaaattcc cccaagtaaa ggaaaaccaa acatggtgta  
2101 tgaagaaatt atagcaagag ggaaatatta gctagaaaaa tcttggcaga tgcaaggatg  
2161 atttgatact gaacctatct cttaagaaga ctagaaccaa ggatcctcaa aattggcact  
2221 gctatctttg gaagagaggt aggtcttcaa tcacccaaag gcaaggagct ggccagggtga  
2281 tcttgggggg catctgttct gctctactaa caaagacaca ggtcaggatt ttgttctgaa  
2341 gatagagggg catggtggct ccgtataggt atctacttca taggtggcct tgggtgggtcc  
2401 cagatttcaa agaagagatg gaaactccca aaagtgtgca caactggcca ccaggctatg  
2461 tgccactcac tgatccttta gtccccgcac cgagcagtg gacagtgtg gactgttcag  
2521 aatgtggggc ctgggcagtg atgtgctggt aaatgttcaa caactgactc ttctgaagaa  
2581 aagatccctg ctttataaca tttgttgatt ttcatgggat aaatgcccc actgtggtca  
2641 gtttcaagct accaaccatgc tgaatgtgga gtggggaaga gatgcacgca attggcattt  
2701 ataaaccagt ataagccagc cagcgcacca taggcctggg tgtctttcac catcacagac  
2761 tgcctactc tgctcagaga ctcaccaact cccaggtggg aagacactag cagtggagg  
2821 tccaggatcc agggctatac tgaccactgt gccagtggcc ttgaggcaga ctctgcagta  
2881 gacaacanc agggctggcc nattagatga caacatgncc ttgtccctc tcgggcccc  
2941 cccagacacc tctg  
1 atggaaactc caaacaccac agaggactat gacacgacca cagagtttga ctatggggat  
61 gcaactccgt gccagaaggt gaacgagagg gcctttggg cccaactgct gccccctctg  
121 tactccttgg tatttgtcat tggcctggtt ggaaacatcc tgggtgctct ggtccttgtg  
181 caatacaaga ggctaaaaaa catgaccagc atctacctcc tgaacctggc catttctgac  
241 ctgctcttcc tgttcacgct tcccttctgg atcgactaca agttgaagga tgaactgggt  
301 tttggtgatg ccatgtgtaa gatcctctct gggttttatt acacaggctt gtacagcgag  
361 atctttttca tcatcctgct gacgattgac aggtacctgg ccatcgcca cgccgtgtt  
421 gccttggggg caggaccgt cacttttgtt gtcacacca gcacatcat ttgggcccctg  
481 gccatcttgg cttccatgcc aggttatac tttccaaga ccaatggga attcactcac  
541 cacacctgca gccttcactt tcttcacgaa agcctacgag agtggaagct gtttcaggct  
601 ctgaaactga acctctttgg gctggtattt cctttgttgg tcatgatcat ctgctacaca  
661 gggattataa agattctgct aagacgacca aatgagaaga aatccaaagc tgcctgttg  
721 atttttgtca tcatgatcat ctttttctc ttttggacc cctacaattt gactatactt  
781 atttctgttt tccaagactt cctgttcacc catgagtgtg agcagagcag acatttggac  
841 ctggctgtgc aagtgcgga ggtgatcgcc tacacgcact gctgtgtcaa cccagtgtc

901 ta...tttcg ttggtgagag gttccggaag tacctgcggc ttgtttcca caggcgtgtg  
 961 gctgtgcacc tggttaaatg gctccccttc ctctccgtgg acaggctgga gagggctcagc  
 1021 tccacatctc cctccacagg ggagcatgaa ctctctgctg ggttctgact cagaccatag  
 1081 gaggccaacc caaaataagc aggcgtgacc tgccaggcac actgaccagc agcctggctc  
 1141 tccagccag gttctgactc ttggcacagc atggagtcgg cctcttggat agagaggat  
 1201 gtaatgggtg cctggggctt ctgaggcttc tgggcttgag tcttttccat gaacttctcc  
 1261 cctggtagaa aagaagatga atgagcaaaa ccaaatttcc cagagactgg gactaagtgt  
 1321 accagagaag ggcttgact caagcaagat ttcagatttg tgaccattag catttgtcaa  
 1381 caaagtcacc cacttcccac tattgcttgc acaaaccaat taaaccagat agtggtgact  
 1441 gtgggctcca ttcaaagtga gtcctaagc catgggagac actgatgtat gagga

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1068 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

1 atgacaacct cactagatac agttgagacc ttggtacca catcctacta tgatgacgtg  
 61 ggcctgctct gtgaaaaagc tgataccaga gcactgatgg cccagtttgt gcccccgtg  
 121 tactccctgg tgttactgt gggcctcttg ggcaatgtgg tgggtgtgat gatcctcata  
 181 aaatacagga ggctccgaat tatgaccaac atctacctgc tcaacctggc catttcggac  
 241 ctgctcttcc tcgtcaccct tccattctgg atccactatg tcagggggca taactgggtt  
 301 ttggccatg gcatgtgtaa gtcctctca gggttttatc acacaggctt gtacagcgag  
 361 atctttttca taatcctgct gacaatcgac aggtacctgg ccattgtcca tgctgtgtt  
 421 gcccttcgag cccggactgt cacttttggg gtcacacca gcatcgctac ctggggcctg  
 481 gcagtgttag cagctcttcc tgaatttatt ttctatgaga ctgaagagtt gtttgaagag  
 541 actctttgca gtgctcttta cccagaggat acagtatata gctggaggca ttccacact  
 601 ctgagaatga ccatcttctg tctcgttctc cctctgctcg ttatggccat ctgctacaca  
 661 ggaatcatca aaacgtgctg gaggtgcccc agtaaaaaaa agtacaaggc catccggctc  
 721 attttgtca tcatggcggg gtttttcatt ttctggacac cctacaattg ggctatcctt  
 781 ctctcttctc atcaatccat cttatttggg aatgactgtg agcggagcaa gcatctggac  
 841 ctggatcatg tggtagacag ggtgatcgcc tactccact gctgcatgaa cccggtgatc  
 901 tacgcctttg ttggagagag gttccggaag tacctgcgcc acttcttcca caggcacttg  
 961 ctcatgcacc tgggcagata catccattc cttcctagtg agaagctgga aagaaccagc  
 1021 tctgtctctc catccacagc agagccgga ctctctattg tgttttag

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

1 tttttcttct tctatcacag ggagaagtga aatgacaacc tcactagata cagttgagac  
 61 ctttgggtacc acatcctact atgatgacgt gggcctgctc tgtgaaaaag ctgataccag  
 121 agcactgatg gccagtttg tgccccgct gtactccctg gtgttcaactg tgggcctctt  
 181 gggcaatgtg tggtgtgtga tgatcctcat aaaatacagg aggcctccga ttatgaccaa  
 241 catctacctg ctcaacctgg ccatttcgga cctgctcttc ctgcgcaccc ttccattctg  
 301 gatccactat gtcagggggc ataactgggt ttttggccat ggcagtgtga agctctctc  
 361 aggtgtttat cacacaggct tgtacagcga gatcttttcc ataactctgc tgacaatcga  
 421 caggtagctg gccattgtcc atgctgtgtt tgcccttcga gcccgactg tcacttttgg  
 481 tgtcatcacc agcatcgta cctggggcct ggcagtgtga gcagctcttc ctgaatttat  
 541 cttctatgag actgaagagt tgtttgaaga gactctttgc agtgcctttt acccagagga  
 601 tacagtatat agctggaggc atttccacac tctgagaatg accatcttct gtctcgttct  
 661 cctctgctc gttatggcca tctgtacac aggaatcatc aaaacgtgc tgagggtgcc  
 721 cagtaaaaaa aagtacaagg ccattccggct catttttgc atcatggcg tgttttcat  
 781 ttcttgagca ccctacaatg tggctatcct tctctcttcc tatcaatoca cttatttgg  
 841 aaatgactgt gagcggagca agcatctgga cctggtcagt ctggtgacag aggtgatcgc  
 901 ctactccac tgctgcatga acccggtgat ctacgccttt gttggagaga ggttccggaa  
 961 gtacctgcgc cacttcttcc acaggcactt gctcatgcac ctgggcagat acatccatt  
 1021 cttcctagt gagaagctgg aaagaaccag ctctgtctct ccattccacag cagagccgga  
 1081 actctctatt gtgttttagg tcagatgcag aaaattgcct aaagaggaag gaccaaggag  
 1141 atgaagcaaa cacattaagc cttccacact cacctctaaa acagtcttcc aaacttccag  
 1201 t

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1699 base pairs



- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

1 aatccttttc ctggcacctc tgatattcctt ttgaaattca tgttaaagaa tccctaggct  
61 gctatcacat gtggcatcct tgttgagtag atgaataaat caactggtgt gttttacgga  
121 ggatgattat gcttcattgt gggattgtat ttttcttctt ctatcacagg gagaagtga  
181 atgacaacct cactagatac agttgagacc ttgtgtacca catcctacta tgatgacgtg  
241 ggctgctctt gtgaaaaagc tgataccaga gcaactgatg cccagtttgt gcccccgctg  
301 tactccctgg tgttcactgt gggcctcttg ggcaatgtgg tgggtggtgat gatcctcata  
361 aaatacagga ggctccgaat tatgaccaac atctacctgc tcaacctggc catttcggac  
421 ctgctcttcc tcgtcacctt tccattcttg atccactatg tcagggggca taactgggtt  
481 tttggccatg gcatgtgtaa gctcctctca gggttttatc acacaggctt gtacagcgag  
541 atctttttca taatcctgct gacaatcgac aggtacctgg ccattgtcca tgctgtgttt  
601 gcccttcgag cccggactgt cacttttggt gtcataccca gcatcgctac ctggggcctg  
661 gcagtgttag cagctcttcc tgaatttatc ttctatgaga ctgaagagtt gtttgaagag  
721 actcttttga gtgctcttta cccagaggat acagtatata gctggaggca ttccacact  
781 ctgagaatga ccatcttctg tctcgttctc cctctgctcg ttatggccat ctgctacaca  
841 ggaatcatca aaacgctgct gaggtgcccc agtaaaaaaa agtacaaggc catccggctc  
901 atttttgtca tcatggcggg gtttttcatt ttctggacac cctacaatgt ggctatcctt  
961 ctctcttctt atcaatccat cttatttggg aatgactgtg agcggagcaa gcatctggac  
1021 ctggtcatgc tgggtgacaga ggtgatcgcc tactccact gctgcatgaa cccggtgatc  
1081 tacgcctttg ttggagagag gttccggaag tactgctgcc acttcttcca caggcacttg  
1141 ctcatgcacc tgggcagata catcccattc ctctctagt gagaagctgga aagaaccagc  
1201 tctgtctctc catccacagc agagccgga ctctctattg tgttttaggt agatgcagaa  
1261 aattgcctaa agaggaagga ccaaggagat naagcaaaca cattaagcct tccacactca  
1321 cctctaaaac agtcttcaa accttccagt gcaacactga agctcttaag acactgaaat  
1381 atacacacag cagtagcagt agatgcattg accctaaggt cattaccaca gggcaggct  
1441 gggcagcgta ctcatcatca acctaaaaag cagagctttg ctctctctc taaaatgagt  
1501 tacctatatt ttaatgcacc tgaatgttag atagttacta tatgccgcta caaaaaggtg  
1561 aaacttttta tattttatac attaatctca gccagctatt atataataa aacattttca  
1621 cacaatacaa taagttaact attttatttt ctaatgtgcc tagttcttct cctgcttaat  
1681 gaaaagctt

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2968 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

1 atgacaacct cactagatac agttgagacc ttgtgtacca catcctacta tgatgacgtg  
61 ggctgctctt gtgaaaaagc tgataccaga gcaactgatg cccagtttgt gcccccgctg  
121 tactccctgg tgttcactgt gggcctcttg ggcaatgtgg tgggtggtgat gatcctcata  
181 aaatacagga ggctccgaat tatgaccaac atctacctgc tcaacctggc catttcggac  
241 ctgctcttcc tcgtcacctt tccattcttg atccactatg tcagggggca taactgggtt  
301 tttggccatg gcatgtgtaa gctcctctca gggttttatc acacaggctt gtacagcgag  
361 atctttttca taatcctgct gacaatcgac aggtacctgg ccattgtcca tgctgtgttt  
421 gcccttcgag cccggactgt cacttttggt gtcataccca gcatcgctac ctggggcctg  
481 gcagtgttag cagctcttcc tgaatttatc ttctatgaga ctgaagagtt gtttgaagag  
541 actcttttga gtgctcttta cccagaggat acagtatata gctggaggca ttccacact  
601 ctgagaatga ccatcttctg tctcgttctc cctctgctcg ttatggccat ctgctacaca  
661 ggaatcatca aaacgctgct gaggtgcccc agtaaaaaaa agtacaaggc catccggctc  
721 atttttgtca tcatggcggg gtttttcatt ttctggacac cctacaatgt ggctatcctt  
781 ctctcttctt atcaatccat cttatttggg aatgactgtg agcggagcaa gcatctggac  
841 ctggtcatgc tgggtgacaga ggtgatcgcc tactccact gctgcatgaa cccggtgatc  
901 tacgcctttg ttggagagag gttccggaag tactgctgcc acttcttcca caggcacttg  
961 ctcatgcacc tgggcagata catcccattc ctctctagt gagaagctgga aagaaccagc  
1021 tctgtctctc catccacagc agagccgga ctctctattg tgttttag  
1 tttttcttct tctatcacag ggagaagtga aatgacaacc tcaactagata cagttgagac  
61 ctttggtagc acatcctact atgatgacgt gggcctgctc tgtgaaaaag ctgataccag  
121 agcactgatg gccagtttg tgcccccgct gtactccctg tgtttcactg tgggcctctt  
181 gggcaatgtg gtggtggtga tgatcctcat aaaatacagg aggtccgaa ttatgaccaa  
241 catctacctg ctcaacctgg ccatttcgga cctgctcttc ctgctcacc ttccattctg  
301 gatccactat gtcagggggc ataactgggt ttttggccat ggcagtgtga agctctctc  
361 agggttttat cacacaggct tgtacagcga gatcttttct ataactctgc tgacaatcga  
421 caggtaacct gccattgtcc atgctgtgtt tgcccttcga gcccggaact tcaatttttg  
481 tgtcatcacc agcatcgta cctggggcct ggcagtgtga gcagctcttc ctgaatttat  
541 ctctatgag actgaagagt tgtttgaaga gactctttgc agtgccttcc acccagagga

601 tacagtatat agctggaggc atttccacac tctgagaatg accatcttct gtctcgttct  
661 ccctctgctc gttatggcca tctgctacac aggaatcatc aaaacgctgc tgaggtgccc  
721 cagtaaaaaa aagtacaagg ccacccggct catttttgtc atcatggcgg tgtttttcat  
781 tttctggaca cctacaatg tggctatcct tctctcttcc tatcaatcca tcttatttgg  
841 aaatgactgt gagcggagca agcatctgga cctggtcattg ctgggtgacag aggtgatcgc  
901 ctactccacac tgctgcatga acccgggtgat ctacgccttt gttggagaga ggttccggaa  
961 gtacctgctc cacttcttcc acaggcactt gctcatgcac ctgggcagat acatcccatt  
1021 ccttcctagt gagaagctgg aaagaaccag ctctgtctct ccacccacag cagagccgga  
1081 actctctatt gtgttttagg tcagatgcag aaaattgcct aaagaggag gaccaaggag  
1141 atgaagcaaa cacattaagc cttccacact cacctctaaa acagtccttc aaacttccag  
1201 t

1 aatccttttc ctggcacctc tgatctcctt ttgaaattca tgttaaagaa tccctaggct  
61 gctatcacat gtggcatctt tgttgagtac atgaataaat caactgggtg gttttacgga  
121 ggatgattat gcttcattgt gggattgtat ttttcttctt ctatcacagg gagaagtga  
181 atgacaacct cactagatac agttgagacc tttggtacca catcctacta tgatgacgtg  
241 ggctgtctct gtgaaaaagc tgataccaga gcaactgatg cccagtttgt gccccgctg  
301 tactccctgg tgttactgt gggcctcttg ggcaatgtgg tgggtgtgat gatcctcata  
361 aaatacagga ggctccgaat tatgaccaac atctacctgc tcaacctggc catttcggac  
421 ctgctcttcc tcgtcacctt tccattcttg atccactatg tcagggggca taactgggtt  
481 tttggccatg gcatgtgtaa gctcctctca ggtttttatc acacaggctt gtacagcgag  
541 atctttttca taactctgct gacaatcgac aggtacctgg ccattgtcca tgcgtgtttt  
601 gcccttcgag cccggactgt cacttttggg gtcacacca gcatcgtcac ctggggcctg  
661 gcagtgttag cagctcttcc tgaatttacc ttctatgaga ctgaagagtt gtttgaagag  
721 actctttgca gtgctcttta cccagaggat acagtatata gctggaggca tttccacact  
781 ctgagaatga ccactctctg tctcgttctc cctctgctcg ttatggccat ctgctacaca  
841 ggaatcatca aaacgctgct gaggtgcccc agtaaaaaaa agtacaaggc catccggctc  
901 atttttgcata tcatggcggt gtttttcatt ttctggacac cctacaatgt ggctatcctt  
961 ctctcttctc atcaatccat cttatttggg aatgactgtg agcggacgaa gcatctggac  
1021 ctgggtcatgc tgggtgacaga ggtgatcgcc tactccact gctgcatgaa cccggtgatc  
1081 tacgcctttg ttggagagag gttccgggag tacttgcgcc acttcttcca caggcacttg  
1141 ctcatgcacc tgggcagata catcccattc cttcctagtg agaagctgga aagaaccagc  
1201 tctgtctctc catccacagc agagccggaa ctctctattg tgttttaggt agatgcagaa  
1261 aattgcctaa agaggaagga ccaaggagat naagcaaaaca cattaagcct tccacactca  
1321 cctctaaaaa agtccttcaa accttccagt gcaacactga agctcttaag acactgaaat  
1381 atacacacag cagtagcagt agatgcattg accctaaggt cattaccaca gggcagggct  
1441 gggcagcgta ctcatcatca acctaaaaag cagagctttg cttctctctc taaaaagagt  
1501 tacctatatt ttaatgcacc tgaatgttag atagttacta tatgccgcta caaaaaggtg  
1561 aaacttttta tattttatac attaaactta gccagctatt atataataa aacattttca  
1621 cacaatacaa taagttaact attttatttt ctaatgtgcc tagttcttct cctgcttaat  
1681 gaaaagctt

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2961 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

1 tctagagcca aggtcacgga agccagagg gcatcttctg gctcgggagt agctctctgc  
61 tgtcttctca gctctgctga caatacttga gattttcaga tgtcaccaac caccaagaga  
121 gcttgatatg actgtatata gtatagtcac aaagaacctg aacttgacca tatacttatg  
181 tcatgtggaa aatttctcat agcttcagat agattatata tggagtgaag aatcctgcc  
241 cctatgtatc tggcatagtg tgagtcttca taaatgttta ctgggttgaa gggcaacaaa  
301 atagtgaaca gagtgaaaat cccactaag atcctgggtc cagaaaaaga tgggaaacct  
361 gtttagctca cccgtgagcc catagttaaa actctttaga caacaggttt tttccgttta  
421 cagagaacaa taatattggg tgggtgagcat ctgtgtgggg gttgggggtg gatagggat  
481 acggggagag tggagaaaaa gggggcacag ggttaatgtg aagtcaggga tccccctca  
541 catttaagt tggtttaagt tggctttaat taatagcaac tcttaagata atcagaattt  
601 tcttaacctt ttagccttac tgttgaaaag cctgtgatc ttgtacaaat catttgcttc  
661 ttggatagta atttctttta ctaaaatgtg ggcttttgac tagatgaatg taaatgttct  
721 tctagctctg atatccttta ttctttatat tttctaacag attctgtgta gtgggatgag  
781 cagagaacaa aaacaaaata atccagttag aaaagccctg aaataaactt tcagaccaga  
841 gatctattct ctagcttatt ttaagctcaa cttaaaagga agaactgttc tctgattctt  
901 ttgccttca atacacttaa tgatttaact ccaccctctc tcaaaagaaa cagcatttcc  
961 tacttttata ctgtctatat gattgatttg cacagctcat ctggccagaa gagctgagac  
1021 atccgttccc ctacaagaaa ctctccccgg taagtaacct ctcagctgct tggcctgtta  
1081 gttagcttct gagatgagta aaagacttta caggaaacct atagaagaca tttggcaaac  
1141 accaagtgtc catacaatta tcttaaaata taatctttaa gataaggaaa gggtcacagt  
1201 ttggaatgag tttcagacgg ttataacatc aaagatacaa aacatgattg tgagtgaag

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1261 actttaaagg gagcaatagt attttaataa ctaacaatcc ttacctctca aaagaaagat
1321 ttgcagagag atgagtcctta gctgaaatct tgaaatctta tcttctgcta aggagaacta
1381 aaccctctcc agtgagatgc cttctgaata tgtgccacac agaagttgtg tctaagtctg
1441 gttctctttt ttctttttcc tccagacaag agggaagcct aaaaatggct aaaattaata
1501 ttaaatataa aacgccaaat aaaattttcc tctaataat cagtttcatg gcacagttag
1561 tatataattc tttatggttc aaaattaaaa atgagctttt ctaggggctt ctctcagctg
1621 cctagtctaa ggtgcaggga gtttgagact cacagggttt aataagagaa aattctcagc
1681 tagagcagct gaacttaaat agactaggca agacagctgg ttataagact aaactacca
1741 gaatgcatga cattcatctg tgggtggcaga cgaaacattt tttattatat ttttcttgg
1801 gtatgtatga caactcttaa ttgttgcaac tcaaaactaca aacacaaact tcacagaaaa
1861 tgtgaggatt ttacaattgg ctgtgtcat ctatgacctt ccctgggact tgggcacccg
1921 gccatttcac tctgactaca tcatgtcacc aaacatctga tggctctggc ttttaattct
1981 ctttttgagg actgagaggg agggtagcat ggtagttaag agtgcaggct tccgcattc
2041 aaaatcgggt gcttactagc tgtgtggctt tgagcaagtt actcaccctc tctgtgctt
2101 aaggtccttg tctgcaaaat gtgaaaaata tttcctgcct cataaggttg ccctaaggat
2161 taaatgaatg aatgggtatg atgcttagaa cagtgtattg catccagtat gtgccctcga
2221 ggctctttaa ttattactgg cttgctcata gtgcatgttc tttgtgggct aactctagcg
2281 tcaataaaaa tgttaagact gagggtgagc agggagtagc cttgagccca ggagttcgag accagccttg
2341 gcattctagg aggtgaggc agggagtagc cttgagccca ggagttcgag accagccttg
2401 gcaacatagt gtgatcttgt atctataaaa ataaacaaaa ttagcttggt gtggttgctg
2461 ctgtagtccc cagccacttg gaggggtgag gtgagaggat tgcttgagcc cgggatgac
2521 caggtctgag tgagccatga tctgtccact gactccagc ctgggagaca gaggtagacc
2581 ctgtctcaca acaacaacag caacaaaaag gctgagctgc accatgcttg acccagttt
2641 ttaaaattgt tgtcaaagct tcattcactc catggtgcta tagagcacia gattttattt
2701 ggtgagatgg tgctttcatg aattccccca acagagccaa gctctccatc tagtggacag
2761 ggaagctagc agcaaacctt cccttacta caaaacttca ttgcttggtc aaaaagagag
2821 ttaattcaat gtagacatct atgtaggcaa ttaaaaacct attgatgat aaaacagttt
2881 gcattcatgg agggcaacta aatacattct aggactttat aaaagatcac tttttattta
2941 tgacagggtt ggaacaagat g

```

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3383 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```

1 agaagagctg agacatccgt tcccctacaa gaaactctcc ccgggtggaa caagatggat
61 tatcaagtgt caagtccaat ctatgacatc aattattata catcggagcc ctgccaaaaa
121 atcaatgtga agcaaatcgc agcccgctc ctgctccgc tctactcact ggtgttcac
181 tttggttttg tgggcaacat gctggtcac ctcatcctga taaactgcaa aaggctgaag
241 agcatgactg acatctacct gctcaacctg gccatctctg acctgtttt ccttcttact
301 gtccccttct gggctcacta tgctgccgcc cagtgggact ttggaaatac aatgtgtcaa
361 ctcttgacag ggctctattt tataggcttc ttctctggaa tcttcttcat catcctcctg
421 acaatcgata ggtacctggc tgctgtccat gctgtgtttg ctttaaaagc caggacggtc
481 acctttgggg tggtgacaag tgtgatcact tgggtgggtg ctgtgtttgc gtctctccca
541 ggaatcatct ttaccagatc tcaaaaagaa ggtcttcatt acacctgcag ctctcatttt
601 ccatacagtc agtatcaatt ctggaagaat ttccagacat taaagatagt catcttgggg
661 ctggtctctg cgctgcttgt catggtcatc tgctactcgg gaatcctaaa aactctgctt
721 cgggtgctga atgagaagaa gaggcacagg gctgtgaggc ttatcttcac catcatgatt
781 gtttattttc tcttctgggc tccctacaa attgtccttc tctgaacac cttccaggaa
841 ttctttggcc tgaataattg cagtactctt aacaggtttg accaagctat gcaggtgaca
901 gagactcttg ggatgacgca ctgctgcac aaccccatca tctatgcctt tgcggggag
961 aagttcagaa actacctctt agtcttcttc caaaagcaca ttgccaaacg cttctgcaaa
1021 tgctgttcta tttccagca agaggctccc gagcgagcaa gctcagttta caccgatcc
1081 actggggagc aggaaatata tgtgggcttg tgacacggac tcaagtgggc tggtgacca
1141 gtcagagttg tgcacatggc ttagttttca tacacagcct gggctggggg tgggtggga
1201 gaggtctttt ttaaaaggaa gttactgtta tagagggtct aagattcatc catttatttg
1261 gcatctgttt aaagtagatt agatctttta agcccatcaa ttatagaaag ccaaatcaaa
1321 atatgttgat gaaaaatagc aaccttttta tctccccttc acatgcatca agttattgac
1381 aaactctccc ttcactccga aagttcctta tgtatattta aaagaaagcc tcagagaatt
1441 gctgattctt gaggtttagt atctgaacag aaataccaaa attatttcag aaatgtacaa
1501 ctttttacct agtacaaggc aacatatagg ttgtaaatgt gtttaaaaca ggtctttgtc
1561 ttgctatggg gagaaaagac atgaatatga ttagtaaaag aatgacactt tcatgtgtg
1621 atttcccctc caaggtatgg ttaataagtt tcaactgact agaaccaggc gagagacttg
1681 tggcctggga gagctgggga agcttcttaa atgagaagga atttgagttg gatcatctat
1741 tgctggcaaa gacagaagcc tcaactgcaag cactgcatgg gcaagcttgg ctgtagaagg
1801 agacagagct ggttgggaag acatggggag gaaggacaag gctagatcat gaagaacctt
1861 gacggcattg ctccgtctaa gtcatgagct gagcagggag atcctgggtg gtgttcaga

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1921 aggtttactc tgtggccaaa ggagggtcag gaaggatgag catttagggc aaggagacca
1981 ccaacagccc tcaggtcagg gtgaggatgg cctctgctaa gctcaaggcg tgaggatggg
2041 aaggagggag gtattcgtaa ggatgggaag gagggaggta ttcgtgcagc atatgaggat
2101 gcagagtcag cagaactggg gtggatttgg tttggaagtg agggtcagag aggagtcaga
2161 gagaatccct agtcttcaag cagatttgag aaacccttga aaagacatca agcacagaag
2221 gaggaggagg aggttttagt caagaagaag atggatttgg gtaaaaggat gggctctggtt
2281 tgcagagctt gaacacagtc tcaccagac tccaggctgt ctttctactga atgcttctga
2341 cttcatagat ttcttcccca tccagctga aatactgagg ggtctccagg aggagactag
2401 atttatgaat acacgaggta tgaggcttag gaacatactt cagctcacac atgagatcta
2461 ggtgaggatt gattacctag tagtcatttc atgggttgtt gggaggattc tatgaggcaa
2521 ccacaggcag catttagcac atactacaca ttcaataagc atcaaaactct tagttactca
2581 ttcagggata gcaactgagca aagcattgag caaaggggtc ccatataggt gagggaaagcc
2641 tgaanaacta agatgctgac tgcccagtg acacaagtgt aggtatcatt ttctgcattt
2701 aaccgtcaat aggcaaaggg gggaaggagc atattcattt ggaaataagc tgccttgagc
2761 cttaaaaccc acaaaagtac aatttaccag cctccgtatt tcagactgaa tgggggtggg
2821 gggggcgctt taggtactta tccagatgc cttctccaga caaacacaaa gcaacagaaa
2881 aaatcgtctc tccctccctt tgaaatgaat atacccttga gtgtttgggt atattcattt
2941 caaagggaga gagagaggtt ttttctgtt ctttctcata tgattgtgca catacttgag
3001 actgttttga atttggggga tggctaaaac catcatagta caggtaaggt gagggaaatag
3061 taagtggtag gaactactca gggaatgaag gtgtcagaat aataagaggt gctactgact
3121 ttctcagcct ctgaatatga acggtgagca ttgtggctgt cagcaggaag caacgaaggg
3181 aaatgtcttt ccttttgctc ttaagtgtg gagagtcaa cagtagcata ggacctacc
3241 cttggggcca agtcaaagac attctgacat cttagtattt gcatattctt atgtatgtga
3301 aagttaaaaa ttgcttgaag gaaaatatgc atctaataaa aaacacctc taaaataaaa
3361 aaaaaaaaaa aaaaaaaaaa aaa

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## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143068 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

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1 aagcttcagt atgcaaat tcaatgacat gtgctgtgg attctgaaaa ttcacagatc
61 tgtctatcct tagctgagac tgaaggcatc tacttcccaa tgaccaaact cgtgtctgt
121 ggcgacactg agcaggaact ccattagaat atcaatatca ctctgcagac attccatgat
181 gtaagctatg ttttctcttg ttgcaattac acttaattta ccaccagctg cttcaatgtc
241 atgggctatc ttgaaaaatg aagctccttt cgtagtcaaa ctggatgcaa gacacagcaa
301 atgagaagtt actaaattgt tggagtcctc atagctactg cctgctttaa tgaacaaacc
361 aattcttgat gcagggcata gttttccaaa ggagaaatca taaaaccatt tggaaatttg
421 atgatctcaa ggtcctgatg atgtggagcc actcctatgg gggtagctgt ggctttaact
481 ttgggggcaa ctttgaggga ataaagtctc aaaaagaggg aataaagtct caagattgtt
541 cgtgacccat agtaacttct ggcttaaaag accattcggc aagtttttaa atgtattttc
601 tataatttcc atgtagtctt ttatttttct tttttcttat ttaaaacctc tattttagct
661 cgtttccttt gacactgctc tggcagggaa aggggtggca ctgcctcatt actgccaggt
721 aggggtagaa gtccattatc cacttggctc ccattgatac ccaaagtggg gagaggctcc
781 tgttactgct ggtgagggtg ggagtcctcc cactaagttt ctgctaatac tgtcctggtg
841 gcttgctact attcccatga agcctccact gatactacat tacttttggg tgggtgcaaa
901 tgtcctgctc ctccactagc cctcctgctc taaaacaacc cgagtaggga gtgggaagga
961 agctttgtta ctggtagggt ggagctgaag tccagacttg ccacattgtc ccactgatgc
1021 tacagggagg aggaagcggg ccacattact gcctgatagg gatgaaagcc ccagctccct
1081 acctggcctt cgctgatacc agcctgtctc aggagtgaag agagatttga aggcctcaat
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1201 ggggccatag ctgtctctgt actgcttggc tagagtggag tatttgaggt ccaaaagtgt
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1321 tttacctgtt gtatttccag gttcctagct tctccagcac agtctgggat gtgtgagaca
1381 cagagaaaat ccagtgatgt tactaccgta tggtttcttg ggtcccaacg tctctagcta
1441 atctgtctca ccttttggag ttttcttatt tgttttagat cagggattta gtcataat
1501 ataggagaaa tatggaaaaa tacttctact ctatcttctt ggaagtttct gtttattttt
1561 tatgtccttt tctctggtc agaccgtaag agacttacga aacaaacact tacacattct
1621 actaaactca atgtccaaag ttgtgtaact tcttgaatat tgcttggtca tttccacccc
1681 cagtcactga ctgaatctcc ctgctgtctg tctacaatgc caatgagctt ctggttaact
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1801 tttgttgggt cttaatccct tggcctagtg ccaccatact cctccagcag agcaaccaat
1861 tcttacatta taggacagca catatccact aaaaacagtt catgccacac caaccacatt
1921 tccctttgtc aacaaaatta ctgtagatag aattccagga atgcctgatg aagctgattg
1981 acaacaagat atttggcaga ctctctgctg cctatacata ccttagcatg tggaaactcaa
2041 gtaatgagag gtccatttaa ttggattgaa ttgggctgga taggattgga ttgaatcctg
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2161 tgactaatga gttaatttta ctctcaaaga cagtctttag tagtaagctg taatgcatta
2221 tatcaacta tttccagtc aatgatttat aagttacttg aataaggatg ctaaagatgt
2281 gccttattga aatggcaatt agcacaaagt tgggaatgaa atctaattag ttaaataaca

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2341 gaatcacata aaaaaggact tgaataaatg tagcatccta ccatgttccct ggatagaaa  
2401 actgctatcg taaagatatt cattctctc aggttaaatt ataaactcaa tgcaattcaa  
2461 caggatttta aaaaactaga caaagtgatt ccaagtttac gtggaaaata aaatgtgagg  
2521 gaccaacaa tatttgaata agaaagagaa taaaatctca tcttccaga taccacaatg  
2581 tattataaag caatagtaat taacatgagg gcagaaatga gcaagcaagt gaacaaaata  
2641 agacagatag tcacaggaaa ctcatatatt tataggtgct ttgctataa tgaagatggt  
2701 ccttcaaatc agttgggaaa agatgggtta ttcaataaat ggtgttgggt aaatgtggt  
2761 atacattggt gagaaataaa gtgaaactcc tactttgtat catatgcaa aaatagattc  
2821 cagacagatg aatatattaa atgtaaaaa taaaattcta aaactactag aaaaaaaga  
2881 agaataatatt tattcctttg aaatagaaaa ggtcttacta agcaaacac agaagtaata  
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3061 acaagaaaat atttacaaca tttgacaggc cacagattat tatccagcct catctgataa  
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3841 aatatcacta cagatcctac agatataaaa agtataaggg catactttga ataattttat  
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5581 attgaatcat gggggcagg ctttcccatg ctgttttcac gatactgaat aagtctcaca  
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6421 atgaaaatga acctccttgc ttctgaccag tggatgagtt gcttggccgt gttcctacag  
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6661 cacatgagag tttagttag tgtattgaa gactgggttg gctctgtcgc tagtggctac  
6721 atcatcttgc tcaagtcatg ccagtctcag gacctcattc agtctcttca gctgtaatat  
6781 ggggtgggtg caccacataa ccagaaagat cccttccagc tctaccact tacaacatgg

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6961 tcactaccgt ctacttccag aactcttcat ctgtgcaaac tgaacctctg ttgtcattag  
7021 tcactaacta ttctctctcc cccctccttc taggccttgg caatcaccat tctactttct  
7081 gtgcgtatga atttgactac tctaggtaac ttatataagt ggaatcacag catttgccct  
7141 attatgactg gtttagttga cttagcaca cctcctaagg ctcaaccaca ttttagcatg  
7201 tgtcagaatt ttctttgttt ttaaggctga ataataattct gttgtatctg taaataacat  
7261 ctttattcat ttgtccatca acagactgtt gagttcctcc catcttttga ctattgtgaa  
7321 aaatgctgct atgaacctga gtgtacagac atctggttga gtactgcttt caattcattg  
7381 tttatatgga tcatatggta attttatggt taattttttt ggaactgcta cattgttttc  
7441 cacagtgtac atcattttac atttccatca gcaatgcaca aagggtccaa tttctccaca  
7501 ttcttaccaa cattttttat tttctgtttc ttattttatt gtttatttat tctgagacag  
7561 agtctcactc tgtcacctag gctggagtgc agcaggggtga tctcagctca ctgcaacctc  
7621 tgcctcccat gttcaagtga ttctcctccc tcagcctccc aagtaaatgg aattacaggt  
7681 gcccaccacc acgcccaggt aatttttggc ttttttttag tagtgatgag tttccaccat  
7741 gttggtcagg ctggtcttga actcctgacc tcaagtgtac caccgcctc agcctcccaa  
7801 agtgctggga ttacaggtat gaacctgtc acccaggcca ttttttgctt tttagataat  
7861 agtcatccta gtgggtatga agtggatttt cattgtggtt ttgatttata tttccctaatt  
7921 gatcagtgat attgagcatc ttccaagtgc ttattggcca ttttcttctt tggagaaattg  
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## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149412 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

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1157

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1158

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1170

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## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5133 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

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1172

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3781 aagacctgct gagggaccag ccaagagggc tgcaaaagt agggcttgc attaccagac  
3841 ggttcaccag cctctcttgg ttcttctctt ggaagagaat gtctgatcta aatgtggaga  
3901 aactgtagtc tcaggacctg ggtatgttct ggccctcacc cctgcctgg gatgtccaca  
3961 gatgcctcca ccccccagaa cctgtccttg cacactcccc tgcactggag tccagtctct  
4021 tctgctggca gaaagcaaat gtgacctgtg tcaactacgt actgtggcac acgccttgtt  
4081 cttggccaaa gaccaaattc cttggcatgc cttccagcac cctgcaaaat gagacctcg  
4141 tggccttccc cagcctcttc tagagccgtg atgcctccct gttgaagctc tggtagaccc  
4201 agcctttctc ccaggccagg ctcttctctg tcttcttgca ttcaccagca cagctccctc  
4261 tgctgaacc ttccatctcg cccacccctc ctctcttgac cagcagatcc cagctcacgt  
4321 cacacacttg gttgggtcct cacatctttc acacttccac caccctgcac tactccctca  
4381 aagcacacgt catgtttctt catccggcag cctggatgtt ttttccctgt ttaatgattg  
4441 acgtacttag cagctatctc tcagtgaact gtgagggtaa aggtatact tgccttgttc  
4501 accttgggat gacgcccgat gatatgtcag ggcgtgggac atctagttag tgcctgacat  
4561 aatttcaact aattaatgac agagccagtg ggaagataca gaaaaagagg gccggggctg

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4621 ggcgcggtgg ttcacgcctg taatcccagc actttgggag gccaaaggag gtggatcacc  
 4681 tgaggtcagg agtttagagg cagcctggcg aaaccccatc tctactaaaa atacaaaatc  
 4741 caggcgtggt ggcacacacc ttagtccca gctactcagg aggttgaggt aggagaattg  
 4801 cttgaacctg ggaggtggag gttgcagtga gccaaagattg cgcattgca ctccagcctg  
 4861 ggcaacacag cgagactccg tctcaaggaa aaaataaaaa taaaaagcgg gcacgggccc  
 4921 ggacatcccc acccttggag gctgtcttct caggctctgc cctgcctag ctccacaccc  
 4981 tctcccagga cccatcacgc ctgtgcagtg gccccacag aaagactgag ctcaagggtg  
 5041 gaaccacgtc tgctaacttg gagccccagt gccaagcaca gtgcctgcat gtatttatcc  
 5101 aataaatgtg aaattctgtc caaaaaaaaa aaa

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

1 ggatccagaa gggtcattca atcagttctc agtcttatca ggtctaagtt cctttcttat  
 61 caggtcctaa aggcctaatac ttatcattgt gacaaagata actgtagagt ctgttaaact  
 121 ttttttttaa taacatgaag attatgattt atagctgaat ttctcccttt tattccaatt  
 181 caacaatttt catggctttt tgtgtttgtt ttgttctgga cataattaca gaaaattacc  
 241 tgaagagttc caacctgagg cctcctcatg gatgggtcaa acgtgacatc atttgttgtt  
 301 gaggaaccca cgaacatctc aactggcagg aacgcctcag tcgggaatgc acatcggcaa  
 361 atccccatcg tgactgggt cattatgagc atctcccag tggggttgt tgagaatggg  
 421 attctcctct ggttcctgtg cttccggatg agaagaaatc ccttactgt ctacatcacc  
 481 cacctgtcta tcgcagacat ctcactgtc ttctgtattt tcatctgtc tatcgactat  
 541 gctttagatt atgagctttc ttctggccat tactacacaa ttgtcacatt atcagtgact  
 601 tttctgtttg gctacaacac gggectctat ctgctgacgg ccattagtgt ggagaggtgc  
 661 ctgtcagtc tttaccccat ctggtaccga tgccatcgcc ccaagtacca gtcggcattg  
 721 gtctgtgccc ttctgtgggc tctttcttgc ttggtgacca ccattggagta tgtcatgtgc  
 781 atcgacagag aagaagagag tcaactcagg aatgactgcc gagcagtcac catctttata  
 841 gccatcctga gcttcctggt cttcacgccc ctcatgctgg tgtccagcac catcttgggc  
 901 gtgaagatcc ggaagaacac gtgggcttcc cattcctcca agctttacat agtcatcatg  
 961 gtcaccatca ttatattcct catcttcgt atgcccata gactccttt cctgctgtac  
 1021 tatgagtatt ggtcgacctt tgggaaccta caccacattt cctgctctt ctccacaatc  
 1081 aacagtagcg ccaacccttt catttacttc ttgtgtggaa gcagtaagaa gaagagattc  
 1141 aaggagtcct taaaagttgt tctgaccagg gctttcaaag atgaaatgca acctcggcgc  
 1201 cagaaagaca attgtaatac ggtcacagtt gagactgtcg tctaagaact gtgagggag  
 1261 ttgtggataa aaatggtgga acacaggtca tttttagttt gtgcttgaa tatgacttaa  
 1321 gtatctccta aatgtgatac agaagaacat ctcatcccat atgcatgaga tactaattaa  
 1381 tgatgaaa

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

1 gagcagtgcc cagcttgtcg cagatattga agcctgttaa aataaatgcc tttgattggt  
 61 cacactttaa gcaatattgg tacaatatta aacccattgt cccaggcact cctctcctt  
 121 actgcttatg gcaattcatg tattaataaa tgacagtggc agcattgccc agacatgcgt  
 181 tttgtcatca agtcttaatg cagtcacact ggtccctcag gcaaatgaat ggaggcacag  
 241 aagatgaaat gattttcaaa atgccattag gaaagctcag gccagaactg gaaatgggtc  
 301 ccgcacaggg cactcggcca ctcttgctg gccatctct ttttggcact aagcacacaa  
 361 tgatatagaa tgaatgggta tcaactgggga tcc

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

1 ggatccagaa gggtcattca atcagttctc agtcttatca ggtctaagtt cctttcttat  
 61 caggtcctaa aggcctaatac ttatcattgt gacaaagata actgtagagt ctgttaaact  
 121 ttttttttaa taacatgaag attatgattt atagctgaat ttctcccttt tattccaatt  
 181 caacaatttt catggctttt tgtgtttgtt ttgttctgga catatttaca gaaaattacc  
 241 tgaagagttc caacctgagg cctcctcatg gatgggtcaa acgtgacatc atttgttgtt  
 301 gaggaaccca cgaacatctc aactggcagg aacgcctcag tcgggaatgc acatcggcaa



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361 atccccatcg tgcactgggt cattatgagc atctccccag tggggtttgt tgagaatggg  
421 attctcctct ggttcctgtg cttccggatg agaagaaatc ccttcactgt ctacatcacc  
481 cactgtcta tcgcagacat ctcactgtct ttctgtatct tcatcttctc tatcgactat  
541 gcttttagatt atgagctttc ttctggccat tactacacaa ttgtcacatt atcagtgact  
601 tttctgtttg gctacaacac gggcctctat ctgctgacgg ccattagtgt ggagagggtgc  
661 ctgtcagtc tttaccccat ctggtaccga tgccatcgcc ccaagtacca gtccggcattg  
721 gtctgtgccc ttctgtgggc tctttcttgc ttggtgacca ccattggagta tgtcatgtgc  
781 atcgacagag aagaagagag tcactctcgg aatgactgcc gagcagtcac catctttata  
841 gccatcctga gcttcctggt cttcacgccc ctcagtctgg tgtccagcac catcttggtc  
901 gtgaagatcc ggaagaacac gtgggcttcc cattcctcca agctttacat agtcacatg  
961 gtcacatca ttatattcct catcttcgct atgcccata gactccttta cctgtgtac  
1021 tatgagtatt ggtcgacctt tgggaacctt caccacattt ccctgtctct ctccacaatc  
1081 aacagtagcg ccaacccttt catttacttc tttgtgggaa gcagtaagaa gaagagattc  
1141 aaggagtcct taaaagtgtg tctgaccagg gctttcaaag atgaaatgca acctcggcgc  
1201 cagaaagaca attgtaatac ggtcacagtt gagactgtcg tctaagaact gtgagggag  
1261 ttgtggataa aaatggtgga acacagggtca tttttagttt gtgcttggaa tatgacttaa  
1321 gtatctccta aatgtgatac agaagaacat ctcatcccat atgcatgaga tactaattaa  
1381 tgatgaaa

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3169 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

1 ggatccagaa ggttcattca atcagttctc agtcttatca ggtctaagtt cctttcttat  
61 caggctcctaa aggcctaatac ttatcattgt gacaaagata actgtagagt ctgttaaact  
121 ttttttttaa taacatgaag attatgattt atagctgaat ttctcccttt tattccaatt  
181 caacaatttt catggctttt tgtgtttgtt ttgttctgga catatttaca gaaaattacc  
241 tgaagagttc caacctgagg cctcctcatg gatgggtcaa acgtgacatc atttgttgtt  
301 gaggaaccca cgaacatctc aactggcagg aacgcctcag tcgggaatgc acatcggaac  
361 atccccatcg tgcactgggt cattatgagc atctccccag tggggtttgt tgagaatggg  
421 attctcctct ggttcctgtg cttccggatg agaagaaatc ccttcactgt ctacatcacc  
481 cactgtcta tcgcagacat ctcactgtct ttctgtatct tcatcttctc tatcgactat  
541 gcttttagatt atgagctttc ttctggccat tactacacaa ttgtcacatt atcagtgact  
601 tttctgtttg gctacaacac gggcctctat ctgctgacgg ccattagtgt ggagagggtgc  
661 ctgtcagtc tttaccccat ctggtaccga tgccatcgcc ccaagtacca gtccggcattg  
721 gtctgtgccc ttctgtgggc tctttcttgc ttggtgacca ccattggagta tgtcatgtgc  
781 atcgacagag aagaagagag tcactctcgg aatgactgcc gagcagtcac catctttata  
841 gccatcctga gcttcctggt cttcacgccc ctcagtctgg tgtccagcac catcttggtc  
901 gtgaagatcc ggaagaacac gtgggcttcc cattcctcca agctttacat agtcacatg  
961 gtcacatca ttatattcct catcttcgct atgcccata gactccttta cctgtgtac  
1021 tatgagtatt ggtcgacctt tgggaacctt caccacattt ccctgtctct ctccacaatc  
1081 aacagtagcg ccaacccttt catttacttc tttgtgggaa gcagtaagaa gaagagattc  
1141 aaggagtcct taaaagtgtg tctgaccagg gctttcaaag atgaaatgca acctcggcgc  
1201 cagaaagaca attgtaatac ggtcacagtt gagactgtcg tctaagaact gtgagggag  
1261 ttgtggataa aaatggtgga acacagggtca tttttagttt gtgcttggaa tatgacttaa  
1321 gtatctccta aatgtgatac agaagaacat ctcatcccat atgcatgaga tactaattaa  
1381 tgatgaaa  
1 gagcagtgcc cagcttctcg cagatattga agccgtgtaa aataaatgcc tttgattgtt  
61 cacactttaa gcaatattgg tacaatatta aaccattgt cccaggcact cctctcctt  
121 actgcttatg gcaattcatg tattaaaaaa tgacagtggc agcattgccc agacatgcgt  
181 tttgtcatca agtcttaatg cagtccacct ggtccctcag gcaaatgaat ggaggcacag  
241 aagatgaaat gattttcaaa atgccattag gaaagctcag gccagaactg gaaatgggtc  
301 ccgcacaggg cactcgccca ctcttgctg gccatctcct ttttggcact aagcacacaa  
361 tgatatagaa tgaatggtta tcaactggga tcc  
1 ggatccagaa ggttcattca atcagttctc agtcttatca ggtctaagtt cctttcttat  
61 caggctcctaa aggcctaatac ttatcattgt gacaaagata actgtagagt ctgttaaact  
121 ttttttttaa taacatgaag attatgattt atagctgaat ttctcccttt tattccaatt  
181 caacaatttt catggctttt tgtgtttgtt ttgttctgga catatttaca gaaaattacc  
241 tgaagagttc caacctgagg cctcctcatg gatgggtcaa acgtgacatc atttgttgtt  
301 gaggaaccca cgaacatctc aactggcagg aacgcctcag tcgggaatgc acatcggaac  
361 atccccatcg tgcactgggt cattatgagc atctccccag tggggtttgt tgagaatggg  
421 attctcctct ggttcctgtg cttccggatg agaagaaatc ccttcactgt ctacatcacc  
481 cactgtcta tcgcagacat ctcactgtct ttctgtatct tcatcttctc tatcgactat  
541 gcttttagatt atgagctttc ttctggccat tactacacaa ttgtcacatt atcagtgact  
601 tttctgtttg gctacaacac gggcctctat ctgctgacgg ccattagtgt ggagagggtgc  
661 ctgtcagtc tttaccccat ctggtaccga tgccatcgcc ccaagtacca gtccggcattg



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721 gtctgtgccc ttctgtgggc tctttcttgc ttggtgacca ccatggagta tgtcatgtgc  
781 atcgacagag aagaagagag tcaactctcg aatgactgcc gagcagtcac catctttata  
841 gccatcctga gcttcctggt cttcacgccc ctcagtctgg tgtccagcac catcttggtc  
901 gtgaagatcc ggaagaacac gtgggcttcc cttcctcca agctttacat agtcatcatg  
961 gtcaccatca ttatattcct catcttcgct atgcccata gactccttta cctgctgtac  
1021 tatgagtatt ggtcgacctt tgggaacctt caccacattt ccctgctctt ctccacaatc  
1081 aacagtagcg ccaacccttt catcttacttc tttgtgggaa gcagtaagaa gaagagattc  
1141 aaggagtcct taaaagttgt tctgaccagg gctttcaaag atgaaatgca acctcggcgc  
1201 cagaagaca attgtaatac ggtcacagtt gagactgtcg tctaagaact gtgagggaag  
1261 ttgtggataa aaatggtgga acacaggtca tttttagttt gtgcttggaa tatgacttaa  
1321 gtatctccta aatgtgatac agaagaacat ctcacccat atgcatgaga tactaattaa  
1381 tgatgaaa

## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

1 gggcccgag aaagagctgt ccccggggccc ttggggacag ggtgacagcc acccagagat  
61 catggagaag gggacgtaag gaagacctca cagaggagtc atcctgcgac tgtgttgggt  
121 gggccttca ggaagcagag tcccaggagt tggaagcata agaggaatac tgcgggcaat  
181 gcctgagaaa gataacaggg accgggagca ggagtgaatt gggcagggga aggatcaggc  
241 ccacaatgcc aggtcacac ctgcagagga gggaagaaga agaagggccc cacatcagcc  
301 cagcggggga tgttacgccc acagacgccc cggggctcag ttactgtcta agtgttagaa  
361 ataaattttc ggtgccacaa aagaaatagc actcagatta aatgttcccc gcaaggcaat  
421 tttacttcta tagaagggtg catctcacag atggagcaat ggcaagagca cactgaaca  
481 agggaaagga aggggttttt atccctaagg caggtagccc ctacagctgt gttgtcccc  
541 tattggtcag ggttggacca caccgtctga gctaattgtt actggctatt ttaaagagag  
601 caggggtaag agccggattg gcagggtaag tagtttgga ggaggacgg tcacagaaca  
661 ggtgactcag gatgactcag gtcagagcag gtgaccagt gtgactcagt tcggagcagg  
721 tgatagaagc taggaggggg ttgtttactg aaactagggg caaggagacg aagagaacat  
781 gaaagttaaa cttaagatg aagaacaaag ctgaacatac tgatgcattg gatctttgga  
841 gaggatctca gaactcattg tacttaattt acaggctaaa acctagaag aggaatttat  
901 tatatcctac acaagactcc aggggaagcac atggccttgg actgaaggct ggcacttggg  
961 agctgtcagc caccagcacc ttctgcagca ggtacctgct ctctaagagg gaggcctggg  
1021 tgggtcacct ccagagctgc ccaggctggg cctcaaggaa gaaaaagatt ttcatttgtc  
1081 agaggcggaa gggagagggt gagggaaacag cacagcagcg gccagggggc aggggaagcac  
1141 aggaccatta gggagacacg agaaagcccc tttgtctaga acagaggatt caagcagtgc  
1201 accaaggaaa atgagggcca ggccaatgtg ctggagtggc tttgttcttg gctgaggggt  
1261 ttgggtagtg ccaaagcgta aggttaagccc tgctttccag aagaatctag cagagtgtgg  
1321 agcccagatg ggactggaag gcctgggagg ggtcaggtgg ccacagggac gggccacagc  
1381 cagtgggtgca ggcaagaaga caatggccat ccagtgtggc tcacacctgg aatcccagcc  
1441 cattgggagg tcgaggcagg tggatcacct gaggtcagga gttcgagacc agcctggtca  
1501 acatggtgaa accctgtctc taataaaatt ataaaaatta gccgggcgtg gtggtgggta  
1561 cctgtaattc cagctactca ggaggctggg tcaggagaat cgcttgaacc caggaggcgg  
1621 aggttacagt gagctgagat agcaccattg cattccagcc tggacaacaa aagcgagact  
1681 ctgtctcaaa aaaaaaaaaa aattagccag gcgtgggtgt ggggtcctgt cgtcctcggg  
1741 aggctgaggc atgagaatca ctccgggagg cagaggttgc aatgaaccaa gatcacacca  
1801 ctgcactcca gcctgggtga cagagcaaga ctctgtctaa aaaaaaaaaa aagacagaag  
1861 gatgtcagca tctgatgctg cctgtcacct tgaccctgag gatgccagtc acagctccat  
1921 taactgggac ctaggaaaat gagtcatect tggatcatgca catttcaaat ggtggcttaa  
1981 tatggaagcc acacttggga tctgttgtct cctccagcat ggtagaagat gccctgaaaag  
2041 taggggtctg atcccattcc ctgcctcact ggggaaggcga ggtggtgggg tgggggtggg  
2101 cctcaggctt ggggtcatgg gacaaagccc aggtgaatg ccgcccctcc atctccctcc  
2161 tctgagaca ggggcagcag ggcacactag tgtccaggag cagcttatga gggcccttca  
2221 cctcccgatc ctccaaaact ggcagacccc accttcttct gtgtgacccc agagctctga  
2281 gcacagcccc ttcttccgct ctgcggccc cccaccagg cccaccccaa ccttatctc  
2341 cactgctttt cagaggagtc tggccaacac aaatcctctt gtttgtttgt ctgtctgtct  
2401 gctgctccta gtctctgcct ctcccagctc ctcagcttcc gtttctttct taaactttct  
2461 ctcagtctct gaggtctcga aatcacgagg cttcagcccc tgtggaccag atgccagct  
2521 agtggccttt ctccagcccc tcagatggca cagaactaca aaccccagca tgcactctgg  
2581 cctgaagtgc ctggagagtg ctggtgtacc ccacctgcat tctgggaact gtagtttccc  
2641 tagtccccc tgctccacc agggcatcaa gctcttccct ggcgggctga cctgcctca  
2701 gccctagtct ctctgctgac ctgcggcccc ggggaagcgt cgctactgaa tgacaggggt  
2761 ggggtggagg cactggaagg cagcttctct ctcttttgtg tccccactt gagtcatggg  
2821 ggtgtggggg ttccaggaaa ttggggctgg gaggggaagg gataccctaa tgtcagactc  
2881 aaggacaaaa agtcactaca tcctgtctgg gcctctatcc ccaagaaccc aaaaggactc

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2941 aaggggtgggg atccaggagt tcttgtatgt atgggggggag gtgaaggaga gaacctgcat  
3001 gaccctagag gtccctgtgg tctactgagag tgtgggctgc catccctgc tacagaaacg  
3061 gtgctcacct tctgccaac cctccaggga aaggcacaca ggggtgaggc cgaaccttcc  
3121 gtctgggtgcc acatcacaga aggaccttta tgacccctg gtggctctac cctgccactc  
3181 cccaatgccc cagcccccac gctgcagccc cagggtctctg ctggacacct gggctccac  
3241 ttatcagcct cagtctcac agcggaaccc aggcgtccg ccccccaccc ttcaggccaag  
3301 cgggcgtgga gctgaggctt tagagcctcc cagccgggct tgttctgtc ccattgtgta  
3361 tgggatatagg gcggggcgag ggccagcact ggagagcccc ctcccactgc cccctcctct  
3421 cgggtccctc cctcttccca aggaaaaggc cagggtctctg ctggagcagg cagcagagtg  
3481 gacgcacagt aacatgggca acttgaagag cgtggcccag gagcctgggc caccctgcgg  
3541 cctggggctg gggctgggccc ttgggctgtg cggcaagcag ggccc

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23142 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

1 ggatcccatg ccttgcctca ctgggaaggc gaggtggtgg ggtgggggtgg ggcctcaggc  
61 ttgggggtcat gggacaaagc ccaggctgaa tgcgcccctt ccatctccct cctcctgaga  
121 cagggggcagc agggcacact agtgtgcagg agcagcttat gagggccctt caccctccat  
181 cctccaaaac tggcagaccc caccttcttg gtgtgacccc agagctctga gcacagcccg  
241 ttcttctccg ctgcccggccc cccacccagg cccaccccaa ccttatcctc cactgctttt  
301 cagaggagtc tggccaacac aaatcctctt gtttgtttgt ctgtctgtct gctgtccta  
361 gtctctgcct ctcccagctt ctgagcttcc gtttctttct taaactttct ctgagctctt  
421 gaggtctcga aatcacgagg ctctgacccc tgtggaccag atgcccagct agtggccttt  
481 ctccagcccc tcagatgaca cagaactaca aaccccagca tgcactctgg cctgaagtgc  
541 ctggagagtg ctggtgtacc ccacctgcat tctgggaact gtagtctccc tagtccccca  
601 tgctcccacc agggcatcaa gctcttccct ggctggctga cctgcctca gccctagtct  
661 ctctgctgac tgcggccccc ggaagcgtgc gtcactgaat gacaggggtg ggggtgaggc  
721 actggaaggc agcttctctg tctttgtgtt ccccaacttg agtcatgggg gtgtgggggt  
781 tccaggaaat tggggctggg aggggaaggg atacccta atgtcagacta aggacaaaa  
841 gtcactacat ccttgtctgg cctctatccc caagaaccca aaaggactca aggtggggga  
901 tccaggagtt cttgtatgta tggggggagg tgaaggagag aacctgcatg accctagagg  
961 tccctgtggt cactgagagt gtgggctgcc atccctgct acagaaacgg tgctcacctt  
1021 ctgcccaccc ctccaggga aggacacag ggtgagccg aaggccctt cgtctggtgc  
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1141 ccagccccc tctgagccc ccagggtctt gctggacacc tgggtcccca cttatcagcc  
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15061 ccctgcaccc caggttctgt gtgttcgggc tcggctccc ggcatacccc cacttctgcg  
15121 ctttgtctg tgcgtggac acacggctg aggaactgg cggggagcg ctgctgcagc  
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19141 ctcagagttc tgccctgaaa ctatagctcc cagagccaga gctggtatca aaccggctgg  
19201 ccctgtggct ttctgaaagc ttctgtgttc ctctctatgt ccctgggctg tctgatgtg  
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19981 acataaacta aataccacta ttaaggatac ttaaaataaa cacacttagt gaaccatta  
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23041 tcaggctcgt aatcgagaag gcaggtgcag cactcagctg ccaggagtgg ggcctgccag  
23101 aaacaagat cacagagatg tgcaacagcc atgagcaagc tt

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3690 base pairs

(B) TYPE: nucleic acid



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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

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121 cgccccctga gcccagccgg gcccagcat ccctactccc accagcgcca gaacacagcc  
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3241 tcaccgcctt ctcccggga cctgacaacc ccaagacct cgtgcaggac atcctgagga  
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(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30417 base pairs



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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

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 241 ccacaatgcc aggtcacac ctgcagagga ggaagaaga agaagggcct cacatcagcc
 301 cagcggggga tgttacgccc acagacgccc cggggctcag ttactgtcta agtgttagaa
 361 ataaattttc ggtgccacaa aagaatagc actcagatta aatgttccca gcaaggcaat
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481 aagccgaggt ggcagccaca ggcacctacc agcttaggga gagcgagctg gtgttcgggg  
541 ctaagcaggc ctggcgcaac gctcccgcgt cgtggggcg gatccagtgg gggaagctgc  
601 aggtgttcga tgcccgggac tgcaaggtctg cacaggaaat gttcacctac atctgcaacc  
661 acatcaagta tgccaccaac cggggcaacc ttcgctcggc catcacagtg ttcccgcagc  
721 gctgccctgg ccgaggagac ttccgaatct ggaacagcca gctggtgcgc tacgcggtt  
781 accggcagca ggacggctct gtgcgggggg acccagccaa cgtggagatc accgagctct  
841 gcattcagca cggctggacc ccaggaaacg gtgcgttcga cgtgctgccc ctgctgtgc  
901 agggcccaaga tgagccccc gaactcttcc ttctgcccc cgagctgggc cttgaggtgc  
961 cctggagca ccccagctg gagtgggttg cagccctggg cctgcgctgg tacgccctcc  
1021 cggcagtgtc caacatgctg ctggaaattg ggggctgga gttcccgcga gcccccctca  
1081 gtggctggtg catgagcact gagatcgga cgaggaaact gtgtgacct caccgctaca  
1141 acatcttggg ggtgtggtg gtctgcatgg acctggatac ccggaccacc tgcctcctgt  
1201 ggaaagacaa ggcagcagtg gaaatcaacg tggcgtgct gcacagttac cagctagcca  
1261 aagtcacat cgtggaccac cagcgcccca cggcctctt catgaagcag ctggagaatg  
1321 agcagaaggc cagggggggc tgccctgcag actgggctg gatcgtgccc cccatctcgg  
1381 gcagcctcac tctgttttc catcaggaga tggtaacta tttcctgtcc ccggccttcc  
1441 gctaccagcc agacccttg aaggggagtg ccgccaagg caccggcatc accaggaaga  
1501 agaccttaa agaagtggc aacgcccgtg agatctccgc ctgctcatg ggcaggtga  
1561 tggcgaagcg agtgaaggcg acaatcctgt atggtccga gaccggccgg gccagagct



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1621 acgcacagca gctggggaga ctctccgga aggcctttga tccccgggtc ctgtgtatgg  
1681 atgagtatga cgtggtgtcc ctcgaaacag agacgctggt gctggtgtga accagcacat  
1741 ttgggaatgg ggtatccccg gagaatggag agagctttgc agctgccttg atggagatgt  
1801 ccggccccca caacagctcc cctcgggcgg aacagcacaa gagttataag atccgcttca  
1861 acagcatctc ctgctcagac ccactggtgt cctcttggcg gcggaagagg aaggagtcca  
1921 gtaacacaga cagtgcaggg gccctgggca ccctcaggtt ctgtgtgttc gggctcggct  
1981 cccgggcata cccccacttc tgcgcctttg ctctgcccgt ggacacacgg ctggaggaaac  
2041 tgggcgggga gcggctgtg cagctgggcc agggcgacga gctgtgcggc caggaggagg  
2101 ccttccgagg ctgggcccag gctgccttcc agggcgctg tgagaccttc tgtgtgggag  
2161 aggatgccaa ggccgcccgc cgagacatct tcagcccaaa acggagctgg aagcgccaga  
2221 ggtaccggct gagcgcccag gccgagggcc tgcagttgct gccaggtctg atccacgtgc  
2281 acaggcggaa gatgttccag gctacaatcc gctcagtga aaacttgcaa agcagcaagt  
2341 ccacgagggc caccatcctg gtgcccctg acaccggagg ccaggagggg ctgcagtacc  
2401 agccggggga ccacataggt gtctgcccgc ccaaccggcc cggccttctg gaggcgctgc  
2461 tgagccgctg ggaggaccg ccggcgccca ctgagcccgt ggcagtagag cagctggaga  
2521 agggcagccc tgggtggcct cccccggct ggggtgcggga cccccggctg cccccgtgca  
2581 cgctgcgcca ggctctcacc ttcttctgg acatcacctc cccaccaccc cctcagctct  
2641 tgcggctgct cagcaccttg gcagaagagc ccagggaaca gcaggagctg gaggccctca  
2701 gccaggatcc ccgacgtac gaggagtga agtggttccg ctgcccacg ctgctggagg  
2761 tgctggagca gttcccctg gtggcgctgc ctgcccact gctcctcacc cagctgcctc  
2821 tgctccagcc ccggtactac tcagtccagt cggcacccag caccacccca ggagagatcc  
2881 acctcactgt agctgtgtg gcatacagga ctccaggtgg gctgggcccc ctgcactatg  
2941 gagtctgtc cacgtggcta agccagctca agcccggaga cctgtgccc tgcctcatcc  
3001 ggggggctcc ctccctccgg ctgccaccg atcccagctt gccctgctt ctggtgggtc  
3061 caggcactgg cattgcccc ttccggggat tctggcagga gcggctgcat gacattgaga  
3121 gcaaaaggct gcagccact cccatgactt tgggtgttcg ctgccgatgc tcccaacttg  
3181 accatctcta ccgacgag gtgcagaacg ccagcagcg cggggtgtt ggccgagtc  
3241 tcaccgcctt ctcccggaa cctgacaacc ccaagacctt cgtgcaggac atcctgagga  
3301 cggagctggc tgcggagggt caccgcgtgc tgtgcctcga gcggggccac atgtttgtct  
3361 gcggcgatgt taccatggca accaacgtcc tgcagaccgt gcagcgatc ttggcgacg  
3421 agggcgacat ggagctggac gagggcggg acgtcatcg cgtctgcgg gatcagcaac  
3481 gctaccacga agacatttcc gggctcagc tgccgacca ggaggtgaca agccgatac  
3541 gcaccagag cttttccttg caggagcgtc agttgcgggg cgcagtgcct tggcggttcg  
3601 accctcccg ctcagacacc aacagccct gagagccgcc tggctttccc ttccagttcc  
3661 gggagagcgg ctgcccagct caggtccgcc

## (2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1872 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

1 aggagtttcg acccgcgctg gcgagtcag agcgccaagt ttcccactgg cgcgcaaaact  
61 tgagttactt ttgagcgtgg atactggcga agaggctgcg ggcggtatta gcgtttgcag  
121 cgacttggct cgggcagctg acccaagtgt cctgtcttcc ttccctcgtc tgtctctagg  
181 ctctgaaact gcggagcggc caccggacgc cttctggagc aggtagcagc atgcagccgc  
241 ctccaagtct gtgcggaccg gccctgggtg cgtgtgttct tgccctgcggc ctgtcggga  
301 tctggggaga ggagagaggc ttcccgcctg acaggggccac tccgcttttg caaacgcag  
361 agataatgac gccaccact aagaccttat ggcccaaggg ttccaacgcc agtctggcgc  
421 ggtcgttggc acctgcggag gtgcctaaag gagacaggac ggcaggatct ccgccagca  
481 ccattctccc tccccctgca caaggacca tcgagatcaa ggagactttc aaatacatca  
541 acacggttgt gtccctgcctt gtgttcgtgc tggggatcat cgggaactcc acacttctga  
601 gaattatcta caagaacaag tgcatgcgaa acgggtccca tatcttgatc gccagcttgg  
661 ctctgggaga cctgctgcac atcgtcattg acatccctat caatgtctac aagctgctgg  
721 cagaggactg gccatttga gctgagatgt gtaagctggg gcctttcata cagaaagcct  
781 ccgtgggaat cactgtgctg agtctatgt ctctgagtat tgacagatat cgactggctg  
841 cttcttggag tagaattaaa ggaattgggg ttccaaaatg gacagcagta gaaattgttt  
901 tgatttgggt ggtctctgtg gttctgctg tccctgaagc cataggtttt gatataatta  
961 cgatggacta caaaggaaat tatctgcgaa tctgcttgc tcatcccggt cagaagacag  
1021 ctttcatgca gttttacaag acagcaaaag attggtggct attcagtttc tatttctgct  
1081 tgccattggc catcactgca tttttttata cactaatgac ctgtgaaatg ttgagaagaa  
1141 aaagtggcat gcagattgct ttaaagtatc acctaaagca gagacgggaa gtggccaaaa  
1201 ccgtcttttg cctggtcctt gctcttgccc tctgctggct tccccctcag ctgagcagga  
1261 ttctgaagct cactctttat aatcagaatg atcccaatag atgtgaaact ttgagctttc  
1321 tgttgggtatt ggactatatt ggtatcaaca tggcttcaat gaattcctgc attaacccaa  
1381 ttgctctgta tttggtgagc aaaagattca aaaactgctt taagtcatgc ttatgctgct  
1441 ggtgccagtc atttgaagaa aaacagtcct tggaggaaaa gcagtcgtgc ttaaagtcca  
1501 aagctaataa tcacggatat gacaacttcc gttccagtaa taaatacagc tcatcttgaa



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1561 agaagaacta ttcactgtat ttcattttct ttatattgga ccgaagtcac taaaacaaaa  
1621 tgaacacatt gccaaaacaa acaaaaaaac tatgtatttg cacagcacac tattaataa  
1681 ttaagtgtaa ttattttaac actcacagct acatatgaca ttttatgagc tgtttacggc  
1741 atggaaagaa aatcagtgga aattaagaaa gcctcgtcgt gaaagcactt aattttttac  
1801 agtttagcact tcaacatagc tcttaacaac ttccaggata ttcacacaac acttaggcctt  
1861 aaaaatgagc tc

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4286 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

1 gagacattcc ggtgggggac tctggccagc ccgagcaacg tggatcctga gagcactccc  
61 aggtaggcat ttgccccggt gggacgcctt gccagagcag tgtgtggcag gccccctgg  
121 aggatcaaca cagtggctga acactgggaa ggaactggta cttggagctt ggacatctga  
181 aacttggtct tgaactgagc cagcggccac cggacgcctt ctggagcagg tagcagcatg  
241 cagccgcctc caagtctgtg cggacgcgcc ctggttgccg tggttcttgc ctgcccctg  
301 tcgcggtatc ggggagagga gagaggcttc ccgcctgaca ggccactcc gcttttgcaa  
361 accgcagaga taatgacgcc accactaag accttatggc ccaagggttc caacgccagt  
421 ctggcgcggt cgttggcacc tgcggaggtg cctaaaggag acaggacggc aggatctccg  
481 ccacgcacca tctccctcc cccgtgcaa ggaccatcg agatcaagga gactttcaaa  
541 tacatcaaca cgttctgtgc ctgccttggt ttcgtgctgg ggaatcagg gaactccaca  
601 cttctgagaa ttatctacaa gaacaagtgc atgcgaaacg gtcccaatat cttgatcgcc  
661 agcttggtct tgggagacct gctgcacatc gtcattgaca tccctatcaa tgtctacaag  
721 ctgctggcag aggactggcc atttgagctc gagatgtgta agctgggtgc tttctacag  
781 aaagcctccg tgggaatcac tgtgctgagt ctatgtgctc tgagtattga cagatatcga  
841 gctgttgcct cttggagtag aattaaagga attgggttcc caaatggac agcagtagaa  
901 attgttttga tttgggtggt ctctgtggtt ctggctgtcc ctgaagccat aggttttgat  
961 ataattacga tggactacaa aggaagttat ctgcgaatct gcttgcttca tcccgttcag  
1021 aagacagctt tcatgcagtt ttacaagaca gcaaaagatt ggtggctggt cagtttctat  
1081 ttctgcttgc cattggccat cactgcattt ttttatacac taatgacctg tgaatggtg  
1141 agaagaaaaa gtggcatgca gattgcttta aatgatcacc taaagcagag acgggaagtg  
1201 gccaaaaccg tcttttgctt ggtcctgtgc tttgcccctc gctggcttcc ccttcacctc  
1261 agcaggattc tgaagctcac tttttataat cagaatgatc ccaatagatg tgaacttttg  
1321 agctttctgt tggatttggc ctatattggt atcaacatgg cttcactgaa ttcctgcatt  
1381 aacccaattg ctctgtattt ggtgagcaaa agattcaaaa actgctttta gtcagtctta  
1441 tgctgctggt gccagtcatt tgaagaaaaa cagtccttgg aggaaaagca gtcgtgctta  
1501 aagttcaaaag ctaatgatca cggatatgac aacttccgtt ccagtaataa atacagctca  
1561 tcttgaaaaga agaactattc actgtatttc attttcttta tattggaccg aagtcattaa  
1621 acaaaaatga aacatttgcc aaaacaaaaa aaaaaactat gtatttgac agcacactat  
1681 taaaatatta agtgaatta ttttaacact cacagctaca tatgacattt tatgagctgt  
1741 ttacggcatg gaaagaaaat cagtgggaat taagaaagcc tcgtcgtgaa agcacttaat  
1801 tttttacagt tagcacttca acatagctct taacaacttc caggatattc acacaact  
1861 taggcttaaa aatgagctca ctccagaattt ctattcttcc taaaaagaga tttattttta  
1921 aatcaatggg actctgatat aaaggaagaa taagtcactg taaaacagaa ctttttaagt  
1981 aagcttaaat tactcaattt aaaattttta aatcctttta aacaactttt caattaatat  
2041 tatcacacta ttatcagatt gtaattagat gcaaatgaga gacagttta gttgtgcat  
2101 ttttcggaca ctggaaacat ttaaatgatc agggaggagt aacagaaaga gcaaggctgt  
2161 ttttgaaaat cattacactt tcaactagaag cccaaacctc agcattctgc aatatgtaac  
2221 caacatgtca caaacaagca gcatgtaaca gactggcaca tgtgccagct gaatttaaaa  
2281 tataatactt ttaaaaagaa aattattaca tccctttacat tcagttaaga tcaaacctca  
2341 caaagagaaa tagaatgttt gaaaggctat cccaaaagac ttttttgaaat ctgtcattca  
2401 cataccctgt gaagacaata ctatctacaa ttttttcagg attattaaaa tcttcttttt  
2461 tcactatcgt agcttaaaat ctgtttgggt ttgtcatctg taaatactta cctacataca  
2521 tcgcatgtag atgattaaat gagggcagcc cctgtgctca tagctttacg atggagagat  
2581 gccagtgacc tcataataaa gactgtgaac tgccctggtc agtgtccaca tgacaaaggg  
2641 gcaggtagca cctctctca cccatgctgt ggttaaaaat gtttctagca tatgtataat  
2701 gctatagtta aaatactatt tttcaaaatc atacagatta gtacatttaa cagctacctg  
2761 taaagcttat tactaatttt tgtattattt ttgtaaatag ccaatagaaa agtttgcttg  
2821 acatggtgct tttctttcat ctgagggcaa aactgctttt tgagaccgta agaacctctt  
2881 agctttgtgc gttcctgcct aattttttata tcttctaagc aaagtgcctt aggatagctt  
2941 gggatgagat gtgtgtgaaa gtatgtacaa gagaaaacgg aagagagagg aaatgaggtg  
3001 gggttggagg aaacctatgg ggacagattc ccattcttag cctaactgtc gtcattgcct  
3061 cgtcacatca atgcaaaagg tctgattttt gttccagcaa aacacagtcg aatgttctca  
3121 gagtgaactt cgaaataaat tgggcccag agctttaact cggctttaa atatgcccaa  
3181 atttttactt tgtttttctt ttaataggct gggccacatg ttggaaataa gctagtaagt  
3241 ttgttttctg tcaatattga atgtgatggt acagtaaaac aaaacccaac aatgtggcca

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3301 gaaagaaaga gcaataataa ttaattcaca caccatatgg attctattta taaatcaccc
3361 acaaacttgt tctttaattt catcccaatc actttttcag aggcctgtta tcatagaagt
3421 catttttagac tctcaatttt aaattaattt tgaatcacta atattttcac agtttattaa
3481 tatattttaat ttctattttta atttttagatt atttttatta ccatgtactg aatttttaca
3541 tcctgatacc ctttcctttt ccatgtcagt atcatgttct ctaattatct tgccaaattt
3601 tgaaactaca cacaaaaagc atacttgcag tatttataat aaaattgcat tcagtggcct
3661 tttaaaaaaa atgtttgatt caaaacttta acatactgat aagtaagaaa caattataat
3721 ttctttacat actcaaaacc aagatagaaa aagggtgctat cgttcaactt caaaacatgt
3781 ttcctagtat taaggacttt aatatagcaa cagacaaaat tattgttaac atggatgtta
3841 cagctcaaaa gatttataaa agatttttaac ctattttctc ccttattatc cactgctaata
3901 gtggatgtat gttcaaacac ctttttagtat tgatagctta catatggcca aaggaatata
3961 gtttatagca aaacatgggt atgctgtagc taactttata aaagtgtaat ataacaatgt
4021 aaaaaattat atatctggga ggattttttg gttgcctaaa gtggctatag ttactgattt
4081 tttattatgt aagcaaaacc aataaaaaatt taagtttttt taacaactac ctattttttc
4141 actgtacaga cactaattca ttaataacta attgattggt taaaagaaat ataatgtga
4201 caagtggaca ttatttatgt taaatataca attatcaagc aagtatgaag ttattcaatt
4261 aaaatgccac atttctgggc tctggg

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## (2) INFORMATION FOR SEQ ID NO:37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

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1 gggctgcagg ttctgaccg cgctggcgag tcatgagcgc caagtttccc actggcgcg
61 aaacttgagt tacttttgag cgtggatact ggcgaaagagg ctgcggggcg tattagcgtt
121 tgcagcgact tggctcgggc agctgacccc aaagtgtctg tcttccttcc tctgcttgctc
181 tctaggctct gaaactgcgg cggccaccgg acgcttctgg agcaggtagc agcatgcagc
241 cgcctccaag tctgtgcgga cgcgccttgg ttgcgctggt tcttgccctgc ggcctgtcgc
301 ggatctgggg agaggagaga ggcttcccgc ccgacagggc cactccgctt ttgcaaacgg
361 cagagataat gacgccaccc actaagacct tatggcccaa gggttccaac gccagtctgg
421 cgcggtcggt ggcacctgcg gaggtgccta aaggagacag gacggcagga tctccgccac
481 gcaccatctc cctcccccgc tggcaaggac ccatcgagat caaggagact ttcaaatata
541 tcaacacggt tgtgtcctgc cttgtgttcg tgctggggat catcgggaaac tccacacttc
601 tgagaattat ctacaagaac aagtgcctgc gaaacggctc caatatcttg atcgccagct
661 tggctctggg agacctgctg cacatcgta ttgacatccc tatcaatgtc tacaagctgc
721 tggcagagga ctggccattt ggagctgaga tgtgtaagct ggtgcctttc atacagaaag
781 cctccgtggg aatcactgtg ctgagcttat gtgctctgag tattgacaga tatcgagctg
841 ttgcttcttg gtagaattt aaaggaattg gggttccaaa atggacagca gtagaattg
901 ttttgatttg ggtggtctct ctggttctgg ctgtccctga agccataggt ttgatataa
961 ttacgatgga ctacaaagga agttatctgc gaatctgctt gcttcatccc gttcagaaga
1021 cagctttcat gcagttttac aagacagcaa aagattgggt gctgttcagt ttctatttct
1081 gcttgccatt ggccatcact gcattttttt atactaatat gacctgtgaa atgttgagaa
1141 agaaaagtgg catgcagatt gctttaaatg atcacctaaa gcagagacgg gaagtggcca
1201 aaaccgtctt ttgcttggtc cttgtctttg cctctgctg gcttcccctt cacctcagca
1261 ggattctgaa gctcactctt tataatcaga atgatcccaa tagatgtgaa cttttgagct
1321 ttctgttggt attggactat attggtatca acatggcttc actgaattcc tgcattaaac
1381 caattgctct gtatttggtg agcaaaagat tcaaaaactg ctttaagtca tgcttatgct
1441 gctggtgcca gtcatttgaa gaaaaacagt ctttgaggga aaagcagtcg tgcttaaagt
1501 tcaaagctaa tgatcacgga tatgacaact tccgttccag taataaatac agctcatctt
1561 gaaagaagaa ctattcactg tatttcattt tctttatatt ggaccgaagt cattaaaaca
1621 aatgaaaca tttgcaaaaa caaaacaaaa aactatgtat ttgcacagca cactattaaa
1681 atattaagtg taattatttt aaaaaaaaaa aaaaaaaaaa

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## (2) INFORMATION FOR SEQ ID NO:38:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4156 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

1 cccactatgt tggccaggat ggtcttgatt tcttgacctc gtgttctgccc cgcctctacc
61 tcccaaagtg ccgggattac aggcgtgact gctgtgcccg gccccagcat cacttttata
121 gctttctgtg cctcttcctc tgggccttgg tgatgaagc cacttgccct tctctgttgg
181 gaagcgagca gaatcagatt gctactcatg atgcagtcgg ggcagggcat actgtcacct
241 ttggctgtgg acacagttgt caggataggg gagaagccct ttaggtccgt cttcttgaca
301 cagccctcct acctggttac gctgggtctt tcgcttggtt tagacaacca agacacttga
361 gaattatgct gtcctcagaa tgrctgatga aaagaacaga ttcacttttt ggacacaatg

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421 cccattagcc atctttggca gtgtttctga tcaaagggtc cccatgcctg ccttaggaaa
481 gtaaaccttt ttcagaataa atcctcaaat ggattactga gtagtctttg caccattccc
541 atcagcctaa tcagactgaa tggcacgct cagtgcacaa agctgttttg ctgttaggat
601 gtttcagtg tcttgtctt tcttgaaca gtccagttgt ttaaatttag taattcaatc
661 ctgaccagtg taaacccact taattattgc agcctaaaaga attcagctac ttctactctt
721 cataaatgtg cccaagtaaa tatgtgtttt taatattcaa ccctggaaaa ttagtaattc
781 agatgataaa agctcatgtt ttggtgtctt tgtactcaga ttgtgaacag gcatatttca
841 ctgatttaga cttagtatac ttgatgagaa tgctcaggtt gaagagatag ttctgacagc
901 aatccaacat ctatagcaat gtggaaaaag taatcaactc atatttcacg aatttgatgt
961 atgttgtgat ttagagggca tgagataaag tttatatttg aactgtgtgg ggtaggggga
1021 agaagagggt gcttaagcaa atgggggggt gattgaggaa caagatgtct ctaagatgag
1081 aagttatttt cttgcatcat agaagcactc tythyacccg ngagtgttg tgtaactat
1141 aaatcattta tatctgtaca ttaaagcaga ttccctcaat taggcaaat tggttagcca
1201 agcccaagtt attgtttgta cttgaaagta ataaagctgc atttcttaa aaatatattc
1261 tgtagttaag actttgtctt gctttccgga attcctgttt tcttttctc ctagagacct
1321 cggcttgcaa ctggatcaaa cgctgtcgaa aggatgtaaa taggcagagc aactgttacc
1381 aagaaggcca ccacccccac ccaaaggcag tgaggagtgt ggggctcgt ctgggctccc
1441 ccgagtctca acagtaatca acagtcaggt gttgattgca acttttcaag gtcagccacc
1501 gggagttagc tattccctct aggaaccttg gagggcatat cttgctggga ctcaacttgg
1561 ctgagaaatg cacaagatgc caaaggagga aggattatag ggggctgtg tgtgaccccc
1621 aagaccgatc ttccgctatc accctaactc ccggttcccc gctacccggg cgggggtgag
1681 tatgtgacat gtgcctaact ctcagcagca acttcggcag caggtgtcga tcttaactaa
1741 gcaggagctg cggctgccgg gtgtgccctc accaagccat gcgagccccg ggcgcgttcc
1801 tcgcccgcac gtccggcta ctgctctgct tactgtctca ggtgtctgcc tcttctgccc
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1921 tgatccagcg ccgcggcagg gacgcctggg gaccgggaaa ttctgcaaga gacgttctgc
1981 gagcccgagc acccagggag gagcaggggg cagcgtttct tgccggaccc tcttgggacc
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2161 aggagccttc tgaactttg gggagagggg ggtcccagag gcgctgtcat ttccgggcgt agccaggagc
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2281 agagtgtgaa gacagtcccc ggagccagcg atctttttta ctgtccaagg agagccggga
2341 aactccaggg ttcccaccac aagcccctgt ccaagacggc caatggactg gcggggcacg
2401 aagggtggac aattgcactc ccgggcccgg cgctggccca gaatggatcc ttgggtgaag
2461 gaatccatga tccctggggg ccccgccggg gaaacagcac gaaccggcgt gtgagactga
2521 agaaccctt ctaccgcgtg acccaggagt cctatggagc ctacgcggtc atgtgtctgt
2581 ccgtggtgat cttcgggacc ggcattcatt gcaacctggc ggtgatgtgc atcgtgtgcc
2641 acaactacta catgcgagc atctccaact ccccttggc caacctggtc ttctgggact
2701 ttctcatcat cttcttctgc cttccgctgg tcatcttcca cgagctgacc aagaagtggc
2761 tgggtggagga cttctcctgc aagatcgtgc cctatataga ggtcgcttct ctgggagtca
2821 ccactttcac cttatgtgct ctgtgcatag accgcttccg tgctgccacc aacgtacaga
2881 tgtactacga aatgatcgaa aactgttctt caacaactgc caaacttgct gttatatggg
2941 tgggagctct attgttagca cttccagaag ttgttctccg ccagctgagc aaggaggatt
3001 tggggtttag tggccgagct ccggcagaaa ggtgcattat taagatctct cctgatttac
3061 cagacaccat ctatgttcta gccctcacct acgacagtgc gagactgtgg ttgtattttg
3121 gctgttactt ttgtttgccc acgcttttca ccatcacctg ctctctagtg actgcgagga
3181 aaatccgcaa agcagagaaa gcctgtaccc gagggataaa acggcagatt caactagaga
3241 gtcagatgaa ctgtacagta gtggcactga ccattttata tggattgggc attattcctg
3301 aaaatatctg caacattggt actgcctaca tggctacagg ggtttcacag cagacaatgg
3361 acctccttaa tatcatcagc cagttccttt tgttctttaa gtcctgtgtc accccagctc
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3481 gtgaggaatg cattcagaag tcttcaacgg tgaccagtga tgacaatgac aacgagtaca
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3661 tcatatcccc tgaaagtatt taattcatat ttttccttat agggaaaaat gcaaaaaaga
3721 aacaataaag aaagaaatat taactactgt agaactgatt ttcaaaatta atatttgtgc
3781 ttgaaaaaaa agtttctatt tagttattta agaagaatga gaaggccaat agtttttagat
3841 tattttatct ggtatggtgc taatatttta tttgaaaaaa gttactgcaa cttactataa
3901 aattgctaac gtttttctt cttttaaaaa tattaattat gtatattaat tatagcaatg
3961 tgattttgta ggttatttta tatttgagtt gtgattgaaa gtatgttgta tatggtattg
4021 tgagatgatt tgtacttggg agcattcaca aagtagcacc aaataaatta cactttattc
4081 tttaatgtca ttgtcaatct acttttaacc aatattcaat aaatcttcta attgccttaa
4141 aaaaaaaaaa aaaaaa

```

## (2) INFORMATION FOR SEQ ID NO:39:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1578 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```
1 gggctgcagg ttctgaccgg cgctggcgag tcatgagcgc caagtttccc actggcgcg  
61 aaacttgagt tacttttgag cgtggatact ggcgaagagg ctgcgggcgg tattagcggt  
121 tgacgcgact tggctcgggc agctgacccc aaagtgtctg tcttccttcc tctgcttgtc  
181 tctaggctct gaaactgcgg cggccaccgg acgcttcttg agcaggtagc agcatgcagc  
241 cgctccaag tctgtgcgga cgcgccttgg ttgcgctggg tcttgccctgc ggctgtgcgc  
301 ggatctgggg agaggagaga ggcttcccgc ccgacagggc cactccgctt ttgcaaaccg  
361 cagagataat gacgccaccc actaagacct tatggcccaa gggttccaac gccagcttgg  
421 cgcggtcggt ggcacctgcg gaggtgccta aaggagacag gacggcagga tctccgccac  
481 gcaccatctc cctcccccgg tgccaaggac ccacgcagat caaggagact ttcaaatata  
541 tcaacacggg tgtgtcctgc cttgtgttgc tgctggggat catcggaac tccacacttc  
601 tgagaattat ctacaagaac aagtgcctgc gaaacggtcc caatatcttg atcgccagct  
661 tggctctggg agacctgctg cacatcgta ttgacatccc tatcaatgtc tacaagctgc  
721 tggcagagga ctggccattt ggagctgaga tgtgtaagct ggtgccttcc atacagaaag  
781 cctccgtggg aatcactgtg ctgagctctat gtgctctgag tattgacaga tatcgagctg  
841 ttgcttcttg gagtagaatt aaaggaaattg gggttccaaa atggacagca gtagaattg  
901 ttttgatttg ggtggtctct gtggttcttg ctgtccctga agccataggt tttgatataa  
961 ttacgatgga ctacaaagga agttatctgc gaatctgctt gcttcatccc gttcagaaga  
1021 cagctttcat gcagttttac aagacagcaa aagattggtg gctgttcagt ttctatttct  
1081 gcttgccatt ggccatcact gcattttttt atacactaat gacctgtgaa atgttgagaa  
1141 agaaaagtgg catgcagatt gctttaaatg atcacctaaa gcagagacgg gaagtggcca  
1201 aaacgctctt ttgctgtgct cctgtcttgg cctctgctg gcttccctt cactcagca  
1261 ggattctgaa gctcactctt tataatcaga atgatcccaa tagatgtgaa cttttgagct  
1321 ttctgttggg attggactat attggtatca acatggcttc actgaattcc tgcattaaac  
1381 caattgctct gtatttgggt agcaaaagat tcaaaaactg ctttaaggct gggccacatg  
1441 ttggaataa gctagtaatg ttgtttctg tcaatattga atgtgatggt acagtaaac  
1501 aaaacccaac aatgtggcca gaaagaaaga gcaataataa ttaattcaca caccatattg  
1561 attctattta taaatcac
```

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13611 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```
1 aggagtttctg acccgcgctg gcgagtcattg agcgccaagt ttccactgg cgcgcaaact  
61 tgagttactt ttgagcgtgg atactggcga agaggctgcg ggcggtatta gcgtttgcag  
121 cgacttggct cgggcagctg acccaagtgt cctgtcttcc ttcctctgct tgtctctagg  
181 ctctgaaact gcggagcggc caccggacgc cttctggagc aggtagcagc atgcagccgc  
241 ctccaagtct gtgcggaccg gccctggttg cgctggttct tgcctgcggc ctgtcgcgga  
301 tctggggaga ggagagaggc ttcccgcttg acagggccac tccgcttttg caaaccgcag  
361 agataatgac gccaccact aagaccttat ggcccaaggg ttccaacgcc agtctggcgc  
421 ggtcgttggc acctgcggag gtgcctaaag gagacaggac ggcaggatct ccgccacgca  
481 ccactctccc tccccgtgc caaggaccca tcgagatcaa ggagactttc aaatacatca  
541 acacggttgt gtctgcctt gtgttcgtgc tggggatcat cgggaactcc acacttctga  
601 gaattatcta caagaacaag tgcattgcga acggtcccaa tatcttgatc gccagcttgg  
661 ctctgggaga cctgctgcac atcgctattg acatccctat caatgtctac aagctgtctg  
721 cagaggactg gccatttga gctgagatgt gtaagctggg gcctttcata cagaagcct  
781 ccgtgggaat cactgtgctg agtctatgtg ctctgagtat tgacagatat cgagctgttg  
841 cttcttgag tagaattaaa ggaattggg ttccaaaatg gacagcagta gaaattgttt  
901 tgatttgggt ggtctctgtg gttctggctg tccctgaagc cataggtttt gatataatta  
961 cgatggacta caaagggaat tatctgcgaa tctgcttgc tcatccggt cagaagacag  
1021 ctttcatgca gttttacaag acagcaaaaag attggtggct attcagtttc tatttctgct  
1081 tggcattggc catcactgca ttttttata cactaatgac ctgtgaaatg ttgagaaaga  
1141 aaagtggcat gcagattgtt ttaaattgat acctaaagca gagacgggaa gtggccaaaa  
1201 ccgtcttttg cctggtcctt gtctttgccc tctgctggct tcccttccac ctgacagga  
1261 ttctgaagct cactctttat aatcagaatg atcccaatag atgtgaactt ttgagctttc  
1321 tgttggtatt ggactatatt ggtatcaaca tggcttccat gaattcctgc attaacccaa  
1381 ttgctctgta tttggtgagc aaaagattca aaaactgctt taagtcatgc ttatgctgct  
1441 ggtgccagtc atttgaagaa aaacagtcct tggaggaaaa gcagtcgtgc ttaaagttca  
1501 aagctaatag tcacggatat gacaacttcc gttccagtaa taaatacagc tcatcttgaa  
1561 agaagaacta ttcactgtat ttcattttct ttatatgga ccgaagtcac taaaacaaa  
1621 tgaacattt gccaaaacaa aacaaaaaac tatgtatttg cacagcacac tattaaata  
1681 ttaagtgtaa ttattttaac actcacagct acatatgaca ttttatgagc tgtttacggc  
1741 atggaaagaa aatcagtggt aattaagaaa gcctcgtcgt gaaagcactt aattttttac  
1801 agttagcact tcaacatagc tcttaacaac ttccaggata ttcacacaac acttaggctt  
1861 aaaaatgagc tc
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61 aggtaggcat ttgccccggt gggacgcctt gccagagcag tgtgtggcag gcccccggtg  
121 aggatcaaca cagtggctga acactgggaa ggaactggta cttggagtct ggacactctga  
181 aacttggtc tgaaactgcg cagcggccac cggacgcctt ctggagcagg tagcagcatg  
241 cagccgctc caagtctgtg cggacgcgcc ctggttgccg tggttcttgc ctggcgctg  
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421 ctggcggtt cgttggcacc tgcggagggt cctaaaggag acaggacggc aggatctccg  
481 ccacgcacca tctccccctc cccgtgccaa ggacccatcg agatcaagga gactttcaaa  
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661 agcttggtc tgggagacct gctgcacatc gtcattgaca tccctatcaa tgtctacaag  
721 ctgctggcag aggactggcc atttgagctt gagatgtgta agctgggtgc tttcatacag  
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1621 acaaaaatga aacatttgcc aaaacaaaac aaaaaactat gtatttgca acacactat  
1681 taaaatatta agtgtaatta ttttaacact cacagctaca tatgacattt tatgagctgt  
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3301 gaaagaaaga gcaataataa ttaattcaca caccatatgg attctattta taaatcacc  
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3601 tgaaactaca cacaaaaagc atacttgcat tatttataat aaaattgcat tcagtggctt  
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3961 gttttagca aaacatgggt atgctgtagc taactttata aaagtgaat ataacaatgt  
4021 aaaaaattat atatctggga ggattttttg gttgcctaaa gtggctatag ttactgattt

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4081 tttattatgt aagcaaaacc aataaaaatt taagtttttt taacaactac cttatttttc  
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901 ttttgatttg ggtggtctct gtggttctgg ctgtccctga agccataggt tttgatataa  
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1021 cagctttcat gcagttttac aagacagcaa aagattgggt gctgttcagt ttctatttct  
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1501 aaaacccaac aatgtggcca gaaagaaaga gcaataataa ttaattcaca caccatattg  
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## (2) INFORMATION FOR SEQ ID NO:41:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12461 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear



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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

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121 gtaatccaca gcaactgtgg aggccaaggt aagaggattg cttgaggcca ggatttcaag  
181 accagcctag gcaacatagt gagatcccta tctctacgaa aaaattttta aacttagctg  
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8461 tctatgatta aagtgttctg agctcaggcc aggcagtcac gaactacttc tgagtgtgtt  
8521 actactgatt tgtggggcag cctcagctat cggtttcttc acacctgctt atgagagtat  
8581 ccataattat ggtcgcaggc agtaatgctc cccacgagat cagtttctga actaaccttg  
8641 aattttttat gggtttttat tatggccaact attaaatcaa cattacagtt cttccctctg  
8701 tatttctcct gtaaaacatt aggcctgcaa aaaaaaaaaa tcttttttaa aataattgcc  
8761 ataaagtatt tgctctgggc cractgtatg cttcttttyt ttttctctct tttcaactaa  
8821 gtcaccgtca atttattaag atggccataa ctattcaaaa cctatgctga gttcctcaag  
8881 gcagggtcgc atagtgtatg aggttgggat ggggctacgg aagaaaccag aacaactcta  
8941 gtttatttaa aacctgtatt tactgccac ttcctcttag acttgaccat atgacctctt  
9001 gctcccatc ctaagcatag gggcaggctt tatttttaca atggtaatat atgatattac  
9061 ttgaggtttt atcaaagagt tgcggcgggt ggtgaaagt cacaaccaga ttcaggtttt  
9121 gtttgtgcca gattctaatt ttacatgttt cttttgcaa aggtgtattt ttttaaaata  
9181 acatttgttt tctcttatct tgctttatta ggtcggagac catgagaaac agcgtcaaat  
9241 catcttttca tgatcccaag ctgaaaggca agccctccag agagcgttat gtgaccaca  
9301 accgagcaca ttggtgacag acctcgggg cctgtctgaa gccatagcct ccacggagag  
9361 cctgtgggcc gactctgcac tctccacctt ggctgggatc agagcaggag catcctctgc  
9421 tggttcctga ctggcaaagg accagcgtcc tcgttcaaaa cattccaaga aaggttaagg  
9481 atttccccc accatcttca ctggcttcca tcagtggtaa ctgcttttgt cttcttttct  
9541 atctggggat gacaatggac ctctcagcag aaacacacag tcacattcga attcgggttg  
9601 catectccgg agagagagag aggaaggaga ttccacacag ggggtggagt tctgacgaag  
9661 gtcctaaggg agtgtttgtg tctgactcag gcgcctggca catttcaggg agaaactcca  
9721 aagtcacacac aaagattttc taaggaaatgc acaaattgaa aacacactca aaagacaaac  
9781 atgcaagtaa agaaaaaaa aagaaagact tttgtttaaa tttgtaaaat gcaaaactga  
9841 atgaaactgt tactaccata aatcaggata tgtttcatga atagagctc acctcaccta  
9901 tatgtcactc tggcagaagt atttcccaca ttttaattatt gcctccccc actcttccca  
9961 cccctgctgc cccttccctc atcccccata ctaaatecta gcctcgtaga agtctggtct  
10021 aatgtgtcag cagtagatat aatattttca tggtaatacta ctagctctga tccataagaa  
10081 aaaaaagatc attaaatcag gagattccct gtccttgatt tttggagaca caatggtata  
10141 gggttgttta tgaatatat tgaaaagtta gtgtttgtta cgctttaaag cagtaaaatt  
10201 attttcttt atataaccgg ctaatgaaag aggttggatt gaattttgat gtacttattt  
10261 ttttatagat atttatattc aaacaattta ttccttatat ttaccatgtt aaatatctgt  
10321 ttgggcaggc catattgggt tatgtatttt taaaatatgt atttctaatt gaaattgaga  
10381 acatgctttg ttttgcctgt caaggtaatg actttagaaa ataaatattt ttttcttac  
10441 tgtactgatt tggaaatcatt actgaaattt gtaaggagtg ggccaacgtg attaagtacc  
10501 ataaaggcaa ataaatggtt aaagacggtt tcatagaaaa gtgacaatta gaaggatatt  
10561 acggtctaag ctaattatat aaagaatttt atctgtatct taaatgttga ttttatactg  
10621 cattgaggta aaaacacaaa acaaaaaagc agctttaaca cctctgtctt ctcttgggta  
10681 gcagcctcct gcttctcctt cacctgaaaa attctccagg gacttcatcc attaacttgg  
10741 ctacggctat tggcaggatt cacagtttaa gctgatggtg tggtagaga tcttttatcc  
10801 atattaatgg actgaaggaa gtaatgtcga gacaacccc caaaacatac ctaattatac  
10861 aaagtatat accaaagtgt cttttagaaa atggcctgct cagagcaagt agaggtttcc  
10921 aatggctttt tattttctca cattaaggat gttgtttctt aaggaacatt gagtaccatt  
10981 gcttctctgt gatagcctag gactgccgtg tgcccattgga ggtagagaca ccaggtactg  
11041 attctaaggc ctctgccaca aagcaccact tcctctccac tttgccttgg ctggccttgt  
11101 cagctcactg gagagcacag tattgcaatt gcagtattgc aaatggtcac tactaactga  
11161 attctctaag agcttgatta gccctcgaga atcttctctg cccttctcta atagtgtctg  
11221 aggaattcc tggcatttaa caaattatg catgtagtga tcactgtcgt cctaacagtg  
11281 acacatcaga aggatttcaa ataacagtct tcaggcatgc gtaatcaatg tctgtgcag  
11341 agtctccgtc ctcatgtatc ctcattttct tctttaaggc acagtccaat gtctttgggg  
11401 aattgtttat aaagcttact ttatccataa actgtttctc agtgcgtgac tctgaagaaa  
11461 attttgaagt tttgccatg ttgacaagggt gcttgggtctg aacttggcca gtatttaatc  
11521 ttgagcaaac gattcaattt ccttctatcg tgagttttct catctatgaa acaaggaggt  
11581 tgaggggagt ttctttcata cctctgagaa agagtttgag attacataaa gaagtgaag  
11641 tggcatgaaa aaaaataaag atctgagctt agaagacatg gatctaatac atttaagagg  
11701 aagtcagaat cagagaagcc actgaacaaa acagtccaaa cggagcatag taagtcagat  
11761 tgatgagttt tgggtgggtt tttcatcagt caaaccttgg agccccctt tcccatgctt  
11821 cctgcttcag tatccagtag gaaaaatgaa agggatgatg tagacactct agggcatgag  
11881 gatttgcagt aaataagttg ggagactcac agaaaattaa tatttttcaa acatgaagac  
11941 gaaacattca attatattac agtccacatc agcttgaagg gtaaaactgat gggatgatct  
12001 gtcacatttc ttgctctgtt tccagtaaaa gcatgggttc tggaaaccca cttaggacag  
12061 ctttctctct ttacactgat agcccaggca agctttgatc tcagaactcc agaaaccaga  
12121 gaactctagg tggaaatgtg taacttttgc cagggcagag ggaacaccta ctaataggtg

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12181 cttcatttgc accaccagag attggcatct tttttgatgg atccactggc tttgatactg  
 12241 cctgtactcc cccaaaacac agcttgggta ttggactaat cttagactcc ctcaggagaa  
 12301 ctcttgctga cattaagaaa gagcaacatt ttgtctttcc aggtgaaaat ccaaggccaa  
 12361 aaagggagtg actcacctaa gatcacagaa ggagctgtag catctctgga gcttgaacac  
 12421 ttaagttaag cagcactatt tcacgcagag ggcattgaatt c

## (2) INFORMATION FOR SEQ ID NO:42:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

1 ggagctggtt acccccactc taatagggtt tcaatataaa aagccggcag agagctgtcc  
 61 aagtcagacg cgccctctga tctgcgccag gcgaacgggt cctgcgcctc ctgcagtcce  
 121 agctctccac caccgcgcgc tgcgcctgca gacgctccgc tcgctgcctt ctctcctggc  
 181 aggcgctgcc ttttctcccc gttaaagggc acttgggctg aaggatcgct ttgagatctg  
 241 aggaacccgc agcgctttga gggacctgaa gctgtttttc ttcgttttcc tttgggttca  
 301 gtttgaacgg gaggtttttg atcccttttt ttcagaatgg attatttgct catgattttc  
 361 tctctgctgt ttgtggcttg ccaaggagct ccagaaacag cagtcttagg cgctgagctc  
 421 agcgcggtgg gtgagaacgg cggggagaaa cccactccca gtccaccctg gcggctccgc  
 481 cgggtccaagc gctgctcctg ctctgcccctg atggataaag agtgtgtcta cttctgccac  
 541 ctggacatca tttgggtcaa cactcccagc cacgttggtc cgtatggact tggagccct  
 601 aggtccaaga gagccttggg gaatttactt cccacaaaag caacagaccg tgagaataga  
 661 tgccaatgtg ctaggccaaa agacaagaag tgctggaatt tttgccaaagc aggaaaagaa  
 721 ctgagggctg aagacattat ggagaaagac tggataatc ataagaaagg aaaagactgt  
 781 tccaagcttg gaaaaaagtg tatttatcag cagttagtga gaggaagaaa aatcagaaga  
 841 agttcagagg aacacctaag acaaacccag tcggagacca tgagaacacg cgtcaaatca  
 901 tcttttcatg atcccaagct gaaaggcaag cctccagag agcgttatgt gaccacaaac  
 961 cgagcacatt ggtgacagac ttcggggcct gtctgaagcc atagcctcca cggagagccc  
 1021 tgtggccgac tctgcaactc ccaccctggc tgggatcaga gcaggagcat cctctgctgg  
 1081 ttcttgactg gcaaggacc agcgtcctcg ttcaaaacat tccaagaaag gtttaaggagt  
 1141 tcccccaacc atcttctact gcttccatca gtggtaactg ctttggcttc ttctttcatc  
 1201 tggggatgac aatggacctc tcagcagaaa cacacagtca cattcgaatt c

## (2) INFORMATION FOR SEQ ID NO:43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1166 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

1 ctgcgcagg cgaacgggtc ctgcgcctcc tgcagtccea gctctccacc gccgcgtgag  
 61 cctgcagacg ctccgctcgc tgccttctct cctggcagcg gctgcctttt ctccccgtta  
 121 aagggcactt gggctgaagg atcgctttga gatctgagga acccgacagc ctttgaggga  
 181 cctgaagctg tttttcttcg ttttctttg gggtcagttt gaacgggagg tttttgatcc  
 241 ctttttttca gaatggatta tttgtctatg attttctctc tgctgtttgt ggcttgccaa  
 301 ggagctccag aaacagcagt cttaggcgct gagctcagcg cgggtgggtg gaacggcggg  
 361 gagaaaccca ctcccagtc accctggcgg ctccgcccgt ccaagcgtg ctctgctcg  
 421 tccctgatgg ataaagagtg tgtctacttc tgccacctgg acatcatttg ggtcaacact  
 481 cccgagcagc ttgttccgta tgagcttggg agccctaggt ccaagagagc cttggagaat  
 541 ttaactccca caaaggcaac agaccgtgag aatagatgcc aatgtgctag ctaaaaagac  
 601 aagaagtgtt ggaatttttg ccaagcagga aaagaactca gggctgaaga cattatggag  
 661 aaagactgga ataatacataa gaaaggaaaa gactgttcca agcttgggaa aaagtgtatt  
 721 tatcagcagt tagtgagagg aagaaaaatc agaagaagt cagaggaaca cctaagacaa  
 781 accaggtcgg agaccatgag aaacagcgtc aaatcatctt tcatgatcc caagctgaaa  
 841 ggcaagccct ccagagagcg ttatgtgacc cacaaccgag cacattgggtg acagacttcg  
 901 gggcctgtct gaagccatag cctccacgga gagccctgtg gccgactctg cactctccac  
 961 cctggctggg atcagagcag gagcctcctc tgctgggttc tgactggcaa aggaccagcg  
 1021 tcctcggtta aaacattcca agaaagggtta aggagttccc ccaacctct tcaactggctt  
 1081 ccatcagtggt taactgcttt ggtctcttct ttcactctggg gatgacaatg gacctctcag  
 1141 cagaaacaca cagtcacatt cgaattc

## (2) INFORMATION FOR SEQ ID NO:44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14878 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

1 gatatactat taatacagag atacagaaag aaatacataa aaaatagttt tatcaaatatc  
 61 tttccagcat tcaagtgtag cctcaaaaagc aagaataggc caggagtggg ggctcacgct  
 121 gtaatccaca gcaactgtggg aggccaaagg aagaggattg cttgaggcca ggatttcaag  
 181 accagcctag gcaacatagt gagatcccta tctctacgaa aaaattttta aacttagctg

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241 ggcatggtgc ttgagcctgt tgtcccagct actcaggagg tgaagtagga gtgtcacttg  
301 agcccaggag gttgagggtc cagttagcta taactgcacc actgcactcc agccttggag  
361 acagagttag accctgtccc caaaaaaatt aaaatttgaga aaaaaaaaaa ggcaagaaca  
421 gccacagcaa acrtttctatt ggggaaaaaa aaaaatcctc ctctttacat ctctcccttc  
481 ctcccttccc ctttctgaga gtgactgtgg ccaaaggag cattttcccc ctgcagtcct  
541 ctgaggggtg ggttggggct atgaagctat ctttcatatt cactcctttg tccagctctt  
601 ttcacctcta gttcttctcc ccgcatctct gtctagcagt gccttaagtg gaggagggtg  
661 gggggcatca agcttgtaaa actggtttgt tggggttctc cttctccctt catttcttga  
721 ttcttgggaa aatgtcttgc tgggaggctg cctggcgagt gccctagctg ccttctgttg  
781 gcttgaatgg ggcttccctc tgcccctaca ggaggaaaag ggagctgtg ccagaggag  
841 aaatggagag atggacagag aaggcagggt ccaccctcg cccctgacac acaagaaaa  
901 agacacggaa attctctctc tctcttctct tctctatct ctctctctct cctctctct  
961 ctctctctct ctctctctca cacacacaca cacacacaca cacacacaca caggcgcgcg  
1021 ccgcgcgcg aggcacacgt cttgcaaaat caggattcaa agagacagg gcaccattat  
1081 atttggcacg gtggggcctt ccagggtctga aatcctgcat tcttctttac tatttacttt  
1141 ccccgagctc gagaagggcc aggtgtgggc ggatggctgg ccacgttttg tgtttccaa  
1201 tcatattcac gggatgacac agacggggcg tggtagtgct tgttggaggc gcttgggcag  
1261 tttcattttg cccacttctt ccacctgaag gctggcggtt gctggaacct gcaggggcag  
1321 cctcagcaag gtgggttggc gtggagtggt gtgggagaag ggaactccagc tgaagtagaa  
1381 ccagggtctg acctgagaat attggggagg gcatgggcgg tggtttccgg gtaggggcct  
1441 ttgaggacatg ttgttcttga ctgttgcag tgtttggtca aagtttcaaa aagtttcaaa  
1501 aaaaaaaagt agggggagtc tctgccaaga catattttcc aggccacctt tcttccgagg  
1561 gagtgttggg ggggagggcg tgccttgaac ctgtgaatgt gacatcagct cctctctct  
1621 ctcccaaggt cggcttttga gaggagggtc agggcacctt tgcttggcac aggcacgtg  
1681 gcttccggct cagtgcggcc tgcctctcgg gagctgtgct cctcctgggc cccggggcta  
1741 ggctgaggtg agcgacacgc ggaggccagg cgcgcggcca gaggcctgg ggtatagggtg  
1801 gaggcatctc tgggtgtggg tgggtgtgtg ggtgtgggag ggagagttct tgcctctctc  
1861 tctcccatct ccaactcttg cttcagtggt tcttttagag gatgcagtgc attatggacc  
1921 tgtcgtgcc actgtccctg tccccacagc tgtgacttgc agggagggtc ggggatctga  
1981 gtctgtccaa acccacggct ttgctgttgg gataaaaact gtcttttga ttttagaagg  
2041 aggaggga aaaggtttcc cagcatgtgt gttgtgccag tcttggaaat tcatccgtg  
2101 ttgaattcca cctccatcc ccagaaaaac tggagtaaaa caaaaagagg agatggacaa  
2161 agtgtgtatt tgatggcatc ccttgggaag agactctaaa tttatcccat aggtcttact  
2221 gggccactgt gagcgcttgg tgggagaaca aaaaaaatt ctgggtgtct agttgtctaa  
2281 ctgaaaaat gggactagcg gaaaaagcca atgtgttcca tgcactttt gctttcttta  
2341 ttaaggcatg atgtcacctg tacagtaact gccctgtgtg tacttcaggg ggggatttca  
2401 aggttagata gacaggaaat tgttttgaat atgtaaacac attattaaat gtgaagtatt  
2461 atctgattcc ttgttcgaat ggcatttctt tctcagcacc accttccctg catattcact  
2521 taaccttgta caagaacacc tttttgcctt aaatgaagac acccccccaa aaaaagagt  
2581 ccagaaaaat atgtccctgc ttgtgcggga ataaatagaa tattctgagg tgcattcctc  
2641 ctctctatgt taggcaacat tcttgcacc tctcggccc ccaagccagg ttgcgtttt  
2701 ttctgccatt tagaagggtt ttctttttg tcttagtaaa acatcagccc ctgtagctct  
2761 tcatctcccc ctggtgttct tctcccgcca tgtcttaaga ttggtggcac cgaccaatct  
2821 taagatttaa gttctgtgtg aaaaacacct ttgcttttca atcagtttat cagctcctc  
2881 cgcaggggaa tgtggacaca caaaaagaat tatcggggct tctcatcagt gatagggaaa  
2941 agactggcat gtgcctaaac gagctctgat gttattttta agtcccttt cttgccaatc  
3001 cctcacggat ctttctccga tagatgcaaa gaacttcagc aaaaaagacc cgcaggaagg  
3061 ggcttgaaga gaaaagtacg ttgatctgcc aaaaatgtct gacccccagt agtgggcagt  
3121 gacgaggag agcattccct tgtttgactg agactagaat cggagagaca taaaaggaaa  
3181 atgaagcgag caacaattaa aaaaaattcc ccgcacacaa caatacaatc tatttaact  
3241 gtggctcata cttttcatac caatggatg acttttttct tggagtcccc tcttctgatt  
3301 cttgaactcc ggggtctggca gcttgcaaa ggggaagcgg ctcagcact gcacgggcag  
3361 gtttagcaaa ggtctctaag ggttatttct ttttcttag cctgcccc gaattgtcag  
3421 acggcgggcg tctgcttctg aagtttagcag tgatttctt tcgggcccgt cttatctccg  
3481 gctgcacgtt gcctgttggg gactaataac acaataacat tgtctggggc tggataaag  
3541 tcggagctgt ttacccccac tctaataagg gttcaatata aaaagccggc agagagctgt  
3601 ccaagtca ga cgcgctctg catctgcgcc aggcgaacgg gtccctgcgc tcttgcagtc  
3661 ccagctctcc accgcccgtt gcgctcgag acgctccgtt cgttgccttc tctctggca  
3721 ggcgctgcct tttctccccg ttaaaggcca cttgggctga aggatcgctt tgagatctga  
3781 ggaacccgca gcgctttagg ggacctgaag ctgttttct tctgtttctt ttgggttcag  
3841 tttgaacggg aggtttttga tccctttttt tcagaatgga ttatttgcct atgattttct  
3901 ctctgctgtt tgtggttgc caaggagctc cagaaacagg taggcacgtt cgttgacttg  
3961 taagtctcgg aattacaagt tagtgtgttc ttatccacct tcatgtttt ctgtctcta  
4021 tttttccccg ttctttttat gactgcagct tagagagcaa gtgtctgaga attattgctg  
4081 aaacgtactt taagtcttct agtgtaaaat gtaaaattcc tctactgaat acaattaggt  
4141 gcaattgact ataacatgac attaaaaata cttatcgttt tattattatt attccattat  
4201 gtgtttcctt ggcttttaaa aaatgagaag agtatggaca tatacaattt agtcaattgt  
4261 atgtttgtaa tatatgtgtt tatacaggtt cacaggccat ataggacatt aaactattat  
4321 taaacactat ttttaatagt tgttaacgtg taaaatattt aagcattcca gcttgaagcc  
4381 aaggaattgt atccagctgt tcaagcaatg tatgttcagt aaaatcacct gcagagcaaa  
4441 agtctgttga ctaactaccg cctccccccg cccccacca ccccccgag gcggtttctg  
4501 ggtgaagcag atgttttctt taaaatttgc catcattgac tttaggtttc ttttggcag  
4561 tttttggcac ccaaaacagt gtgagctctc ttttcagctt tattcacctg tctgggagg  
4621 ggagctagga taattcttgg ctgccgaagg atttaggcag tgcgtgtgca tctgcccggg  
4681 tccccccgt ttttagggct agtgcacttt ttttgcctt tctgaccct gactaaagag

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4741 aaaggatgtc aagggaaatga aaatcctgga atgtgtctga tcatttgaaa tgtacaaaat  
4801 tgggcagata agctgcatgg ctaaattgtt aggggaaga ggcaaggcag tagtggagaa  
4861 gggggaggca gtggatccca cacaagcctg atgccaggg attcggaaatt caaaaatcccc  
4921 ccagcctacc ttcagtcctc tgacctgctt ctcagcccca ccttaggtca ctggtttcta  
4981 tggagttacc ctactgaatt gaattattgaa tagttaattt ctctctccaa tcattttccc  
5041 cacctaattt tgaaagatat acatcatctg gggtagccctg tgcctacac agcatgtgaa  
5101 gtggatgggt accccctaaa gagaggggtca tctgaatgg ggaagtggcc ccaaagctag  
5161 gaataactgt gatttcttgt ctttagtcat gtgccaatgt taagtaagct tcagtgagata  
5221 gtgctgtcct accaagtctc ttgtagaagc cagccggatt ttcaacaggc agcattccac  
5281 agcatttccc tgagcctgct tcaagagggg tgggggaaqt ccttttcag gtgtttatct  
5341 cctctgcatt tgtgtaattt cctgaaggt ggataagcca agggcatgag ggggaggcaa  
5401 aaggtgaact catgttaagg agggaaaaaa ataaagagcc ctttttctg tgtttcttgc  
5461 tgatggcagg ctgtgtgctt catctgcttt tatctgctct gctagctctg actctactgt  
5521 gatccagcat gtctctcggc gtttgaggag acatccccc ctgacctgct ctttctctcc  
5581 ccagcagctt taggcgctga gctcagcgcg gtgggtgaga acggcgggga gaaacccact  
5641 cccagtcac cctggcggct ccgcccgtcc aagcgctgct cctgctcgtc cctgatggat  
5701 aaagagtgtg tctacttctg ccacctggac atcatttggg tcaacactcc cgagtgaatc  
5761 tctagagggc attgtaaccc tattcattca ttagcgctgg ctccactgga gccagtttt  
5821 agagtctctt ttctagggac tctgaaggta gtctttctaa caccatccaa gtgcctcagt  
5881 ggggacagtt tcctctatt cctgaaaaata acgacagctt cgttcttagc aaaccaaggg  
5941 agggctctct gagggcccgt agctcaggtt actcatgat ggacaagcag gaggccactg  
6001 cactgtttcaa atgaggaact ttcagtgaga gggcctcagg gggacactct cacagtggca  
6061 tctgatgggg ttctgggaat aattgccgag gtcagatgtg ggttagtgca acctgtgctt  
6121 ctcatgggag ggtggagact gagaggcaga agtgatgata tagaggggta gaatcactta  
6181 attttagtta cagaaaaacc taggctcaaa gtgttgaagc catttggtga ggaagtgaat  
6241 ttagcagag ctagaactgg agcccggtt tcttttctg ctatattttc ctttagataa  
6301 tgcccatttc agaactgaaa tagaaatact gtccataggc ttctctttca cctacagaga  
6361 agaaaagcag atttctctct tctgccctgg acactagttc atcatctgtc ggaagcagtc  
6421 ataaacaagc acacatttac tatgcataca atgtaccgtt atgacaaagg aggaccaaaa  
6481 tccaaacaat atcaaaccac accaaaaacc acaaggagcc taataattac taagtgata  
6541 ctcccaaagg gaggaactta ttcttagat gagaatgaaa atggacacat tggaaattat  
6601 tggagagccc tctggctatg agtccttcca caacctatg gtaccaccga ctggcaggag  
6661 aaatgtgtga acatgtgctt cctctcccca accactgggg ccggtggggg gacggtggca  
6721 cttttagcag tatcctcctg ggtttgagtt gaaaaataagt tttaaaaatc ctgtgagta  
6781 tggttttgca ttgaaacctc ttcccactgt gtaccacaaa atagttact aaatagacca  
6841 tttagaaaag aagaaaaat aaagcagatg ccaagcagag atgtcctaatt tttgacaaa  
6901 aaagcaatgt tgcttgtgtc aagaagaaac tgaactttgt gaagagttga aatggaattc  
6961 cactgaatta gaaaaacttg tttctcctg cctggataca tacagtcagg gccattgatg  
7021 cacaggtggt cctggctggt gttacacttt accctctgaa atgatgtccc caagtgtat  
7081 gtgatgagct ccttgtgtgc ccagtggaaat aggtgtgtcc atgtgtcatt ttaaagacta  
7141 ttaattacac taatatagtt tctttctctc ttggataat aggcacgttg ttccgtatgg  
7201 acttggagc cctaggtcca agagagcctt ggagaattta cttcccacaa aggcaacaga  
7261 ccgtgagaat agatgccaat gtgctagcca aaaagacaag aagtgtgga atttttgcca  
7321 agcaggaaaa gaactcaggt gagcagaaac acctttgctt tcaactcagt ttaacagcct  
7381 cctgaactcc ttcctatcat ggtactgcct tctgtttta gagagactaa cagagacatt  
7441 gaaagtccag gtaaaactga atataacatt gctgaaatgt ttttcttgt gtattttaac  
7501 agggctgaag acattatgga gaaagactgg aataatcata agaaaggaaa agactgttcc  
7561 aagcttggga aaaagtgtat ttatcagcag ttagttagag gaagaaaaat cagaagaagt  
7621 tcagaggaac acctaagaca aaccaggtaa gaggggaagg agaaaaatta ggtgaagagt  
7681 tcacaagaac aactagcccc agtcagtgat gccagcagcc tgttcctcca gcccttctta  
7741 cccgggcagg tgaagactt agaaaacagt agcagaggag atctatgcat cctatagatt  
7801 aaaaggagca aaagaatccc tcttaaatat ttccatgaag ctctggaatg caaacctatg  
7861 tctctgtac ctttagcaca taccatttca tctacaggtg gatttccaa ccaaatata  
7921 tccagagatg cctttgtcat tgggttatat acagcctttg cctctctgag tcaatgtatt  
7981 taccactttc cctgagaaat cgaaaatcat tttggggagc ggacatttag aaaaagaatc  
8041 aaagtgtcat ggataatcaa attcttcaat aagtgtcagt tattcagatg gccaaaggaa  
8101 aaataaagtc attagatagg gttggtagaa tttagaacat gctgtttttc aggtttatg  
8161 tctttttttt tttttttttt ttttttttaa tagggaaatg tgtttgggtc agagccaatg  
8221 tctttccaaa aagctctctc ttttctggt cagtcagtgt ctgggacaga gaaggatct  
8281 ggattaggca acatcataga gttgctctga gctgctctt ggtgataacc cttccaaatc  
8341 ctaaaacttt tggaattcac aagctcaaaag gaggaaacct actctctgat ctaccacatg  
8401 ttctgcattt ttctatcatg gtctatggaa acttctctta gaaatccagt ggcaagaagt  
8461 tctatgatta aagtgtctg agctcaggcc aggcagtcac gaactactt tgagttgttt  
8521 tctactgatt tgtggggcag cctcagctat cggtttcttc acacctgctt atgagagtat  
8581 ccatatttat ggtcgcaggc agtaatgtc cccacgagat cagtttctga actaacctgg  
8641 aattttttat ggttttttat tatgccaact attaaatcaa cattacagt cttccctctg  
8701 tatttctcct gtaaaacatt aggcctgcaa aaaaaaaaaa tcttttttaa aataattgcc  
8761 ataaagtatt tgctctgggc ctactgtatg cttcttttyt ttttctctt tttcaactaa  
8821 gtaccggtca atttattaag atggccataa ctattcaaaa cctatgctga gttcctcaag  
8881 gcagggtcgc atagtgtatg aggttgggat ggggctacgg aagaaaccag aacaactcta  
8941 gtttatttaa aacctgtatt tactgcccac ttccccttag acttgaccat atgacccctt  
9001 gtcccccatt ctaagcatag gggcaggctt tatttttaca atggtaatat atgatctac  
9061 ttgaggtttt atcaaagat tgccggcggt ggtgaaagt cacaaccaga ttcaggtttt  
9121 gtttgtgcca gatttcaatt ttacatgttt cttttgccaa agggtgattt ttttaaaata  
9181 acatttgttt tctcttatct tgctttatta ggtcggagac catgagaaac agcgtcaaat

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9241 catcttttca tgatcccaag ctgaaaggca agccctccag agagcgttat gtgaccacaca  
9301 accgagcaca ttggtgacag accttcgggg cctgtctgaa gccatagcct ccacggagag  
9361 cccgtgtggc gactctgcac tctccacctt ggctgggatc agagcaggag catctctgac  
9421 tgggttctga ctggcacaag accagcgctc tcgttcaaaa cattccaaga aaggttaagg  
9481 agttccccc accatcttca ctggcttcca tcagtggtaa ctgctttggt ctctcttttc  
9541 atctggggat gacaatggac ctctcagcag aaacacacag tcacattcga attcgggtgg  
9601 catctccgg agagagagag aggaaggaga ttccacacag ggggtggagt tctgacgaag  
9661 gtcctaagg agtggttgtg tctgactcag gcgcttggca catttcaggg agaaactcca  
9721 aagttccacac aaagattttc taaggaaatgc acaaattgaa aacacactca aaagacaaac  
9781 atgcaagtaa agaaaaaaa aagaaagact tttgtttaaa tttgtaaaat gcaaaactga  
9841 atgaaactgt tactaccata aatcaggata tgtttcatga atatgagtct acctcaccta  
9901 ttttgcactc tggcagaagt atttcccaca ttttaattatt gcctcccca acctctccca  
9961 cccctgtctgc ccttccctcc atccccata ctaaaacctc gcctcgtaga agtctggtct  
10021 aatgtgtcag cagtagatat aatattttca tggtaattcta ctagtcttga tccataagaa  
10081 aaaaaagatc attaaatcag gagattccct gtcttggatt tttggagaca caatggtata  
10141 ggggtgttta tgaaatatat tgaaaagtaa gtgtttgtta cgctttaaag cagtaaaatt  
10201 atttctctt atataaccgg ctaatgaaag aggttggatt gaattttgat gtacttattt  
10261 ttttatagat atttatattc aaacaattta ttcccttat taccatgtt aaatatctgt  
10321 ttgggcaggc catattggtc tatgtatttt taaaatatgt atttctaaat gaaattgaga  
10381 acatgctttg ttttgcctgt caaggtaatg acttttagaaa ataaatattt ttttccctac  
10441 tgtactgatt tggaaatcatt actgaaattt gtaaggagtg ggccaacgtg attaagtacc  
10501 ataaaggcaa ataaatggtt aaagacgggt tcatagaaaa gtgacaatta gaaggatatt  
10561 acggtctaa ctaattatat aaagaatttt atctgtatct taaatgttga ttttatactg  
10621 cattgaggta aaaacacaaa acaaaaaagc agctttaaaca cctctgtctt ctcttgggta  
10681 gcagcctcct gcttctcctt cacctgaaaa attctccagg gacttcatcc attaacttgg  
10741 ctcaggctat tggcaggatt cacagttaa gctgatgggt tggtagagag tgctttatcc  
10801 atattaatgg actgaaggaa gtaattggcaa gacaaccccc caaaacatac ctaattatcc  
10861 aaagtatat accaaagtgt cttttagaaa atggcctgct cagagcaagt agaggtttcc  
10921 aatggccttt tattttctca cattaaaggat gtgttttctt aaggaacatt gagtaccatt  
10981 gcttcttctg gatagcctag gactgccgtg tgcccatgga ggtagagaca ccaggtagt  
11041 attctaggtc ctctgccaca aagcaccact tctctccac tttgccttgg ctggccttgt  
11101 cagctcactg gagagcacag tattgcaatt gcagtattgc aaatggtcac tactaactga  
11161 attctctaag agcttgatta gccctcgaga atcttctctg ccttctctca atagtgtctg  
11221 aaggaattcc tggcatttaa caaatattag catgtagtga tcaactgtct cctaacagt  
11281 acacatcaga aggatttcaa ataacagtct tcaggcatgc gtaatcaatg tcttgtgcag  
11341 agtctccgtc ctcatgtatc ctcattttct tctttaaggc acagtccaat gtcttggggg  
11401 aattgtttat aaagcttact ttatccataa actgtttctc agtgctgtac tctgaagaaa  
11461 attttgaagt tttgcccatt ttgacaaggt gcttgggtct aacttgacca gtatttaate  
11521 ttgagcaaac gattcaattt ccttctatcg tgagttttct catctatgaa acaagggagt  
11581 tgaggggagt tcttttcata cctctgagaa agagtttgag attacataaa gaagtgaag  
11641 tggcatgaaa aaaaataaag atctgagctt agaagacatg gatctaatac atttaaggag  
11701 aagtcagaat cagagaagcc actgaacaaa acagtccaaa cggagcatag taagtcagat  
11761 tgatgagttt tgggtgggtt tttcatcagt caaaccttgc agccccctt tccatgctt  
11821 cctgcttcag tatccagtag gaaaaatgaa agggatgatg tagacactct agggcatgag  
11881 gatttgcagt aaataagtgt ggagactcac agaaaattaa tatttttcaa acatgaagac  
11941 gaaacattca attatattac agtccacatc agcttgaagg gtaaaactgat gggatgatct  
12001 gtacatttcc ttgctctgtt tccagtaaaa gcatgggttc tggaaaccca cttaggacag  
12061 ctttctctct ttacactgat agcccaggca agctttgatc tcagaactcc agaaccaga  
12121 gaactctagg tggaaatgtg taacttttgc cagggcagag ggaacaccta ctaataggta  
12181 cttcattttg accaccagag attggcatct tttttgatgg atccactggc ttgtatactg  
12241 cctgtactcc cccaaaacac agcttgggta ttggactaat ctgagctcc ctgaggagaa  
12301 ctcttgctga cattaagaaa gagcaacatt ttgtcttcc aggtgaaaat ccaaggccaa  
12361 aaagggagt actcacctaa gatcacagaa ggagctgtag catctctgga gcctgaacac  
12421 ttaagttaa cagactatt tcacgcagag ggcattgaatt c  
1 ggagctgtt accccactc taatagggt tcaatataaa aagccggcag agagctgtcc  
61 aagtcagacg cgcctctgca tctgcgccag gcgaacgggt cctgcgcctc ctgcagctcc  
121 agctctccac caccgccgag tgcgcctgca gacgtccgc tgcgtgcctt ctctctggc  
181 aggcgctgcc ttttctcccc gttaaagggt acttgggtc aaggatcgct ttgagatctg  
241 aggaaccgc agcgtttga gggacctgaa gctgttttct ttcgttttcc tttgggttca  
301 gtttgaacg gaggttttg atccctttt ttcagaatgg attatttgc catgatttct  
361 tctctgctgt ttgtggcttg ccaaggagct ccagaaacag cagtcttagg cgctgagctc  
421 agcgcggttg gtgagaacgg cggggagaaa cccactccca gtccacctg gcggtccgc  
481 cggtccaagc gctgctcctg ctctgctcctg atggataaag agtgtgtcta ctctgcccac  
541 ctggacatca tttgggtcaa cactcccag cactgtgttc cgtatggact tggaaacct  
601 aggtccaaga gagccttga gaatttactt cccacaaagg caacagaccg tgagaataga  
661 tgccaatgtg ctagccaaaa agacaagaag tgctggaatt tttgccaagc agggaaagaa  
721 ctgagggtg aagacattat ggagaaagac tggaaataatc ataagaaagg aaaagactgt  
781 tccaagcttg ggaaaaagt tatttatcag cagttagtga gaggaagaaa aatcagaaga  
841 agttcagagg aacacctaag acaaacacag tccggagacca tgagaaacag cgtcagaatc  
901 tcttttcatg atcccaagct gaaaggcaag cctccagag agcgttatgt gaccacaaac  
961 cgagcacatt ggtgacagac ttcggggcct gtctgaagcc atagcctcca cggagagccc  
1021 tgtggccgac tctgactct ccaccttggc tgggatcaga gcaggagcat cctctgctgg  
1081 tctctgactg gcaaaggacc agcgtcctcg ttcaaaacat tccaagaaag gttaaggagt  
1141 tcccccaacc atcttctcag gcttccatca gtggtaactg ctttggctct tctttctac  
1201 tggggatgac aatggacctc tcagcagaaa cacacagtca cattcgaatt c

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1 ctgcgccagg cgaacgggtc ctgcgcctcc tgcagtccca gctctccacc ggcgggtgag  
61 cctgcagacg ctcgcgtcgc tgccttctct cctggcagge gctgcctttt ctccccgtta  
121 aagggcactt gggctgaagg atcgctttga gatctgagga acccgagcgc ctttgagggg  
181 cctgaagctg tttttcttcg ttttctttg ggttcagttt gaacgggagg tttttgatcc  
241 ctttttttca gaattggatta tttgctcatg attttctctc tgctgtttgt ggcttgccaa  
301 ggagctccag aaacagcagt cttaggcgct gagctcagcg cgggtgggtga gaacggcggg  
361 gagaacccca ctcccagtc accctggcgg tccgcgcgtt ccaagcgctg ctctgtctcg  
421 tccctgatgg ataaagagtg tgtctacttc tgccacctgg acatcatttg ggtcaacact  
481 cccgagcacg ttgttccgta tggacttggg agccctaggt ccaagagagc cttggagaat  
541 ttactttccc caaaggcaac agaccgtgag aatagatgcc aatgtgctag ccaaaaagac  
601 aagaagtgtc ggaatttttg ccaagcagga aaagaactca gggctgaaga cattatggag  
661 aaagactgga ataatacata gaaaggaaaa gactgttcca agcttgggaa aaagtgtatt  
721 tatcagcagt tagtgagagg aagaaaaatc agaagaagt cagagggaaca cctaagacaa  
781 accaggtcgg agaccatgag aaacagcgtc aaatcatctt tcatgatcc caagtgaag  
841 ggcaagccct ccagagagcg ttatgtgacc cacaaccgag cacattgttg acagacttcg  
901 gggcctgtct gaagccatag cctccacgga gagccctgtg gccgactctg cactctccac  
961 cctggctggg atcagagcag gagcatcctc tgcgtgttcc tgactgtcaa aggaccagcg  
1021 tctctgttca aaacattcca agaaagggtta aggagttccc ccaaccatct tcactggctt  
1081 ccatacagtg taactgtctt ggtctcttct tcatctggg gatgacaatg gacctctcag  
1141 cagaacacac cagtcacatt cgaattc

## (2) INFORMATION FOR SEQ ID NO:45:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

1 aggggcagct ggatcagttc tcacaggagc cacagctcag agactgggaa acatgggttcc  
61 aaaactgttc acttcccaaa tttgtctgct tcttctgttg gggcttatgg gtgtggaggg  
121 ctcaactccat gccagacccc cacagtttac gagggctcag tggtttgcca tccagcacat  
181 cagtctgaac cccctcgtat gcaccattgc aatgggggca attaacaatt atcgatggcg  
241 ttgcaaaaac caaaatactt ttcttcgtac aacttttgct aatgtagtta atgtttgttg  
301 taaccaaagt atacgtgccc ctcataacag aactctcaac aattgtcatc ggagttagatt  
361 ccgggtgccc ttactccact gtgacctcat aaatccaggt gcacagaata tttcaaactg  
421 cagggtatgca gacagaccag gaaggaggtt ctatgtagt gcactgtgaca acagagattcc  
481 acgggattct ccacgggtatc ctgtggttcc agttcacctg gataccacca tctaagctcc  
541 tgtatcagca gtccctcatca tcaactcatc gccaaagctcc tcaatcatag ccaagatccc  
601 atccctccat gtactctggg tatcagcaac tgcctcatc agtctccata ccccttcage  
661 tttcctgagc tgaagtccct tgtgaacct gcaataaact gctttgcaaa ttcaaaaa

## (2) INFORMATION FOR SEQ ID NO:46:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

1 gaacaaccag ctggatcagt tctcacagga gccacagctc agagactggg aaacatggtt  
61 ccaaaactgt tcacttccca aattgtctgt cttcttctgt tgggcttat gggtgtggag  
121 ggctcactcc atgccagacc cccacagttt acgagggctc agtggtttgc catccagcac  
181 atcagtctga acccccctcg atgcaccatt gcaatgggg caattaacaa ttatcgatgg  
241 cgttgcaaaa accaaaatac ttttcttcgt acaacttttg ctaatgtagt taatgtttgt  
301 ggtaaccaaa gtatacgtg cctcataac agaactctca acaattgtca tcggagtaga  
361 ttcgggtgac ctttactcca ctgtgacctc ataaatccag gtgcacagaa tatttcaaac  
421 tgcaggtatg cagacagacc aggaaggagg ttctatgtag ttgcatgtga caacagagat  
481 ccacgggatt ctccacggtg tctgtgtggt ccagttcacc tggataccac catctaagct  
541 cctgtatcag cagtctctcat catcactcat ctgccaagct cctcaatcat agccaagatc  
601 ccatccctcc atgtactctg ggtatcagca actgtcctca tcagtctcca tacccttca  
661 gctttctctg gctgaagtcc cttgtgaacc ctgcaataaa ctgctttgca aattc

## (2) INFORMATION FOR SEQ ID NO:47:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

1 ctgcaccag cgtatagttt tcaccagag tccagatccc accggcaaaa ctctgtctaa  
61 cacaggatga cttggaatta gagtccgtat agcagaaaga gcagcagggc tgtccttggg  
121 tatccgttgc tcagccaagt catcaaataa aaaggatgat tgcacaagtg gaccatgtgt  
181 caatctgtgg gtttctgcat ggccagaccc accaagggaa gctttattta aacagttcca  
241 agtaggggag accagctgcc cctgaacccc agaacaacca gctggatcag ttctcacagg  
301 agccacagct cagagactgg gtaagtcaac aatccccaga gctgggacag gaggggcagc  
361 gacagggcag cacctgaggg agaggtgagc tgaagttagt gcttaggaga tgtggcacac



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421 tttgggggaca ggaagaaaag gaaatgagac cccagagtg ggcagagagg gcttgtgggt  
481 tgagacacta tagagtgtgt cataaccgag accgatagg ggagtagtta cttctcttct  
541 tttcttacag gaaacatggt tccaaaactg ttcacttccc aaatttgtct gcttcttctg  
601 ttggggctta tgggtgtgga gggctcactc catgccagac cccacagtt tacgagggt  
661 cagtgggttg ccatccagca catcagtcgt aacccccctc gatgcacat tgcaatgcgg  
721 gcaattaaca attatcgatg gcgttgcaaa aacaaaata ctttcttctg tacaactttt  
781 gctaagttag ttaatgtttg tggtaaccac agtatagct gccctcataa cagaactctc  
841 aacaattgtc atcggagtag attccgggtg cctttactcc actgtgacct cataaatcca  
901 ggtgcacaga atatttcaaa ctgcaggtat gcagacagac caggaaggag gttctatgta  
961 gttgcatgtg acaacagaga tccacgggat tctccacggg atcctgtggt tccagttcac  
1021 ctggatacca ccatctaagc tccgttatca gcagtcctca tcatcactca tctgccaagc  
1081 tcctcaatca tagccaagat cccatccctc catgtactct gggatcagc aactgtcctc  
1141 atcagtcctc atacccttc agctttctcg agctgaagtc ccttgtgaac cctgcaataa  
1201 actgctttgc aaattcatct ggaagtgtct gtgtgtcttc ctggccgct ctgctgtcat  
1261 ttagtgacaa tctgctctag agatttgggt ttatcatgaa tctctcccc tcaatatctg  
1321 accaaattcc ttgattcccc catcatcctt catgtgatac ctgattccag gctgcctta  
1381 aaaaaaaatc caattgagtc aacttagcat tggctcctt agccttaata tctcctctaa  
1441 gcaattttcc at

## (2) INFORMATION FOR SEQ ID NO:48:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2395 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

1 aggggcagct ggatcagttc tcacaggagc cacagctcag agactgggaa acatgggtcc  
61 aaaactgttc acttccaaa tttgtctgct tcttctgttg gggcttatgg gtgtggaggg  
121 ctcactccat gccagacccc cacagtttac gagggtcag tgggttgcca tccagcacat  
181 cagctcgaac cccctcagat gcaccattgc aatgcgggca attaacaatt atcgatggcg  
241 ttgcaaaaac caaataactt tcttctgtac aacttttgct aatgtagtta atgtttgtg  
301 taaccaaagt atacgtgccc ctcataacag aactctcaac aattgtcatc ggagtagatt  
361 cgggtgccc ttactccact gtgacctcat aaatccaggt gcacagaata tttcaactg  
421 caggatgca gacagaccag gaaggagggt ctatgtagtt gcagtgtgca acagagatcc  
481 accggattct ccacggtatc ctgtggttcc agttcacctg gataaccaca ctaagctccc  
541 tgtatcagca gtctcatca tcaactcatc gccaaagctcc tcaatcatag ccaagatccc  
601 atccctccat gtactctggg tatcagcaac tgcctcatc agtctccata ccccttcagc  
661 tttcctgagc tgaagtccct tgtgaacctt gcaataaact gctttgcaaa ttcaaaaa  
1 gaacaaccag ctggatcagt tctcacagga gccacagctc agagactggg aaacatgggt  
61 ccaaaaactgt tcaacttcca aatttctctg ctttcttctg tggggcttat ggggtgtggg  
121 ggctcactcc atgccagacc cccacagttt acgagggtc agtggtttgc catccagcac  
181 atcagtctga acccccctcg atgcaccatt gcaatgcggg caattaacaa ttatcgatgg  
241 cggttgcaaaa accaaaatac ttttcttctg acaacttttg ctaatgtagt taatgtttgt  
301 ggtaacaaa gtatacgtg cctcataac agaactctca acaattgtca tggagtaga  
361 ttccgggtgc ctttactcca ctgtgacctc ataaatccag gtgcacagaa tatttcaaac  
421 tgcaggtatg cagacagacc aggaaggagg ttctatgtag ttgcatgtga caacagagat  
481 ccacgggatt ctccacggtg tctgtgtggt ccagttcacc tggataccac catctaagct  
541 cctgtatcag cagtcctcat catcactcat ctgccaagct cctcaatcat agccaagatc  
601 ccatccctcc atgtactctg ggtatcagca actgtctcca tcaagttcca tacccttca  
661 gctttctctg gctgaagtcc cttgtgaacc ctgcaataaa ctgctttgca aattc  
1 ctgccagcag cgtatagttt tcaccagag tccagatccc accggcaaaa ctctgtctaa  
61 cacagatga cttggaatta gagtccgtat agcagaaaga gcagcagggc tgtccttggg  
121 tatccgttgc tcagccaagt catcaataa aaaggatgat tgcacaagt gaccatgtgt  
181 caatctgtgg gtttctgcat ggccagaccc accaagggaa gctttattta aacagttcca  
241 agtaggggag accagctgcc cctgaacccc agaacaacca gctggatcag ttctcacagg  
301 agccacagct cagagactgg gtaagtcaac aatccccaga gctgggacag gaggggcagc  
361 gacagggcag cacctgaggg agaggtgagc tgaagttagt gcttaggaga tgtggcacac  
421 ttgggggaca ggaagaaaag gaaatgagac cccagagtg ggcagagagg gcttgtgggt  
481 tgagacacta tagagtgtgt cataaccgag accgatagg ggagtagtta cttctcttct  
541 tttcttacag gaaacatggt tccaaaactg ttcacttccc aaatttgtct gcttcttctg  
601 ttggggctta tgggtgtgga gggctcactc catgccagac cccacagtt tacgagggt  
661 cagtgggttg ccatccagca catcagtcgt aacccccctc gatgcacat tgcaatgcgg  
721 gcaattaaca attatcgatg gcgttgcaaa aacaaaata ctttcttctg tacaactttt  
781 gctaagttag ttaatgtttg tggtaaccac agtatagct gccctcataa cagaactctc  
841 aacaattgtc atcggagtag attccgggtg cctttactcc actgtgacct cataaatcca  
901 ggtgcacaga atatttcaaa ctgcaggtat gcagacagac caggaaggag gttctatgta  
961 gttgcatgtg acaacagaga tccacgggat tctccacggg atcctgtggt tccagttcac  
1021 ctggatacca ccatctaagc tccgttatca gcagtcctca tcatcactca tctgccaagc  
1081 tcctcaatca tagccaagat cccatccctc catgtactct gggatcagc aactgtcctc  
1141 atcagtcctc atacccttc agctttctcg agctgaagtc ccttgtgaac cctgcaataa  
1201 actgctttgc aaattcatct ggaagtgtct gtgtgtcttc ctggccgct ctgctgtcat  
1261 ttagtgacaa tctgctctag agatttgggt ttatcatgaa tctctcccc tcaatatctg  
1321 accaaattcc ttgattcccc catcatcctt catgtgatac ctgattccag gctgcctta  
1381 aaaaaaaatc caattgagtc aacttagcat tggctcctt agccttaata tctcctctaa  
1441 gcaattttcc at



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## (2) INFORMATION FOR SEQ ID NO:49:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 694 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```
1 cacaggagct acagcgcgga gactggaaac atggttccaa aactgttcac ttcccaaatt
61 tgtctgcttc ttctgttggg gcttctggct gtggagggct cactccatgt caaacctcca
121 cagtttacct gggctcaatg gtttgaaacc cagcacatca atatgacctc ccagcaatgc
181 accaatgcaa tgcaggctcat taacaattat caacggcgat gcaaaaacca aaatactttc
241 ctctttacaa cttttgctaa cgtagttaat gtttgtgta acccaaatat gacctgtcct
301 agtaacaaaa ctgcacaaaa ttgtcaccac agtggagcc aggtgccttt aatccactgt
361 aacctcacia ctccaagtcc acagaatatt tcaaactgca ggtatgcgca gacaccagca
421 aacatgttct atatatgttc atgtgacaac agagatcaac gacgagaccc tccacagtat
481 ccggtggttc cagttcacct ggatagaatc atctaagctc ctgtatcagc actcctcatc
541 atcactcatc tgccaaagctc ctcaatcata gccaaagatcc catctctcca tatactttgg
601 gtatcagcat ctgtctcat cagtctccat accccttcag ctttcctgag ctgaagtgc
661 ttgtgaaccc tgcaataaac tgctttgcaa attc
```

## (2) INFORMATION FOR SEQ ID NO:50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```
1 ctgcaggcag catatagttt tcatccagag ttggatcta accagcaaaa ctctgtctta
61 cacaggatga cttggaatta gactccttat agcagaaaaga gcagcagggc tgtccttggg
121 tatccgttgc tcagccaagt catcaataaa aaaggatgat tgcacaagtg gactatgtac
181 caatctgtgg gtttctgcat ggccaagagc cagaccctcc ctctgggctc tgctggccca
241 acccaccaag ggatgcttta tttaaacagt tccaagtagg ggagaccagc tgcccctgaa
301 cccagaaca accagctgga tcagttctca caggagctac agcgcgga ctgggtaagt
361 caacgatccc cagagctggg acagaagggg cagcaatggg gcagcaactg agggagaaga
421 gagctgacgt tagtgcttag gagacgttgc acactttgca gacaggaagt aaaggaaatg
481 ggaccccaga gtggccgcag aggggcctgt ggggtaagac actacagtgt gtgtcataac
541 caagaccgca tcagggagta gttacttctc ttcttttctt acaggaaca tggttccaaa
601 actgttcaact tcccaaattt gtctgttctc tctgttgggg cttctggctg tggagggtc
661 actccatgtc aaacctccac agtttacctg ggctcaatgg tttgaaaccc agcacatcaa
721 tatgacctcc cagcaatgca ccaatgcaat gcaggtcatt aacaattatc aacggcgatg
781 caaaaaccaa aatactttcc ttcttacaac ttttgtaac gtagttaatg tttgtggtaa
841 cccaaatatg acctgtccta gtaacaaaac tcgcaaaaat tgcaccaca gtggaagcca
901 ggtgccttta atccactgta acctcacaac tccaagtcca cagaatattt caaactgcag
961 gtatgcgag acaccagcaa acatgttcta tatagttgca tgtgacaaca gagatcaacg
1021 acgagaccct ccacagtac cgttggttcc agttcacctg gatagaatca tctaagctcc
1081 tgtatcagca ctctcatca tcaactcatc gccaaagctcc tcaatcatag ccaagatccc
1141 atctctccat atactttggg tatcagcatc tgtcctcatc agtctccata cccttcagc
1201 tttcctgagc tgaagtgcct tgtgaaccct gcaataaact gctttgcaa ttcacttgaa
1261 agtgtctgtg tgtcttcatt agccgctctg ctgtcattta gtgacaact actctagaga
1321 tttttcttcc tctaaccctga gacttcggg aaacagagag atttgagat aagagcgt
1381 ttctgtcatg aaacagcaca gtcttatccc tctcctgct ttaggctgag aagctgaggt
1441 ctcaaccgat atctagcaac tgtogaagac tcttgcttg atcaagctt
```

## (2) INFORMATION FOR SEQ ID NO:51:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 735 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```
1 gctgcccctg aacccagaa caaccagctg gatcagttct cacaggagct acaggccgga
61 gactgggaaa catggttcca aaactgttca cttcccaaat ttgtctgctt cttctgttgg
121 ggcttctggc tgtggagggc tcaactcatg tcaaacctcc acagtttacc tgggtcatt
181 ggtttgaaac ccagcacatc aatatgacct ccagcaatg caccaatgca atgcaggtca
241 ttaacaatta tcaacggcga tgcaaaaacc aaaatacttt cttcttaca acttttgcta
301 acgtagttaa tgtttgtgtt aacccaaata tgacctgtcc tagtaacaaa actcgcaaaa
361 attgtcacca cagtgaagc caggtgcctt taatccactg taacctcaca actccaagtc
421 cacagaatat ttcaaactgc aggtatgcgc agacaccagc aaacatggtt tatatagttg
481 catgtgacaa cagagatcaa cgacgagacc ctccacagta tccggtgttt ccagttcacc
541 tggatagaat catctaagct cctgtatcag cactcctcat catcactcat ctgccaagct
601 cctcaatcat agccaagatc ccatctctcc atatactttg ggtatcagca tctgtcctca
661 tcagtctcca tacccttca gctttcctga gctgaagtgc cttgtgaacc ctgcaataaa
721 ctgctttgca aattc
```

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## (2) INFORMATION FOR SEQ ID NO:52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```
1 cacaggagct acagcgcgga gactggaaac atggttccaa aactgttcac ttcccaaatt
61 tgtctgcttc ttctgttggg gctctgggct gtggagggtc cactccatgt caaacctcca
121 cagttttacct gggctcaatg gtttgaaacc cagcacatca atatgacctc ccagcaatgc
181 accaatgcaa tgcaggctcat taacaattat caacggcgat gcaaaaacca aaatactttc
241 cttctttacaa cttttgctaa cgtagttaat gtttgtggtt acccaaatat gacctgtcct
301 agtaacaaaaa ctgcacaaaa ttgtcaccac agtgggaagcc aggtgccttt aatccactgt
361 aacctcacaa ctccaagtcac acagaatatt tcaaactgca ggtatgcgca gacaccagca
421 aacatgtttct atatagtgtc atgtgacaac agagatcaac gacgagaccc tccacagtat
481 ccggtgtgttc cagttcacct ggatagaatc atctaagctc ctgtatcagc actcctcatc
541 atcactcatc tgccaagctc ctcaatcata gccaagatcc catctctcca tatactttgg
601 gtatcagcat ctgtcctcat cagtctccat accccttcag ctttcttgag ctgaagtgcc
661 ttgtgaaccc tgcaataaac tgctttgcaa attc
1 ctgcaggcag catatagttt tcattccagag ttgtgatcta accagcaaaa ctctgtctta
61 cacaggatga cttggaatta gagtccctat agcagaaaga gcagcagggc tgccttggg
121 tatccgttgc tcagccaagt catcaataaa aaaggatgat tgcacaagtg gactatgtac
181 caatctgttg gtttctgcat ggccaagagc cagaccctcc ctctgggctc tgcgtggcca
241 acccaccag ggatgcttta ttaaacagt tccaagtagg ggagaccagc tgcccctgaa
301 cccagacaa accagctgga tcagtcttca caggagctac agcgcgaga ctgggtaagt
361 caacgatccc cagagctggg acagaagggg cagcaatggg gcagcaactg agggagaaga
421 gagctgacgt tagtgcttag gagacgttgc acactttgca gacaggaagt aaaggaaatg
481 ggacccaga gtggccgcag aggggctgt ggggtaagac actacagtgt gtgtcataac
541 caagaccgga tcagggaagta gttacttctc ttcttttctt acaggaacaa tggttccaaa
601 actgttctact tcccaattt gtctgttct tctgttggg cttctggctg tggagggtc
661 actccatgtc aaacctccac agtttacctg ggctcaatgg tttgaaaccc agcacatcaa
721 tatgacctcc cagcaatgca ccaatgcaat gcaggctcatt aacaattatc aacggcgatg
781 caaaaaccaa aatactttcc ttcttacaac ttttgctaac gtagttaatg tttgtggtaa
841 cccaaatag acctgtccta gtaacaaaac tcgcaaaaat tgtcaccaca gtggaagcca
901 ggtgcttcta atccactgta acctcacaac tccaagtcca cagaatattt caaactgcag
961 gtatgcgcag acaccagcaa acatgttcta tatagttgca tgtgacaaca gagatcaacg
1021 acgagacctt ccacagtatc cgtgtgttcc agttcacctg gatagaatca tctaagctcc
1081 tgtatcagca ctctcatca tcaactcatc gccaagctcc tcaatcatag ccaagatccc
1141 atctctccat atactttggg tatcagcatc tgcctcatc agtctccata ccccttcagc
1201 tttcttgagc tgaagtgcct tgtgaaccct gcaataaact gctttgcaaa ttcacttgaa
1261 agtgtctgtg tgtcttcatt agccgctctg ctgtcattta gtgacaatct actctagaga
1321 tttttcttcc tctaacctga gacttccggg aaacagagag atttgaagat aagagacgct
1381 ttctgtcatg aaacagcaca gctttatccc tctccctgct ttaggctgag aagctgaggt
1441 ctcaaccgat atctagcaac tctcgaagac tcttgcttgg atcaagctt
1 gctgcccctg aaccccagaa caaccagctg gatcagttct cacaggagct acaggccgga
61 gactgggaaa catggttcca aaactgttca cttcccaaat ttgtctgctt cttctgttgg
121 ggcttctgyc tgtggagggc tcaactccatg tcaaacctcc acagtttacc tgggtcfaat
181 gggttgaaac ccagcacatc aatatgacct cccagcaatg caccaatgca atgcaggatc
241 ttaacaatta tcaacggcga tgcaaaaacc aaaatacttt cttcttaca acttttgcta
301 acgtagttaa tgtttgtggt aacccaaata tgacctgtcc tagtaacaaa actccgaaaa
361 attgtcacca cagtgggaagc cagggtgcct taatccactg taacctcaca actccaagtc
421 cacagaatat ttcaaactgc aggtatgcgc agacaccagc aaacatgttc tatatagttg
481 catgtgacaa cagagatcaa cgacgagacc ctccacagta tccggtggtt ccagttcacc
541 tggatagaat catctaagct cctgtatcag cactcctcat catcactcat ctgccaagct
601 cctcaatcat agccaagatc ccatctctcc atatactttg ggtatcagca tctgtcctca
661 tcagtctcca tacccttca gctttcctga gctgaagtgc cttgtgaacc ctgcaataaa
721 ctgctttgca aattc
```

## (2) INFORMATION FOR SEQ ID NO:53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```
1 ccatggagga aggtcaatat tcaggtagga ggactctctg gttctaactg tggcagaagc
61 aatgacctt agctactcct ttcacccaga agagaagcgg ggcttcccag tccctctctg
121 ggaagagggt tgaatttcta agaaaggac tgggtgtgag aaggagggtg ggccgactg
181 actttcttgg cacagagcca ggaaggagtg gaaaattgag ggccctcct tttctgatt
241 caacaccttc ctgacaaaaa aagaaaaaga aaaaaaaaaa cggcttcagc tagggagcgg
```

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301 ggacgcaata gagtcagagg ccaaatagaa caggaacttg gaacaagcag aatttagcat  
361 aatgaatcct ccaagccagg gtgagtgcag a

## (2) INFORMATION FOR SEQ ID NO:54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3108 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

1 aagcttggga ataagtcag ctgggccatg ttgtgaggac atggggatga agtcttagtt  
61 ccaggatggg gctgggatgg agtttgggtg ttcttttctg tttttcttct tttttcttct  
121 tctttttttt ttttgtgaga cagaagtttag cttttgttgc ccaggctgga atgcaatggc  
181 ggatctcggc tcaccgcaac ctctgcctcc cggattcaag cgattctcct gcctcagcct  
241 cccgagtagc taggattaca ggtgccacc accatgccca gctaattttt tttttttttt  
301 tttttttttg tattttcagt agatacaggg ttccaccatg ttggccttga actctgacc  
361 tcagatgatc cacctgcctc ggccctccaa agtgctggga ttacaggcgc tgacgatgtg  
421 cccggtctct ctctctctct ttctctctct ctttctttca tctcactgtg ttgcccagg  
481 ctgatcttga actcctgggc tcaagtgatc cactcacctc tgcctcccca gtatctggga  
541 tcacaggcat gcaccaccat gccctgctag tttttatagt tttgtagag acaacggcct  
601 gctatgttgt ccaggctggg cttgaactcc caggcttaag tgatcctccc acctcagcct  
661 cccaaagtgc tgggattaca ggctggaacg tccgtgccag ccaaaactgtc catatttgac  
721 ctgaatatta tctcacgtat ctttctttcc ccccgcttcc ctctctccct cctactcctc  
781 ctctctccctc tcttctcttc tctctttttt ttcccttccc tctgctctc tctctctctc  
841 ccttttttct tgctgggact caaacctggg acatttgacc tgggagccta tttgtcaat  
901 catcaagaga cataatctca tgggtgggtg tctgtggtg agtgccgggt ggcaggatcc  
961 caactccagg ccgtcctctc aaccacaagag gccctgcctc tgcctagagc cttccgtggc  
1021 tccccagggc cctctgtgat cggccatagt ggtatgattc agtgtgcagt aacagtgggt  
1081 cacatcttga cgctaccact cacctccttc agccctgtgg gaacttgctg cttaacatct  
1141 ctagtcttca cccaattctc ttacctgaga aatggagata ataataacac ggacttcacc  
1201 cgggtgtggg gagcaccagg agaggccatg cgtgtaagt tatccgggtg gcaagccat  
1261 atttagtctc atgaaaaatag aagctgtcag tggctctact ttcagaagaa agtgtctctc  
1321 ttctgtctta aacctctgtc tctgacggtc cctgccaatc gctctggtcg acccaacac  
1381 actaggagga cagacacagg ctccaaactc cactaagtga gtacttatct ggtgtgttgg  
1441 ggtttggccc atgggcagtg gagatcaaaag cgcccttggg agaaaacgacc ttgggctgag  
1501 cctcaaggga tgaccagcag gaggtcaciaa ccagagaagg gaggtgggtg gtggtgaggg  
1561 ggcgggggtg gggggcgcag tgtggacaga atctcgaggc attcgagtc ctgatttggg  
1621 gaagtgaag caggccatct ggtctgagat gagcttgggt agtgccgttg gccgatcata  
1681 gagggccctg gggagccatg gaagactcta ggcagaggca ggacctcttg ggttagaagg  
1741 acggcctgga gttgggatcc tgccaccagg cacttaccag tagacacccc accatgagat  
1801 tatgtctcca gatgattgag caaatgggct cccagctcaa gggctccggg tttgattcca  
1861 gtcccaccac tgcgtgatgg ggacaaatga cttacctctc tggaaacctc gttccactga  
1921 gagaggcccc acagaatgag gacagtcccc cagcatcctg ccagtagggt tactgagcac  
1981 ctactgtgtg ctgggtgctt gaatactccc aatttacaga tgagcaaact gagctgctca  
2041 tccagggaga agccaggact cggactcagg tctgtccagc tgcctcccct gacagtcca  
2101 gtcccaggat ggtctctggg ttctctctac aatgtcaaaa gggccagctt gagctgccgc  
2161 taatcagagc ctggccgcgc cacacccccc ctccctgagg ctccgagaga agggacttac  
2221 ctatagtcaa gcagcgaaag aaggtagccc gtgacctcca ggcctgaagg accccaagtc  
2281 ccatgtctct cagcacatag tagatgcttt aaagtacagag gacttggctg ggcgcaggca  
2341 cgcctgtaat cctagcactt tgggaggctg agggaggcag atcacctgtg gtcaggagtt  
2401 cgagaccagg ctgatcaata tggtgaaacc ctgtctctac taaaatacaa aaattagcca  
2461 ggtgtgtgtg tgggtgcctg tagtcccagc tacttgggag gctaagacag gagaatcgct  
2521 tgaacccggg aggtggaggt tgcaagtgag caagatggtg ccattgcact ctagcctggg  
2581 tgacagagcg agactccatc tcaaaaaata aaaaaatagg ccatgcacag gctcacgcct  
2641 gtaatccag cactttggga ggcgaggcgc ggcggatcat gaggtcagga gtttgagact  
2701 agcctggcca acatagtga aaccctgtct tactaaaaat acaaaaaatta tctggtcatg  
2761 gtggcacgtg actatagtc cagctactcg ggaggctgag gcgggagaat cgcttgaacc  
2821 caggaggtgg aggtggcagt gagccgagat cgtgccctcg cactccagcc tgggcaacag  
2881 agcgagactc catttcaata aataaataaa taaataaagt cagagcactt tacagatgcc  
2941 ctggggacat tggcagagga gaaggctgag gcctgggtta tgggctctta gcatttctca  
3001 gtgggacgtg gcacagagta gatgtttcat aaatgtttag aatctgaaga cccactgtgc  
3061 gcagcccgcc accaaaaacc tcaggtatgc tgtgatctca ttggtatcc

## (2) INFORMATION FOR SEQ ID NO:55:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1503 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

1 ctctctgctta aacctctgtc tctgacggtc cctgccaatc gctctggctg accccaacac  
61 actaggagga cagacacagg ctccaaactc cactaagtga ccagagctgt gattgtgccc  
121 gctgagtggg ctgcgttctc agggagttag tgctccatca tccggagaat ccaagcagga  
181 ccgcatgga ggaaggtcaa tattcagaga tcgaggagct tccagaggc cgggtgtgca  
241 ggcgtgggac tcagatcgtg ctgctggggc tggtagaccg cgctctgttg gctgggctgc

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```

301 tgactctgct tctcctgttg cactgggaca ccacacagag tctaaaacag ctggaagaga
361 gggctgcccg gaacgtctct caagtttcca agaacttgga aagccaccac ggtgaccaga
421 tggcgagaaa atcccagttc acgcagattt cacaggaact ggaggaaact cgagctgaac
481 agcagagatt gaaatctcag gacttgagac tgccttgaa cctgaacggg cttcaagcag
541 atctgagcag cttcaagtcc caggaattga acgagaggaa cgaagcttca gatttgctgg
601 aaagactccg ggaggagggt acaaagctaa ggatggagt gcagggtgcc agcggtttg
661 tgtgcaaac gtgccctgaa aagtggatca attccaacg gaagtgtac tactcgga
721 agggcaccaa gcagtgggtc cagcccggt atgcctgtga cgacatggaa gggcagctgg
781 tcagcatcca cagcccggag gagcaggact tctgaccaa gcatgccagc cacaccggct
841 cctggattgg ccttcggaac ttggacctga agggagagt tatctgggtg gatgggagcc
901 atgtggacta cagcaactgg gctccagggg agcccaccag ccggagccag ggcgaggact
961 gcgtgatgat gcggggctcc ggctgctgga acgacgcct ctgcgacgt aagctggcg
1021 cctgggtgtg cgaccggctg gccacatgca cgccgccagc cagcgaaggt tccgaggagt
1081 ccatgggacc tgattcaaga ccagaccctg acggccgcct gccaccccc tctgccctc
1141 tccactcttg agcatggata cagccaggcc cagagcaaga ccctgaagac ccccaaccac
1201 ggcctaaaag cctctttgtg gctgaaagg cctgtgaca tttctgcca ccgaacgga
1261 ggcagctgac acatctcccg ctctctatg gcccctgcct tcccaggagt acaccccaac
1321 agcaccctct ccagatggga gtgccccaa cagcaccctc tccagatgag agtacacccc
1381 aacagcacc tctccagatg cagcccatc tctcagcac ccaggacct gattatcccc
1441 agctcagggt gtgagtctc ctgtccagcc tgcataata aaatggggca gtgatggcct
1501 ccc

```

## (2) INFORMATION FOR SEQ ID NO:56:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

```

1 agtggctcta cttcagaag aaagtgtctc tcttctgt taaacctctg tctctgacgg
61 tccctgccaa tcgctctggt cgaccccaac acactaggag gacagacaca ggctccaaac
121 tccactaacc agagctgtga ttgtgcccgc tgagtggact gcgtgtgacg ggagtgaagt
181 ctccatcatc gggagaatcc aagcaggacc gccatggagg aaggtcaata ttcagagatc
241 gaggagcttc ccaggaggcg gtgttgacgg cgtgggactc agatcgtgct gctggggctg
301 tctgaccgct ctctgtggcg tggctgctg actctgcttc tctgtggca ctgggacgt
361 acacagagtc taaaacagct ggaagagagg gctgcccggg acgtctctca agtttccaag
421 aacttgaaa gccaccacgg tgaccagatg gcgcagaaat ccagctccac gcagatttca
481 caggaactgg aggaacttcg agctgaacag cagagattga aatctcagga cttggagctg
541 tccctggaac tgaacgggct tcaagcagat ctgagcagct tcaagtccca ggaattgaac
601 gagaggaaac aagcttcaga tttgctggaa agactccggg aggaggtgac aaagctaagg
661 atggagtgtc aggtgtccag cggctttgtg tgcaaacagt gccctgaaaa gtggatcaat
721 ttccaacgga agtgctacta cttcggcaag ggcaccaagc agtgggtcca cgcccggtat
781 gcctgtgacg acatggaagg gcagctggct agcatccaca gcccgaggga gcaggacttc
841 ctgaccaagc atgccagcca caccggctcc tggattggcc ttcggaactt ggacctgaag
901 ggagagttaa tctgggtgga tgggagccat gtggactaca gcaactgggc tccaggggag
961 cccaccagcc ggagccaggg cgaggactgc gtgatgatgc ggggctccgg tgcctggaac
1021 gacgccttct gcgaccgtaa gctggcgccc tgggtgtgcg accggtgggc cacatgcacg
1081 ccgcccagcca gcgaaggttc cgcgagctcc atgggacctg attcaagac agaccctgac
1141 ggcgcgctgc ccaccccctc tgcccctctc cactcttgag catggataca gccaggccca
1201 gagcaagacc ctgaagaccc caaacacagg cctaaaagcc tctttgtggc tgaagggtcc
1261 ctgtgacatt ttctgccacc caaacggagg cagctgacac atctcccgt cctctatggc
1321 cctgccttcc ccaggagtac accccaacag caccctctcc agatgggagt gcccccaaca
1381 gcaccctctc cagatgagag tacaccccaa cagcaccctc tccagatgca gccccatctc
1441 ctacgacccc caggacctga gtatccccag ctcaggtggt gagtccctct gtccagcctg
1501 catcaataaa atggggcaggt gatggcctcc

```

## (2) INFORMATION FOR SEQ ID NO:57:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```

1 ccatggaggga aggtcaatat tcaggtagga ggactctctg gttctaactg tggcagaagc
61 aatgaccctt agctactcct ttcacccaga agagaagcgg ggcttcccag tccctctctg
121 ggaagaggag tgaatttcta agaaaggagc tgggtgtgagt aaggagggtg ggcgcgactg
181 actttctctg cacagagcca ggaaggagt gaaaattgag ggcccctcct ttttctgatt
241 caacaccctc ctgacaaaaa aagaaaaaga aaaaaaaaaa cggttcagc tagggagcgg
301 ggacgcaata gagtacagag ccaaatagaa caggaacttg gaacaagcag aatttagcat
361 aatgaatcct ccaagccagg gtgagtgcag a
1 aagcttgagg ataagtcagg ctgggccatg ttgtgaggac atggggatga agtcttagtt
61 ccaggatggg gctgggatgg agtttgggtt ttcttttctg tttttcttct ttttttctt
121 tcttttttct ttttctgaga cagagtcttg cttttgttgc ccaggctgga atgcaatggc
181 ggatctcggc tcaccgcaac ctctgcctcc cggattcaag cgattctcct gcctcagcct
241 cccgagtagc taggattaca ggtgcccacc accatgcccc gctaattttt tttttttt

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301 tttttttttg ttttttcagt agatacaggg tttccaccatg ttggcccttga actcctgacc  
361 tcagatgata cacctgcctc ggccctcccaa agtgcctggga ttacaggcgc tgacgatgtg  
421 cccggctctc ctctctctct tttctctctc tttctcttca tctactgtg ttgccccagg  
481 ctgatcttga actcctgggc tcaagtgtac cactcacctc tgcctcccca gtactgtgga  
541 tcacaggcat gcaccacat gccctgctag tttttatagt tttgttagag acaacggctt  
601 gctatgttgt ccaggctggt cttgaactcc caggcttaag tgatcctccc acctcagcct  
661 cccaaagtgc tgggattaca ggctggaacg tccgtgccag ccaaaactgt catatttgac  
721 ctgaaatatta tctcacgtat cttctcttcc ccccgcttcc ctctctccct cctactcctc  
781 ctctctccctc tctctccttc tgtctttttt tttcccttcc tctgcctctc tctcctcttc  
841 cctttttttct tgcctgggact caaacctggg acatttgacc tgggagccta tttgtctaat  
901 catcaagaga cataatctca tgggtggggtg tctgctggta agtgcgggtg ggcaggatcc  
961 caactccagg ccgtccttct aaccacaagag gccctgcctc tgcctagagc cttccgtggc  
1021 tccccagggc cctctgtgat cggccatagt ggtatgattc agtgtgcagt aacagtgggt  
1081 cacatcttga cgctaccact cacctccttc agccctgtgg gaacttgctg cttaacatct  
1141 ctagtcttca cccaattctc ttacctgaga aatggagata ataataacac ggacttcacc  
1201 cgggtgtggg gagcaccagg agaggccatg cgtgtaagt tcccggtg gcaagccatg  
1261 atttaggtct atgaaaatag aagctgtcag tggctctact ttcagaaaga agtgtctctc  
1321 tctctgctta aacctctgtc tctgacggtc cctgccaatc gctctggtcg accccaacac  
1381 actaggagga cagacacagg ctccaaactc cactaagtga gtacgtatct ggtgtgttgg  
1441 ggggtggccc atgggcagtg gagatcaaaag cgcccttggg agaaacgacc ttgggtgtgag  
1501 cctcaaggga tgaccagcag gaggtcacaa ccagagaagg gaggtgtgg ggtgtgagg  
1561 ggcgggggtg ggggcgcgag tgtggacaga atctcgaggc attcgagtcc ctgatttggg  
1621 gaagtgaag caggccatct ggtctgagat gagcttgggt agtgcgtgg gccgatcata  
1681 gagggccctg gggagccatg gaagactcta ggcagaggca ggacctctg ggttagaagg  
1741 acggcctgga gttgggatcc tggcaccag cacttaccag tagacacccc accatgagat  
1801 tatgtctcca gatgattgag caaatgggct cccagctcaa gggctccggg tttgagcca  
1861 gtcccaccac tgcgtgatgg ggacaaatga cttaccctct tggaaacctc gttccactga  
1921 gagaggcccc acagaatgag gacagtcccc cagcatcctg ccagtaggtt tactgagcac  
1981 ctactgtgtg ctgggtgctt gaatactccc aatttacaga tgagcaaact gagctgtcca  
2041 tccagggaga agccaggact cggactcagg tctgtccagc tgcctccctg gacagtcca  
2101 gctccaggat ggtctctggg ttctctctac aatgtcaaaa gggccagctt gagctgccgc  
2161 taatcagagc ctggccgcgc cacacccac ctccctgagg ctccgagaga agggacttac  
2221 ctatagtcaa gcagcgaag aagtagccc gtgacctcca ggcctgaagg accccaagtc  
2281 ccagtctcct cagcacatag tagatgctt aaagtacag gacttggctg ggcgaggga  
2341 ccctgtaat cctagcact tgggaggctg aggaggcag atcacctgtg ttcaggagt  
2401 cgagaccagc ctgatcaata tgggtgaacc ctgtctctac taaaatacaa aaattagcca  
2461 ggtgtgtgtg tgggtgctg tagtcccagc tacttgggag gctaagacag gagaatcgct  
2521 tgaacccggg aggtggaggt tgcagtgagc caagatgggt ccattgcact ctgacctggg  
2581 tgacagagcg agactccatc tcaaaaaata aaaaaatagg ccattgcacag gctcacgct  
2641 gtaatcccag cactttggga ggccgaggcg ggcggatcat gaggtcagga gtttgagact  
2701 agcctggcca acatagtga aaccctgtc tactaaaaat acaaaaatta tctggtcatg  
2761 gtggcacgtg actatagtcc cagctactcg ggaggctgag gcgggagaat cgcttgaacc  
2821 caggaggtgg aggtggcagt gagccgagat cgtgcccctg cactccagcc tgggcaacag  
2881 agcgagactc catttcaata aataataaaa cagagcactt tacagatgcc  
2941 ctggggacat tggcagagga gaaggctgag gcctgggtta tgggctctta gcatttctca  
3001 gtgggacgtg gcacagagta gatgttcat aaatgtttag aatctgaaga cccactgtgc  
3061 gcagccggc accaaaaacc tcaggatgc tgtgatctca ttggatcc

1 ctctctgctta aacctctgtc tctgacggtc cctgccaatc gctctggtcg accccaacac  
61 actaggagga cagacacagg ctccaaactc cactaagtga ccagagctgt gattgtgccc  
121 gctgagtgga ctgcgttgtc agggagttag tgcctcatca tccggagaat ccaagcagga  
181 ccgccatgga ggaaggtcaa tattcagaga tccaggagct tcccaggagg cgggtgttga  
241 ggcgtgggac tcagatcgtg ctgctggggc tggtagaccg cgctctgtgg gctgggctgc  
301 tgactctgct tctcctgtgg cactgggaca ccacacagag tctaaaacag ctggaagaga  
361 ggctgcccag gaacgtctct caagtttcca agaacttggg aagccaccac ggtgaccaga  
421 tggcgcagaa atcccagtc acgcagattt cacaggaact ggaggaaact cgagctgaac  
481 agcagagatt gaaatctcag gacttggagc tgtcctggaa cctgaacggg cttcaagcag  
541 atctgagcag cttcaagtcc caggaattga acgagaggaa cgaagcttca gatttgtctg  
601 aaagactccg ggaggagggt acaaagctaa ggtgaggtt gcaggtgtcc agcggtttg  
661 ttgtcaaacg gtgccctgaa aagtggatca atttccaacg gaagtgtctac tacttcggca  
721 agggcaccaa gcagtgggtc cagcccggt atgcctgtga cgacatggaa gggcagctgg  
781 tcagcatcca cagcccggag gagcaggact tcttgacca gcatgccagc cacaccggct  
841 cctggatttg ccttcggaac ttggacctga agggagagtt tatctgggtg gttgggagcc  
901 atgtggacta cagcaactgg gctccagggg agccccagc cggagagact gatcgagact  
961 gcgtgatgat gcggggctcc ggtcgttggg acgacgcctt ctgcgaccgt aagctgggag  
1021 cctgggtgtg cgaccggctg gccacatgca cgccgcccag cagcgaaggt tccgaggagt  
1081 ccattgggacc tgattcaaga ccagaccctg acggccgctt gcccaccccc tctgcccctc  
1141 tccactcttg agcatggata cagccaggcc cagagcaaga ccctgaagac ccccaaccac  
1201 ggcctaaaag cctctttgtg gctgaagggt cctgttgaca tttctgcca cccaaacgga  
1261 ggcagctgac acatctcccg ctctctctat gcccctgctt tcccaggagt acaccccaac  
1321 agcaccctct ccagatggga gtgcccccaa cagcaccctc tccagatgag agtacacccc  
1381 aacagcacc cctccagatg cagccccatc tctcagcac cccaggacct gagtatcccc  
1441 agctcaggtg gtgagtcctc ctgtccagcc tgcataata aaatggggca gtgatggcct  
1501 ccc

1 agtggctcta ctttcagaag aaagtgtctc tcttctgct taaacctctg tctctgacgg  
61 tccctgcaa tgcgtctggt cgaccccaac aactaggag gacagacaca ggctccaaac

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121 tccactaacc agagctgtga ttgtgcccgc tgagtggact gcgttgtcag ggagtgagtg
181 ctccatcatc gggagaatcc aagcaggacc gccatggagg aaggtcaata ttcagagatc
241 gaggagcttc ccaggaggcg gtgttgccag cgtgggactc agatcgtgct gctggggctg
301 gtgaccgccg ctctgtgggc tgggctgctg actctgcttc tcctgtggca ctgggacacc
361 acacagagtc taaaacagct ggaagagagg gctgcccga acgtctctca agtttccaag
421 aacttggaaa gccaccacg tgaccagatg gcgcagaaat cccagtccac gcagatttca
481 caggaactgg aggaacttcg agctgaacag cagagattga aatctcagga cttggagctg
541 tcctggaacc tgaacgggct tcaagcagat ctgagcagct tcaagtccca ggaattgaac
601 gagaggaacg aagcttcaga tttgctggaa agactccggg aggaggtgac aaagctaaag
661 atggagttgc aggtgtccag cggctttgtg tgcaacacgt gccctgaaaa gtggatcaat
721 ttccaacgga agtgctacta cttcggaag ggcaccaagc agtgggtcca cgcccggat
781 gcctgtgacg acatggaagg gcagctggtc agcatccaca gcccgaggga gcaggacttc
841 ctgaccaagc atgccagcca caccggctcc tggattggcc ttcggaactt ggacctgaag
901 ggagagttta tctgggttga tgggagccat gtggactaca gcaactgggc tccaggggag
961 cccaccagcc ggagccagg cgaggactgc gtgatgatgc ggggctccg tcgctggaac
1021 gacgccttct gcgaccgtaa gctggcgcc tgggtgtgag accggctggc cacatgcacg
1081 ccgccagcca gcgaaggttc cgcggagtcc atgggacctg attcaagacc agaccctgac
1141 ggcgccttgc ccaccccttc tgccctcttc cactcttgag catggatata gccaggccca
1201 gagcaagacc ctgaagaccc ccaaccacgg cctaaaagcc tctttgtggc tgaagggtcc
1261 ctgtgacatt ttctgccacc caaacggagg cagctgacac atctccgct cctctatggc
1321 cctgccttc ccaggagtac accccaacag caccctctcc agatgggagt gcccccaaca
1381 gcaccctctc cagatgagag tacaccccaa cagcaccctc tccagatgca gccccatctc
1441 ctcagcacc caggacctga gtatccccag ctcagggtgt gagtcctctc gtccagcctg
1501 catcaataaa atggggcagt gatggcctcc

```

## (2) INFORMATION FOR SEQ ID NO:58:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```

1 gtaagtattct tccctctgtg gctaggaaga caaggaatac atttttaaat gtctcctaaa
61 gcaaggacct gaaaccagct ctatgggatt attcttgttc ctcttggtc aatgcagaga
121 catgggaaga accaccaag gtcatgaggg tctcttcag ggatccctgg acattgcctt
181 tccagtggt gtgacaagag ttagaggttg cctacctgc ctctgtcctt agggggcagc
241 agtaggagag ccttcggttt tctcatcttc ttacttgtat gttgaacttt acttaatgca
301 ggctatatcc aaaatacagt gtgaattagg ctagaataga aatgctttct attctacctt
361 cagaaaaaga aaagggtagg gtaggggaaa tcatgggaga gattaaaggc agagaggaaa
421 ccagatggg actgtttaat cccaagcaa gaaaccacta ggaaagagag ataccttccc
481 tctaactttt gtattcgggt cactgacatt gctctctgtg ctggtgggaa attgatttct
541 gtgccaggat gttctaggct gaggccaaga ggggtgctgg cctttaccca gtggaagaaa
601 aaggcaaggg tgaggctttg tagactttcc cattcggagg taatgatgcc tcttcagcc
661 ccacttcttc aaactgactc cacctgctcc catctccaca cccctcggtt tctctatgag
721 ccaaagcaca tcctccttgc agcccaccac tcagcttggc caggtgcgag acatctttcc
781 ccacttcata cctcccctcc ggccagggtga tgtttgcctc ctcag

```

## (2) INFORMATION FOR SEQ ID NO:59:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

```

1 gatcacctga agtcaggagt tcgagaccag cctgaccaac atggagaaac cccgtctcta
61 ctaaaaatac aaaattagtt ggcatgggtc gtgcatgcct gtaatcccag ctactcagga
121 ggctgaggca ggagtatcac ttgaacccag gagacggagg ttgcggtgag ccaagaacat
181 gccattgcac tccagccttg gcaacaagag caaaactccg tctcaagaaa aaaaaaatt
241 tttttttgtc aacctatgtg ggtatgaaat tgtttctcat tatttgcatt tctaataa
301 ctagttaggt caaacatttt tccctcatt tcttatccat taaagtatat tctgtgaatt
361 gccagttcat ggccattttg ggggtgtagt ttttcttact gatttatgta agtttaattg
421 ttttctggaa actaatattt tgctagtgtg gtgaattgta aatatcttct cccactgtat
481 ttttttaaaa actttttatt gtctgaatta gcacatattt agtgaatgcc tctatgtgca
541 attctttttt tttttttttt tttttttttg agatggagtt tcgctcttgt tccccagact
601 ggagtgcagt ggcatgatct aagctcactg caacctcac ctcccgggtt caagtgattc
661 tcctgcctca ggcctcctga gttagctggg ttacagggtc ccgctaccat gaccagctaa
721 ttttttgtat ttttagtaga gacgggggtt catcatgttg gccagggttg tctcgaactc
781 ctgacctcag gtgatccacc cgctcggcc ttccaaagtg tagggattac aggcattgagc
841 cagttagctc agcctctatg tgcaattctt aatgtcaagc tgaggggaga gtctaagaag
901 ttttatataa gtctgacacc cagggtgcct gtaattaaag gtggaatgaa attttaattt
961 gcgagttgat ccttctgttt ttagtttcag tacttctctc tttttagaat gtatgctttc
1021 cagataatta gtgagataaa gatttgattt tcacttttag catttctaaa agctgtaata
1081 tgtaccttaa cttgttttta attcttgctc taacttctga tttttatag ttgtgtattt
1141 tgaattatat tttaaaggat taagtggatt attgcacatg atatttagta aagtgtttgg
1201 gagcatttag cacagcctcc aaaaattaga attccactag cccctgacac ctacatatct

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1213

1261 ggcatcttaa gagtcaataa tagcaaaagt gagagaggca gcttgggtgt gtggaagaa  
1321 catgggtatt ggatccgata gccttaggtt caaatcctgg cttcttcagt aattatcttc  
1381 tgtaatttta gccaaagtgt taatttcctt gagactcagt ttctcgaaga tgaagtgaag  
1441 aatggctttc accaggttgt tgtaaagact gaatacaata gtgtgcatga aaattgcaag  
1501 gcatagtgtc caggacatag ttaacattct taaatatatg ttgaggaatg gtgtgcacct  
1561 gaaaattcct ataaaagctg caaatataca tgccttttga tccagctgtt ccacttcagg  
1621 atatccttac tcatgtgtgc aaagcaattt tttgtagaaa tgtttgtaat agcaaaagac  
1681 tggaaacaac tgaaatgtac actgctaggg aactgattac tctctgggat gtccacgcaa  
1741 tgcagctcta tgaaaaaaag gagtacgtgt caagatatat taacaaataa agtacagaat  
1801 attgtactgt acttatccct tttgtgttta acaaaagaaa gaaaaggaga aaaattagaa  
1861 tatagtatat atttgccctt atgtgcaaaa aaaggaaatc actttttgtt ttttttgaga  
1921 cagggtctca ttctgtcacc caggctgggg tgcagtggcg ctatcacggc tcactgcaac  
1981 ctcaacctcc caggctcaag cgatcctccc gccacagcct cccaagttagc tgggactaca  
2041 ggcacacgcy ccatgcccag ctaatttatt tattttttt tggtagagat ggggtttcgc  
2101 gatgttacc aggtgtgtct caaactcctg agttcaggtg atccacctgt cttggcctcc  
2161 caaagtgtct tgggattaca ggcagagcc actgtgctg acctcttttc ttcttgatgt  
2221 gaaattcttc atagattaga caaatttgcc cattgtgcaa atatgttgca aatatatttt  
2281 ctcagtttgt catttatctt gatttttctt atggttttaa aaaaatgtga ttggatttat  
2341 ggtttctggc attgaaccat agttataaat gtattcttta ctctgaggtt gtccagggaa  
2401 tcttctaatt tctttaattt aattttcatt ttttaaaaac agctctattg atgcataatt  
2461 gatatacaaa aatagcatat atttactact atttgatgag tttggacatg tgtacacacc  
2521 catgaagcca tcagtttaacc tgatgggtgt gatggtttcc tgtaatttta tgcctccatt  
2581 tttcacatct agatctgact tttctggaat ttatctaagt gcacgatgtg aaagatagat  
2641 acagcttatt tttctttcca gatggctata ccttggttcta ggacaattta ttaaatagtc  
2701 catctttttc tttctgatct gagatgctat ctttattata tgctaaattt ctgtacatgt  
2761 ttaaaattat ttgtctcttt tgtttgtctc tttgtacacc agtatctacc tcatgttct  
2821 aattattcga gcttcaggat acatttttaac acttctgggt aggaacagaa ccttctcggt  
2881 actcttacia aattttcttc tttattctgg tttatttttc ctaagaacct taaaagttgg  
2941 cactgaattc caaaatagaa caccaaaana cctgttgatt tttccactgg gattatgtta  
3001 aattttcggg ttaacttagg ggaaaacctat tatttcatga tgttaaatct tactccatga  
3061 gagagcatgg tacgtctttt catctgtaca ggtctttttt tatattgttc agtagcaatt  
3121 taaaaaaatc atccactatg ttcaatgaaa taaaaggcca gatttaaaaa tttggcaagg  
3181 agttgaaaac tataaaaaag aaccataata aaattctttt ttgtccccc taaggcagaa  
3241 gaaatacaaa ttctacaact gaaaaaatat aatatctgat attaagaaat caataaatgg  
3301 tttattatat tagctacatt tgaagagaca actaaaaaag aaaaattttt tcaaaccaac  
3361 tcagaaacaa gaagatggaa aataaagaat acaatgctat ttatatttat atataatagt  
3421 atataataa cacaagttta acataggact gcatttgacg aatagaagag agataatggg  
3481 gagatagcaa cacttgagga aaaaataacg aacacttttt tatttaaggt gcctaacttg  
3541 gctgggtgtg gtggctgaca cctgtaatcc caacactttg ggaggctgag atgggtggat  
3601 catttgagcc caggagttca agaccaactc gggtaacatg gcgaaacccc atctctacag  
3661 aaaaactcca agaaaataaa aacaataatc atctgagtgt ggtagcacat gcctgcgtcc  
3721 ttgtactca ggaggtgggg gtggcagaat taccagggcc tggaggtcaa ggctgcaatg  
3781 agctgtgatc gcatcactat acttcagcct ggttgacgag tgagaccctg tctcaacaaa  
3841 taaaaataaa aataaaaaa aaaaatgccta acttggtgct tggcactttc taaaattgac  
3901 acataaatat tgtacctgtt tatggagtat atgtgatatt ttgatacatg catacaatgt  
3961 gtgtaatgat caaatcagga tatttaagat atccatcatc tcaaacattt ttctttgtgt  
4021 tcagaacatt ccaaatctag ctattttgaa atatacaata aattattaac tatagtcac  
4081 ctaatgtgct attgaatatt attgaattcc atctaattat atgtttgtac caattaacca  
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30241 ctacagctgt gggagccggt cccatgaaaa gggaaaatgg cctccatctt gaaacccctc
30301 tggaccagct tgatgactgc ttttcagaag aggccccaga tgccaccaag cacaagctgt
30361 cctccttctt gttcagttac ttgtctgtgc agactaagaa gaagacgggt cgctccctca
30421 gttgcaacag tgtgccagtg agtgctcaga agccactgcc cacagaggcc tctgtgaaga
30481 atgggggctc ctccagggtc agaattcttt ccaggtttcc agaagacatg atgatgctga
30541 agaaaagtgc cttcaaaaaa ctcatcaaat tctacagcgt cccagctttt cctgaatgca
30601 gctctcaatg tggactccag tgccctgtgt gccctctgca ggccatggtt tagacacagg
30661 gccttcagcc agagtctgag gatatacttc agggactctg tgaacccctc acaattgtat
30721 gccaaacttg tgtgcttatg tgtacatgca tttttcttgg ggcgagtcca taattttaat
30781 caaattctca taggggcttc atgaccacaca ataggatata aacgaagagt ttaagccagc
30841 atgatccaga tgggttcagc agtctgggtc gtgagaaagg gccgagggtg gacaggcagc
30901 ttctgtggtt cagcttggtg catgatatat aacacagaaa taaattatgc ttgtccctga
30961 aacaaaacat accctgtgtc acttaattgg ctgctgaaac attgattaac cagtctggga
31021 gcttaaacat atgtactttt tttgaagcat caattatgag tcaggcactg tggctcatgg
31081 ttcataaatg aggaaccaa cgtttaggct acacagcttt aaataggcaa acccaggtct
31141 cctgcttcca gtgaagccca ggctgttttc accatgcagt actgctcaa gttggacctg
31201 aacaggagct cacagccag caggctgtct gtcctccagt acatttaaat gtttccttct
31261 taggtttgga acttgtgcat tttcccttta ttttcttggg cccgtagtc aaataaaagc
31321 tatgtctaca agtggcttgc ccataattag ttcagaggcc aaacacataa ttttatttcc
31381 atttcagatg gtactttgat aggttgtgac tctgaaatgg gttatgtaaa gagtattaaa
31441 gacaaaacaa gctgggcatt agttagaact ttaaggatag atgttaaaca gtaatatact
31501 atcacaatag ggaaaagggt cccatgtgaa ctgaactcaa cttggatttg tgcaaagggtg
31561 actaggcatt tcacagcgtg aatgggagaa tagggagaag gccagcctag acttagaaga
31621 gtcaggaatg tgaaaaatta caaaaagcgg aaagtgggtg atgtgaaacc cctctgggtt
31681 tgctaactgg tgctttttga agtaagactc ttaccctccc acagagactg ggagtcaggg
31741 cctgtgttcc aggggttcgc tggaacaaac agttaattct ttcggcagct ttgagtttct
31801 ttaagcaggc actttaagggt gagctaggat caacttaggg atgtggcctt gagctgtgag
31861 aaactgtgtt agtgtttgtt caagtcttta taggcaaaag ttgagcccta gttgagaagg
31921 gggctcggag gagcttagct agagtttggt cgagaaaaga atctttgtta agagtttaaa
31981 gctttttttt tttttttttt tttttttttt ttgagactag tgctttctct ctttccagg
32041 ctggagtgtg gaggcacaa catgtcttac tgcagcctca acttcctggg cttgagcaat
32101 cctcctgctt cagcctccca agtagctatt tatttttgag atggggtctc attctgtgag
32161 tgcagtgtt ggaacacagt tcaactgcagc ctcagcctct gaggtcgaag ctgtctttcc
32221 acctcagtc cagcagtagc tgggactatg agtgacacc actatgcctg gctaattttt
32281 ataactttt acagagacag ggtctccctg tgttgccag gctggtctgg aactcctggg
32341 ctcagggtgat c

```

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2371 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

```
1 cgactaagaa gcctgttga cagctgcctt ccagcctcct ctgtctgtct gccaggagga
61 gcaatccaag ggagatgatg gagccctgtg aataccgtga ataccgtgaa tactaccgag
121 ctagagggaa agagatgggt gattacatct cccagtacct gagcactgtg cgggagaggc
181 aggtgactcc aaatgtgcag cctggatacc tgcgagccca gctacctgcg agtgcctccg
241 aggaaccoga cagctgggac agcatctttg gggacattga acgagtcac atgcctgggg
301 tggttcactg gcagagcccc cacatgcacg cctactatcc tgctcttacc tcatggccat
361 ccctgctagg agacatgctg gccgatgcca ttaactgctt aggattcacg tgggcatcta
421 gccagcttg cacagagctg gagatgaaca tcatggactg gctggcgaa agtctggggc
481 tccccaggta cttcctgcac caccatccca gcagccgagg gggagggtgc ttacagagca
541 ctgtcagcga atccacttta attgccctgc tggcagcaag aaagaacaaa atcctagcaa
601 tgacagcgtg cgagccccgat gctaacgagt cctccctgaa cgctcgtctc gttgcctaca
661 cctctgatca ggctcactct tcagtggaga aggtggctt gatttccctt gtgaagatca
721 gatttctacc tgtggacgac aacttctcac tccgaggaga agctctccag aaagctattg
781 aggaagacaa gcaacagggc ttggtgcctg tgtttgtctg tgcaacgtta gggactactg
841 gagtctgtgc atttgacagg ctgtcagaac tggggcccat ctgtgccagt gagggactgt
901 ggctccacgt cgatgctgct tatgcaggca cggcctttct gtgccttgag ctccgagggg
961 tccctggagg catcgagtac gccgactcct tcacctttaa ccttccaaag tggatgatgg
1021 tacactttga ctgtactgga ttctgggtca aggacaagta caagctgcag cagaccttta
1081 gtgtgaacct catctacctc cgacatgcca actctgggtg agccacggac ttcattgcatt
1141 ggcagatccc cttgagccgg cgctttcgct ccattaagct gtggtttgtg attcggctct
1201 tcgggggtga gaattctcaa gcacatgtca gacacggcac agaaatggct aaatactttg
1261 aatctctggt cagaagcgac ccttctctgc aaattcctgc taagaggcac cttgggtttg
1321 tggttttccg tctgaagggt cctaattgtc tcacagaaag tgtgttaaag gaaatagcca
1381 aagctggcca gctctttctc atcccggcta ctatccaaga caagctgatc atccgtttca
1441 ctgtgacgtc ccagtttacc accaaggagg acatcctgag agattggcac ctcatccaag
1501 aggtgcttaa ccttgtctct agccaagcact gcacttccca gccgagccct cgggccaaga
1561 acgtcatccc gccaccgcca gggaccagag ggctatccct ggagtcagtc agcgaggag
1621 gagatgaccc agcacaggcc cggaagatca tcaagcagcc aggagccagt ctggcgagaa
1681 gggaaaggcg ctctgatctg gaaacgatgc cggatccctt tgatgattgc ttctctgaag
1741 agggcccaaa caccaccaag cacaagctgt catcctttct gttcagttac ttgtcggtec
1801 agaacaggag gaagacaacg cggctccctca gctgcaacag tgtgcctatg agtgcacaga
1861 agtcaactcc cgcagacgct tcaactgaaga atgggggctc cttccggggc agaactttt
1921 ccgggttccc agaacaaatg atgatgatga agaaagggtg cttcaaaaag ctgatcaagt
1981 tctacagcgt ccccgacttt cctgaatgca gttctcagt tgctcgccag ctaccgtgct
2041 gccccctgga ggccatggtg tagagtcctc aatcagaatg caagggtgac tgtgcttcag
2101 ggagttgggg aacctcgaa attgcctgca gtttgtgtgc ttattatgtg tgtgtgcatc
2161 ttgagggaa caagcccatt attttgatca taacctcaca ggggtcttct gatccacaac
2221 agattgtaac tgggaagtgt aagcgggcat gctccagagg ttgcaggcgc ttgtgtgata
2281 gaaggggctg agacgggtgc atgctgttaa gcttgtaatg tgaaaaacaa cttagaaata
2341 aattgtgctt atatctaaaa aaaaaaaaaa a
```

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2355 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```
1 cttccacctc ctgcgtgtcc atctgtgaga aggagccaga gcccaaggga gatgatggag
61 cctgaggagt acagagagag agggagagag atggtggatt acatctgcca gtacctgagc
121 actgtgcggg agagacgtgt gacgcagac gtgcagcctg gctacctgcg agccagctg
181 cctgagagtg ctcttgagga ccccgacagc tgggacagca tctttgggga cattgaacga
241 atcatcatgc ctgggggtgt acattggcag agccccata tgcacgccta ctaccagcc
301 ctcacctctt ggccctccct gctaggagac atgctggctg atgccatcaa ctgcttggga
361 ttacactggg catccagccc tgcgtgtaca gagctggaga tgaacgtcat ggactggttg
421 gcaaaaatgc tgggacttcc agagcacttc ttgcaccacc accccagcag ccagggcgga
481 ggcgtcctgc agagcacggt cagtgaatcc actttgattg ccctgctggc agcaaggag
541 aacaaaatcc tggaaatgaa aacgtctgag cccgatgctg atgagtcctg cctaaatgcc
601 cgactcgtgg cctatgcctc tgaccaggct cactcctctg tggaaaaggc tgggttgatt
661 tcccttgtag agatgaaatt tctgcctgtg gatgacaact tctcactccg aggggaaagt
721 cttcagaagg ccatcgagga agacaagcag cggggcttgg tggccgtctt tgtctgtgca
781 aactaggga ccaactgggt ctgtgcattt gactgcctgt cagagctggg ccccatctgt
841 gccctgtagg ggctgtgggt ccacatcgat gctgcttatg caggcactgc cttcctgtgc
901 cccaggttcc gggggtttct gaaggggatt gagtatgccg actccttcc cttaatacct
961 tccaaagtga tgatggtgca ttttgactgt actgggttct gggtaacaga caaggaaagt
1021 ctgcagcaga ccttcagtgt gaatcccatc tacctcaggc atgccaactc aggcgtggcc
1081 accgacttca tgcactggca gatccccctg agccgacggt ttcgctctgt taaactctgg
1141 ttcgtgattc ggtccttcgg ggtgaagaat cttcaagcac atgtcagaca tggtagttaa
1201 atggctaata attttgatc tctgtcaga aacgaccctt ccttggaat tctgccaag
1261 aggcaccttg gcctgggtgt ttttctcta aagggctcta attgtctcac agaaaatgtg
1321 ttaaaggaaa tagctaaagc tggcctctc ttcctcatcc cggccactat ccaggacaa
1381 ttaatcatcc gtttcaactg gacatcccag ttaccacta gggatgacat cctgagagac
1441 tggaaatetca ttcgagatgc tgccactctc atcctgagtc agcactgtac ttcccaacc
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1501 agccctcggg ttgggaacct catctcccaa atcaggggtg ccagagcctg ggccctgtgga
1561 acgtcccttc agtctgtcag tggggcagga gatgatccag tccaggccag gaagatcatc
1621 aagcagccctc agcgtgtggg agccgggtccc atgaaaaggg aaaatggcct ccatcttgaa
1681 accctgcttg acccagttga tgactgcttt tcagaagagg cccagatgc caccaagcac
1741 aagctgtctc ccttctgttg cagttacttg tctgtgcaga ctaagaagaa gacgggtgcg
1801 tccctcagtt gcaacagtgt gccagttagt gctcagaagc cactgccac agaggcctct
1861 gtgaagaatg ggggctctc cagggtcaga atcttttcca ggtttccaga agacatgatg
1921 atgctgaaga aaagtgcctt caaaaaactc atcaaattct acagcgtccc cagctttcct
1981 gaatgcagct ctcaatgtgg actccagctg ccctgttgcc ctctgcaggc catggttag
2041 acacagggtc ttcagccaga gtctgaggat atacttcagg gactctgtga acccctcaca
2101 attgatatgc aactttgtgt gcttatgtgt acatgcattt ttcttggggc gaggttcataa
2161 ttttaatacaa attctcatag gggttcatga cccacaatag gatacaaacg aagagtttaa
2221 gccagcatga tccagatggg ttcagcagtc tggtcagtga gaaagggccg agggtagaca
2281 ggcagcttct gtggttcagc ttgtgacatg atatataaca cagaaataaa ttatgcttgt
2341 ccttgaaaca aaaaa

```

## (2) INFORMATION FOR SEQ ID NO:62:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```

1 agtgcgcagg actggcaaga gggaagccgg gctgctccac gcctttcacg ccttccacct
61 cctgcgtgtc catctgtgag aaggagccag agcccaaggg agatgatgga gcctgaggag
121 tacagagaga gaggagaga gatggtgat tacatctgcc agtacctgag cactgtgcgg
181 gagagacgtg tgacgcaga cgtgcagcct ggctacctgc gagccagct gcctgagagt
241 gctcctgagg accccgacag ctgggacagc atctttggg acattgaacg aatcatcatg
301 cctgggtgtg tacattggca gagcccccat atgcacgct actaccagc cctcacctct
361 tggccctccc tgctaggaga catgctggct gatgccatca actgcttggg attcacctgg
421 gcatccagcc ctgcgtgtac agagctggag atgaacgtca tggactggtt ggcaaaaatg
481 ctgggacttc cagagcactt cttgcaccac caccagca gccaggggcg aggcgtctctg
541 cagcagacgg tcagtgaate cactttgatt gccctgctgg cagcaaggaa gaacaaaatc
601 ctggaaatga aaacgtctga gcccgatgct gatgagtcct gcctaaatgc ccgactcgtg
661 gcctatgcct ctgaccaggc tcaactcctt gtggaaaagg ctggtttgat ttcccttgtg
721 aagatgaaat ttctgcctgt ggatgacaac ttctcactcc gaggggaagc tcttcagaag
781 gccatcgagg aagacaagca gcggggcttg gtgcccgtct ttgtctgtgc aacactaggg
841 accactgggg tctgtgcatt tgactgcctg tcagagctgg gcccatctg tgcccgtgag
901 gggctgtggc tccacatcga tgetgcttat gcaggcactg ccttctgtg ccccgagttc
961 cggggttttc tgaaggggat tgagtatgcc gactccttca cctttaatcc ttccaagtgg
1021 atgatggtgc attttgactg tactgggttc tgggtcaagg acaagtacaa gctgcagcag
1081 acccttcagt tgaatcccat ctacctcagg catgccaaact caggcgtggc caccgacttc
1141 atgcactggc agatccccct gagccgacgg ttctgctctg ttaaaactctg gttcgtgatt
1201 cggctccttc ggggtgaagaa tcttcaagca catgtcagac atggtactga aatggctaaa
1261 tattttgaat ctctgttcag aaacgaccct tcctttgaaa ttcttgccaa gaggcacctt
1321 ggcctggttg ttttctgtct aaagggtcct aattgtctca cagaaaatgt gttaaaggaa
1381 atagctaaaag ctggccgtct cttcctcatc ccggccacta tccaggacaa gttaatcatc
1441 cgtttcactg tgacatccca gtttaccact agggatgaca tccctgagaga ctggaatctc
1501 attcgagatg ctgccactct catcctgagt cagcactgta ctcccaacc cagccctcgg
1561 gttgggaacc tcatctccca aatcaggggt gccagagcct gggcctgtgg aacgtccctt
1621 cagtctgtca gtggggcagg agatgatcca gtccaggcca ggaagatcat caagcagcct
1681 cagcgtgtgg gagccggtcc catgaaaagg gaaaatggcc tccatcttga aacctgtctg
1741 gacccagttg atgactgctt ttcagaagag gcccagatg ccaccaagca caagctgtcc
1801 tcttctctgt tcagtactt gtctgtgcag actaagaaga agacgggtgcg ctccctcagt
1861 tgcaacagtg tgccagttag tgctcagaag ccactgcccc cagaggcctc tgtgaagaat
1921 gggggtcctt ccagggtcag aatcttttcc aggtttccag aagacatgat gatgtgaag
1981 aaaaagtgcct tcaaaaaact catcaaattc tacagcgtcc ccagctttcc tgaatgcagc
2041 tctcaatgtg gactccagct gccctgttgc cctctgcagg ccatggttta gacacagggc
2101 cttcagcaga gtctgaggat atacttcagg gactctgtga acccctcaca attgtatgcc
2161 aactttgtgt gcttatgtgt acatgcattt ttcttggggc gaggttcataa ttttaataca
2221 attctcatag gggctcatga cccacaatag gatacaaacg aagagtttaa gccagcatga
2281 tccagatggg ttcacagtc tggtcagtga gaaagggccg agggtagaca ggcagcttct
2341 gtggttcagc ttgtgacatg atatataaca cagaaataaa ttatgcttgt ccttga

```

## (2) INFORMATION FOR SEQ ID NO:63:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```

1 gtaagtatct tccctctgtg gctaggaaga caaggaatac atttttaaat gtctcctaaa
61 gcaaggacct gaaaccagct ctatgggatt attctgttc ctcttggtc aatgcagaga
121 catgggaaga accaccaaag gtcattggg tctcttccag ggatccctgg acattgcctt
181 tcccagtggt gtgacaagag ttagaggtgg cctaccttgc ctctgtcct aggaggcgac

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241 agtaggagag ccttcggttt tctcatcctc ttacttctat gttgaacttt acttaatgca  
301 ggctatatcc aaaatacagt gtgaattagg ctagaataga aatgctttct attctacctt  
361 cagaaaagga aaagggtagg gttaggggaaa tcatgggaga gattaaaggc agagaggaaa  
421 cccagatggg actgtttaat cccaagcaa gaaaccacta ggaaagagag ataccttccc  
481 tctaaactttt gtattcgggt cactgacatt gctctctgtg ctggtgggaa attgatttct  
541 gtgccaggat gttctaggct gaggccaaaga ggggtgctggc cctttaccga gtggaagaaa  
601 aaggcaagggt tgaggctttg tagactttcc cattcggagg taatgatgcc tcttcagcc  
661 ccacttcttc aaactgactc cacctgctcc catctccaca cccctccgtt tctcatttag  
721 ccaaagcaca tcatccttgc agccaccac tcagcttggc cagggtgcgag acatctttcc  
781 ccacttcata cctccctccc ggccagggtga tgtttgcctc ctacg  
1 gatcacctga agtcaggagt tcgagaccag cctgaccaac atggagaaaac cccgtctcta  
61 ctaaaaaatc aaaattagtt gggcatgggc gtgcatgcct gtaatcccag ctactcagga  
121 ggctgaggca ggagtatcac ttgaaccacg gagacggagg ttgcggtgag ccaagaacat  
181 gccattgcac tccagccttg gcaacaagag caaaactccg tctcaaagaa aaaaaaatt  
241 tttttttgtc aacctatgtg ggtatgaaat tgtttctcat tatttgctat tcactaatta  
301 ctagtggagt caaacatttt ttccctcatt tcttatccat taaagtttat tctgtgaatt  
361 gccagttcat ggccattttg ggggtgtagt ttttcttact gatttattga agtttaattg  
421 ttttctggaa actaatattt tgctagtgtg gtgaattgta aatatcttct cccactgtat  
481 ttttttaaaa actttttatt gtctgaatta gcacatattt agtgaatgcc tctatgtgca  
541 attctttttt tttttttttt tttttttttg agatggagtt tcgctcttgt tcccagact  
601 ggagtgcagt ggcatgatct aagctcactg caaccttcac ctcccggtt caagtgttc  
661 tctgcctca ggccctcctga gtactggga gacggggttt catcatgttg gccaggttg tctcgaactc  
721 tttttgtat ttttagtaga gacggggttt catcatgttg gccaggttg tctcgaactc  
781 ctgacctcag gtgatccacc cgctcggcc ttccaaagt tagggattac aggcattgagc  
841 cagtgcctc agcctctatg tgcaattctt aatgtcaagc tgaggagaa gtctaagaag  
901 ttttatataa gtctgacacc cagggtgcct gtaattaaag gtggaatgaa attttaattt  
961 gcgagttgat ccttctgttt tttagttag tacttctctc tttttagaat gtatgctttc  
1021 cagataatta gtgagataaa gatttgattt tcaacttttag catttctaaa agctgtaata  
1081 tgctacctaa ctgtttttta attcttgctc taacttctga ttttttag ttgtgtattt  
1141 tgaattatat tttaaaggat taagtggatt attgcacatg atatttagta aagtgttttg  
1201 gagcatttag cacagcctcc aaaaattaga attccactag cccctgctc ctacatatct  
1261 ggcatcttaa gagtcaataa tagcaaagt gagagaggca gcttgggtg gtggaagaa  
1321 catgggtatt ggatccgata gccttaggtt caaatcctgg ctcttcagt aattatcttc  
1381 tgtaatttta gccaaagtgt taatttctct gagactcagt ttctcgaaga tgaagtagaa  
1441 aatggctttc accaggttgt tgtaaaagact gaatacaata gtgtgcatga aaattgcaag  
1501 gcatagtgtc caggacatag ttaacattct taaatatatg ttgaggaatg gtgtgcacct  
1561 gaaaattcct ataaaagctg caaatataca tgctttttga tccagctgtt ccacttcagg  
1621 atatccttac tcatgtgtgc aaagcaattt tttgtagaaa tgtttgtaat agcaaaagac  
1681 tggaacaac tgaaatgtac actgctaggg aactgattac tctctggtat gtccacgcaa  
1741 tgcagctcta tgaaaaaag gactacgtgt caagatatat taacaaataa agtacagaat  
1801 attgtactgt acttatccct tttgtgttta acaaaagaaa gaaaaggaga aaaattagaa  
1861 tatagtatat atttgccttt atgtgcaaaa aaaggaaatc actttttgtt tttttgaga  
1921 cagggtctca ttctgtcacc caggctggg tgcaagtggc ctatcacggc tcaactgcaac  
1981 ctcaacctcc caggctcaag cgactctccc gccacagcct cccaagtagc tgggactaca  
2041 ggcacacgcg ccactgccag ctaattttatt tttttatttt tggtagagat ggggtttcgc  
2101 gatgttacc aggtgtgtct caaactcctg agttcagggt atccacctgt cttggcctcc  
2161 caaagtgtc tgggattaca ggcatgagcc actgtgcctg acctcttttc ttctgtatgt  
2221 gaaattcttc atagattaga caaatttgcc cattgtgcaa atatgttgca aatatatttt  
2281 ctcaatttgt catttatctt gatttttctt atggttttaa aaaaatgtga ttggatttat  
2341 ggtttctggc attgaaccat agttataaat gtattcttta ctctgaggtt gtccagggaa  
2401 tcttctaatt ttcttaattt aattttcatc ttttaaaaac agctctattg atgcataatt  
2461 gatatacaaa aatagcatat atttactact atttgatgag tttggacatg tgtacacacc  
2521 catgaagcca tcagttaacc tgatggttgt gatggtttcc tgtaatttta tgcctccatt  
2581 tttcacatt agatctgact tttctggaat ttatctaagt gcacgatgtg aaagatagat  
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1230

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1231

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(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1327 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

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61 ccaggttagag caacactcct cgtcgcaacc caactggctc cccttacctt ctacacacac

121 acacacacac acacacacac acacacacac acacacaaat ccaagacaac actactaagg

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181 ctcttttggg agggggaagt agggataggt aagaggaaag taagggaacc cctatccagc
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1321 gcactgc

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## (2) INFORMATION FOR SEQ ID NO:65:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1601 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```

1 aaaccacaag acagacttgc aaaagaaggc atgcacagct cagcactgct ctgttgctg
61 gtcctcctga ctgggtgag gccagccca gccagggca cccagtctga gaacagctgc
121 acccacttcc caggcaacct gcctaacatg ctctgagatc tccgagatgc cttcagcaga
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1261 gcctgggtcaa catggtgaaa cccgtctct actaaaaata caaaaattag cggggcatgg
1321 tggcgcgcac ctgtaatccc agctacttgg gaggctgagg caagagaatt gcttgaaccc
1381 aggaagatga agttgcagtg agctgatatc atgcccctgt actccagcct ggggtgacaga
1441 gcaagactct gtctcaaaaa aataaaaaata aaaataaatt tggttctaat agaactcagt
1501 ttttaactaga atttattcaa ttctctggg aatgttacat tgtttgtctg tctcatagc
1561 agattttaat tttgaataaa taaatgtatc ttattcacat c

```

## (2) INFORMATION FOR SEQ ID NO:66:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4181 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

1 agatcttgta aactgtagaa tgcacctcc aaaatctatt tgcataagca cacacacaca
61 cacacacaca cacaccccg cagttcttgc ctgcccagat tctctgcag ctaaagtgtat
121 gaaacttact gggcgagct tcctaaaaag attattaggg tctcctgggt tgggtgtcct
181 ttaaaccttt ggactttacc acctcctatc tctcctatct ccttgcaaca aaggttagga
241 gaacaagaat gcagaaaaaa cgggtcctgg atgacatctg agtgctgtct ttgggtctct
301 tgatgagtga gacagaaaat aaaatacaac cccctctttt aaaagccatg cttactcagg
361 ttttcttcca tttgcagcta aatacagaaa tgagagaata ttttggagca gggatggaag
421 aagagaggta tcccccttcc cacaaccttc tgatttccca gtacatcccc cactggaaaa
481 attcatttaa aatcagtata ataagcattg attagatgcc tactatgcat ctgggcttga
541 gggcaactg gactcaggcc ttttggcctc aagaagctca cagtgtgaga gtggcatttg
601 tgtcctctg aaattcacag gactaaattg tgcccaggct gacattctat ccatccatag
661 gtgcctgctt tctcacttcc ctctcttcat gggctcttgc cttgtaccaa aatccaaacc

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721 caaatctcct cacatgtgag tgttggcatt catgtctcag acatgaccta tgggcttggg
781 acttttcccc gtggaccoca gtgacttttc agatgaacag gtatcttcaa aaacttgaga
841 aataggagtc ctgtttgttg ttcttgttgc ttgtcaata taaggcacag ggtctttatt
901 caaatgttca tactatctct tgacagaaat actatgagac atattgatgg agaagccgtt
961 atctccatat gctaaatgag gacttgcacc agggaaacttg cccatggttc tctccaacca
1021 cttaaattct gaaatttga atgagatgg acagtaattt caaatcaatg gggaaagaat
1081 caaatcttca gcaaatggct tgagataatt agctacacat ttcagaacaa ataaagaagt
1141 cagatccggg ccgggcacag tggctcatgc ctgtaatctc agcactctgg gaggccaaag
1201 cgggcggatc ataaggtcag gagatcgaga ccattcctgg taacacagtg aacctctctc
1261 taataaaaaa acaaaaaaaa ataaaaaaac tttagccggg gtggtgccag gcgctgttag
1321 tcccagctac tcgggacgct gaggcaggag aatggcttga actcgggagg cagagcttgc
1381 aggtgagctg agatcatgcc actgcactcc agcctgggca acagagcgag actctgtctc
1441 aaaaaaaaaa aagaagtcag atcctaacct caacctatt taacagatta tagatgaaag
1501 aaagggtacaa atggctttta catacctccc ttctccctga cattttgtat gtgtgtgtgt
1561 gtgtatttac acacacatct catataaggg aagtgaagg aggctgctg catoccttag
1621 tcaactctcc tctcctctg aatgcttacc tgtgccaga ccacctcctt agcctcgcac
1681 cctccaggct tacagggcac tcttctatgc ccattcccaag tatagctgaa ccttccaagg
1741 gccagacttg gtgctaagta ccaagtacgc aaagattaat aaaacaatgt cctgtttcag
1801 gtagctcaaa gctgattcgg cagggcatgg tgtgtacatg aatgataacc acgtagggtt
1861 gcaggtttcc tagtgaggtg agcacaaggc aagatgggaa acaaaggaa gagggttca
1921 cagcctcacc cagagtccag aacctctggc ctgcctggtg cccatgctga gtccacttct
1981 ggaacaccca gctcagagag ggggttagac ctgcaggcta acacagacac agcccagaaa
2041 acccaggagc cgagggggaa ggagaaaggt gcaagaagg gaaaccagg tctgtgtccc
2101 ctctctctct ctctcctggc gcagaactca actataagga aatgaaccag ctaagtctgg
2161 caggaccagt aagttctgag tttagctccat actagtctct agcaggctct ttctcacttc
2221 ctgattctta ggtttctaca ttgacactcc ctgaagagtt gggaagagac accacagtcc
2281 cctgaccctg atccataggt cacacagcag gcatccacag ggtggcggtg ggccctctca
2341 tccctccctc ccactcactt cacgctggct gggccccaag gtgtttgcac ccttgcagt
2401 gagtgcactt ctctagtga gcaagctcag aacctgctgc cactggagt gtccacttgc
2461 tgatgcagaa aggtgaagaa ctagcagaac actggaaatg ccctccatct ggttccatgg
2521 ctacttaatg ctccctggca ggcaggagga caggtgctat tccctgttgg gacagatgaa
2581 aaacagacac agggaggtat agtgatttgc cctgactata gagtggcagg gccaaaggcag
2641 agcccaggcc tctgcacct aggtcagtg tctctccagt tacagtctaa actggaatgc
2701 aggcaaagcc cctgtggaag gggaagggtga aggtcactc aaaggatccc cagagacttt
2761 ccagatatct gaagaagtcc tgatgtcact gccccggctc tccccagggt agagcaacac
2821 tctctgcgcg aacccaactg gctcccctta ccttctacac acacacacac acacacacac
2881 acacacacac acacacacaa atccaagaca acactactaa ggcttctttg ggaaggggaa
2941 gtagggatag gtaagaggaa agtaagggac ctccctatcca gcctccatgg aatcctgact
3001 ttttttctct gttatttcaa ctcttccac cccattcttt aaactttaga ctccagccac
3061 agaagcttac aactaaaaga aactctaagg ccaatttaat ccaaggtttc attctatgtg
3121 ctggagatgg tgtacagtag ggtgaggaaa ccaaattctc agttggcact ggtgtacctt
3181 tgtacaggtg atgtaacatc tctgtgcctc agtttgctca ctataaaata gagacggtag
3241 gggatcatgg gagcactacc tgactagcat ataagaagct ttcagcaagt gcagactact
3301 cttaccactt tcccccaagc acagttgggg tgggggacag ctgaagaggt ggaaacatgt
3361 gcctgagaat cctaatagaa tcggggtaaa ggagcctgga acacatcctg tgaccccgcc
3421 tgtctgttag gaagccagtc tctggaaggt aaaaatggaag ggctgcttgg gaacttttag
3481 gatatttagc ccacccccctc atttttactt ggggaaacta agggccagag acctaaagtg
3541 atgcctaag tttagcaagg gaagtcttgg gtattcatcc caggttgggg ggaccaat
3601 atttctcaat cccattgtat tctggaatgg gcaatttgtc cacgtcactg tgacctagga
3661 acacgcgaat gagaacccac agctgagggc ctctgcgcac agaacagctg ttctccccag
3721 gaaatcaact ttttttaatt gagaagctaa aaaattattc taagagaggt agcccatcct
3781 aaaaatagct gtaatgcaga agttcatgtt caaccaatca tttttgctta cgtatgcaaaa
3841 attgaaaact aagtttatta gagaggttag agaaggagga gctctaagga gaaaaaatcc
3901 tgtgccggga aaccttgatt gtggcttttt aatgaatgaa gaggcctccc tgagcttaca
3961 atataaaagg gggacagaga ggtgaagggtc tacacatcag gggcttgctc ttgcaaaacc
4021 aaaccacaag acagacttgc aaaagaaggc atgcacagct cagcactgtg ctgttgcttg
4081 gtctctctga ctggggtgag ggccagccca ggccagggca cccagtctga gaacagctgc
4141 acccacttcc caggcaacct gcctaacatg cttcgagatc t

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## (2) INFORMATION FOR SEQ ID NO:67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```

1 gggggggggg atttagagac ttgctcttgc actaccaaa g ccacaaagca gccttgacga
61 aaagagagct ccatcatgcc tggctcagca ctgctatgct gctgctctt actgactggc
121 atgaggatca gcaggggcca gtacagccgg gaagacaata actgcacca cttcccagtc
181 ggccagagcc acatgctcct agagctgcgg actgccttca gccaggtgaa gactttcttt
241 caaacaagg accagctgga caacatactg ctaaccgact ccttaatgca ggactttaag
301 ggttacttgg gttgccaaag cttatcgga atgatccagt tttacctggt agaagtgtg
361 ccccaggcag agaagcatgg cccagaaatc aaggagcatt tgaattccct ggggtgagaag
421 ctgaagaccc tcaggatgag gctgaggcgc tgtcatcgat ttctccctg tgaataaag
481 agcaaggcag tggagcaggt gaagagtgt ttaataaagc tccaagacca aggtgtctac

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541 aaaggccatga atgaatttga catcttcac aactgcatag aagcatacat gatgatcaaa
601 atgaaaagct aaaacacctg cagtgtgtat tgagtcctgt ggactccagg acctagacag
661 agctctctaa atctgatcca gggatcttag ctaacggaaa caactccttg gaaaacctcg
721 tttgtacctc tctccgaaat atttattacc tctgatacct cagttcccat tctatttatt
781 cactgagcct ctctgtgaac ttttagaaa gaagcccaat attataattt tacagtattt
841 attattttta acctgtgttt aagctgtttc cattggggac accttatagt atttaaaggg
901 agattatatt atatgatggg aggggttctt ccttgggaag caattgaagc ttctattcta
961 aggctggcca cacttgagag ctgcagggcc ctttgcctat gtgtcctttc aattgtctct
1021 atccctgagt tcagagctcc taagagagtt gtgaagaaac tcatgggtct tgggaagaga
1081 aaccagggag atcctttgat gatcattcct gcagcagctc agaggggtcc cctactgtca
1141 tccccagcc gcttcatccc tgaaaactgt ggccagtttg ttatttataa ccacctaaaa
1201 ttagttctaa tagaactcat ttttaactag aagtaatgca attcctcttg gaatggtgta
1261 ttgtttgtct gcctttgtag cagcatctaa ttttgaataa atggatctta ttcg
```

## (2) INFORMATION FOR SEQ ID NO:68:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7207 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```
1 cagtcaggag agagggcagt gaggtccat gctagctggg tcttgagcct cttctggggt
61 tcagtcctctg atctacagca gtgtgtccac acctaaaaca tcagtcaga gaggcagttg
121 cttctgctgt tggaaacgga catcccaaaa aaaaacaaaa aacagaaatc aaaagggag
181 gagaaagtga aagggtatga ggcagcttgt ccccttccct gtgcttgctg ctggtagaaa
241 actcagcctg gaactgaccg gagcagcagt tcttgagtca attccattcc aacttctaga
301 agattctttt cccgtcgaag agtgtcagga ggagaggcca gacccctctg atcctgatct
361 gccagccact gcatcagata agacgagata accccgagtt cctgttctac cagccctggt
421 gtggttaacc tctccaatgg ggcaggcttg gaacctgtg ccaacgaaga tcttcccccg
481 tactgatgca ggaaggacag cccgggagtg taccctctac atgggtctac ttttatttaa
541 gcaaacattc cctgttcaac aggacgtgta gcattgcccc ccccttggg tcacacagaa
601 aacaggtacc aggaggacaa gtagtgtctt gccagggtg cagaatgaaa ggcaataggg
661 gactctaggc gaattgttctt cccacccaaa ctgaggtagt aggagaaagc cctactgaag
721 ggaaggtcca gacataatca aaggactacc agagatctcc caggatctg tagaagtact
781 aacatctcca tcttcaaca gctacaggtt acacgtctcc aaggctggga cattgtaaaa
841 cagggccatg gtaaggtcta cccgacagca cagagcaagc ctcccagaag tctgagttcc
901 tctcctaac ttctcatgct gggatctgag cttctctgtg aaacacggg cagaggaggc
961 accagaactc tctctgacc aactgcccc cagcacacat atctcctgag gatagctttg
1021 aatacgtgat ggaagaatta aagagagtga ggtctgaaga aaatcagccc tctcgggggt
1081 tcttttgggt aactgagtg taaggtgact tccgagtcag caagaaatat cggacgttca
1141 tcccaggttg agtggaggaa acaattattt ctcaatccta atattgttct gaatagccca
1201 tttatccacg tcattatgac ctgggagtg gtgaatggaa tccacagatg agggcctctg
1261 tacatagaac agctgtctgc ctcaggaaat acaactttta gtattgagaa gctaaaaaga
1321 aaaaaaaatt aaaagagagg tagcccatat taaaaatagc tgtaatgcag aagttcattc
1381 cgaccagttc tttagcgctt acaatgcaaa aaaaagggaa aggaaaaaaa aaaagaaaga
1441 aattaaactc aaaaattgca tggtttagaa gagggaggag gagcctgaat aacaaaaacc
1501 tttgccagga aggccccact gagccttcag tataaaaggg ggaccaagaa caggaggtct
1561 acatttagag acttgctctt gcactaccaa agccacaagg cagccttgca gaaaagagag
1621 ctccatcatg cctggctcag cactgctatg ctgcctgctc ttactgactg gcatgaggat
1681 cagcaggggc cagtacagcc gggaagacaa taactgcacc cacttcccag tcggccagag
1741 ccacatgctc ctagagctgc ggactgcctt cagccaggtg aagactttct ttgtaagtat
1801 gagctcgctt agcctttctt cctgccatca cctgaaatat gcattctgat ggaactgcaa
1861 aatagctctt cttctctctc ctccttctcc tcttctctt tctctctctc tgccttctcc
1921 tcttctctt cctctctctt cttctctctc tctctctctt cttctctctc cagctcttac
1981 ctcagtctgc tctctcccta tttccagcac ctattaccct taaacttaa tctagagagt
2041 cctagggaaa gccatgagtt aaactaaacc caggcacatc cgaaaagcta actagaggt
2101 gaatgcattg tctctcccat gctcaagaac tttctgttaa gtttccaata aggtccatg
2161 ttttgctggc taggacaaaa gtctgtgtgc tctgcgtagt ctctagatct gggggacaga
2221 ggtttggggg tttgaagcag caccagcata gagagcttgc attacaaaa tattccccct
2281 tcagagctcc tggaaactgt atggaggtcc aaagaaggca gagagctatg caaaacaggc
2341 tttctataag ggaactccaga aagggaagggt tgacacaggt gctcttgaaa cctgacttga
2401 ctcatctgaa agaagaccgg gcctgggtct aacttctccc agtcagttaa attcagtcag
2461 aagtttttaa aaacaactgg atcccaagag gaaggacttt gatttaactc cgggctctag
2521 cactgtcaaa tctgttctt aaaactctcc tttccacagt tgccagggca tttgaattga
2581 ttacaattc aaaaactctac aaatggaaaa gtattcaaat gacatgcaca ttgggtattt
2641 tccccagctc ttgcatcac gttctttatg ttcttccagc aaacaaagga ccagctggac
2701 aacatactgc taaccgactc cttaatgcag gactttaagg taagagtccg gtgggtgctg
2761 gggagcgacc aagcgattag ggacgggacg ggaggtgctg cttgtgacag cagagctggg
2821 tctgatgcct tgactttcaa aaagagaagt gagaagacct tgactcagca tatcgccagc
2881 agtcaagggt tgtgaagagc tcattctgtg gtaagggag aaaaatgtaac tagaaggggc
2941 ggggatgggg ggggggtccc taggaacagg acagttccatc aaggttagca gcaacagatc
3001 accattccag taagtcacac ccaacctctg atccctgcct ctagggttac ttgggttgcc
3061 aagccttatc ggaatgatc cagttttacc tggtagaagt gatgccccag gcagagaagc
3121 atggcccaga aatcaaggag catttgaatt ccctgggtga gaagctgaag accctcagga
3181 tgcggctgag gcgctgtgtg agtagcagat gcgttcttcc ccaccccaa tccccctaga
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3241 gccacccaac aaatactgtc tctacagcc cagtcaggcc acatgcatcc agagacacac
3301 acagactaga caggagacta ggtaaatcta gagagacgcc tgtccggtgt cgggtctctt
3361 gctcatctgt ctctgagcga gtgtgggagt gactttgagg cactcacacg tgaagatttg
3421 cgcatagcct tcctgttatt tgtgagtcac tgtgggttat tagctactcc cctctctctc
3481 catgggaagg ctggggcttc agtcatggct ccctcacctc tgggctgcca gctgaggctc
3541 ccaagcacag gaaaaacatc atctctttat ctcatctttt gggaagcaaa ttcagtgga
3601 cagagctggg ctgacaggac gctgggtgtt cagaagggcc agaagactgc tatccctaag
3661 ccagtatcta tgaataatac agtcggggca tctatgtctc tgaagcgatg ccttggctgc
3721 tcttgttttt cttacttctc tcaactgatac tgggacatca gctggagctc acttgtgcaa
3781 cggttctggc ctgacgattt ggccccagta gctgagactt tcgctcctct ctcagacacc
3841 tagaaatagt tcatggtggt tgagattgga gatagacaag aagagacact aaaaacagaa
3901 cagggtgcct ggagctctga gagacaaaac ccgagacctg agttcacacc cacacttagc
3961 aagccatctt agtgattgca aagacataca ttgcatcttt ctaggctgtc ctctgctgtc
4021 cccctcagtc cctaccgaaa tagataagga ccaatcacgg ctcagttctc cctgggagct
4081 aagaagtggg cattgaagat gagcaagggt gtctccttcc tcacacaaca agatagtttc
4141 ccccaagtac catggatgca gaattcaagc aagaattacc aatgctctct ttttctctc
4201 tcagcatcga tttctccctt gtgaaaataa gagcaaggca gtggagcagg tgaagagtga
4261 ttttaataag gtaagtggca aagggggcga gtgtacaag acctctgtct actcaccaaa
4321 gcgcagaagg agggcgggag ctattctgca cctggagtgt gggaaacccg caaatgggtg
4381 gacctctctt gccagttaga aagccaccac ctcagttaca ttgttttctt gcaaagcgtc
4441 tctggcagtt tctaaatgac tgctccactt ttgcaggctt ttggcttaga ctgaccagac
4501 agcctatgag cacagggcac taggtgttga ggagagtga ataggaaaca gaaagtacag
4561 aaagtacctt gttgggaaac aggtgaacc cacaagtaca gaaagcagac atgaattaat
4621 ttactcaggt acatcattgg ggctcagcct ggatgcccc ccccaaatc agaacgagca
4681 gaaagcagaa tcttacttgg tccggggcga ctttccacct ggcaaacaaa atgaggtttc
4741 acacttccaa ctgcctgtga acctattcaa ccctagtctc cagaagccat gtggcctaca
4801 tcatcatctt tgtgggctag gcagagacac ctggcagggc tctaacatta gtgggcatga
4861 attccatgac agcaggtcag agctgcaggg tgaggactgc ctacacactc aaaacataaa
4921 aaaaaaaaaa aaaaaacacc aaccatttcc ctgctatctc tatcactgcc ctgcttcaaa
4981 actgtctcct ctggcatctt tgcatatcat tctgcataag cattatatga gcactggcct
5041 cttaaaaaaa attagttgaa aaggtgccac cctgaagaca gtgctttggg gactgaatgc
5101 ttcccttgct gactcctggc agtgcttaaa gctgggagaa ggttgggtccc accacatcct
5161 gactactaca gtatagttgt ctctcttctt tcatttccct gtccccattt ctttattgta
5221 cataaagtaa ctgggtgatg tgcacacaca tagtgctctc tcttcttttt ctttatttaa
5281 actaaatggc cgatgttctg tttcgggttg catcagatgg agatggtctg ggggaaagta
5341 ctgggtttgt gaaaataccc ccttctccat tagtggcatt ctctttcagc tcttatcttt
5401 atattccagt aagttatttt gctctcattg ttttaacaaa agaaccacac aacaccaaat
5461 ctttgcatac cttgttcgat tggagaattt taatgttttt catttatcat tgtaaaaccg
5521 aggaacaatt tataactttt ttgtacgtgg ctgttacctg tagggcaatc tgtctttaag
5581 tagggataaa ttactcttga ataaaatgat cctagatagt tttcccttca agtcaagcgt
5641 cttgttgttt aaataaactt cttgtttaaa atgaaaaaaa aaaaaacaaa caaacaaaaa
5701 aaagctggga gaaggtatag gagaacacag ggaaggcacg gccccttccc aaagcagacg
5761 gacaaatctt tgggtccttc agctcccaac acaagaaagc agagatcttt ctatgctcag
5821 catccttccc agggcaggga gcccctcagc ccaccaatgg gtactaacca gatgcttctc
5881 tccccacaca gctccaagac caaggtgtct acaaggccat gaatgaattt gacatcttca
5941 tcaactgcat agaagcatac atgatgatca aaatgaaaag ctaaaacacc tgcagtgtgt
6001 attgagtctg ctggactcca ggacctagac agagctctct aaatctgac cagggatctt
6061 agctaacgga aacaactcct tggaaaacct cgtttgtacc tctctccgaa atattttatta
6121 cctctgatac ctcaattccc attctattta ttactgagc ttctctgga actattttaga
6181 aagaagccca atattataat tttacagtat ttattatttt taacctgtgt ttaagctgtt
6241 tccattgggg acactttata gtattttaaag ggagattata ttatatgatg ggaggggttc
6301 ttccttggga agcaattgaa gcttctatct taaggctggc cacacttgag agctgcaggg
6361 cctcttgcta tgggtgtcct tcaattgctc tcatccctga gttcagagct cctaagagag
6421 ttgtgaagaa actcatgggt cttgggaaga gaaaccaggg agatcctttg atgatcattc
6481 ctgcagcagc tcagagggtt cccctactgt catccccag ccgcttcatc cctgaaaact
6541 gtggccagtt tgttatttat aaccacctaa aattagttct aatagaactc atttttaact
6601 agaagtaatg caattctctt gggaaatggg tattgtttgt ctgctttgt agcagactct
6661 aattttgaat aaatggatct tattcgaatt acagtgtggg gtctattgag ttctgtctga
6721 tttaaaagaa aaatccctta aaattccaga gggcagaagc agtgaactct agactccaca
6781 aaaagaatgc cagcaacctc tccaggaagg ggttgagctc ggatcagatc agaggaaagt
6841 cttgcctggc tttcaaagca tcagcataaa ctactgatat cttcaagctc agtcctttaa
6901 aatgtgtcct gaaaccttaa aagcattctt accttccaaa gctagggaa gtagttctaa
6961 gtaaccatcg gaaggaaagt ggaagcatca aagctgaac tctgagacga aatgttgggg
7021 ttaaaaatgg aagctagggg caggagggtg gggagatggc tcagcagtta gagtgtgtgc
7081 cggcaccagt gagacaggag ttcatactct tggaaatcaa ccaacacaca accaacacta
7141 ggcaagagat gcctaattgt tcagtgttg cttcaagctc cagaggtcct ggggtgaact
7201 tagatcc

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## (2) INFORMATION FOR SEQ ID NO:69:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15530 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

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5041 cttaaaaaaa attagttgaa aagggtgccac cctgaagaca gtgctttggg gactgaatgc
5101 ttcccttgct gactcctggc agtgcttaaa gctgggagaa ggttgggtccc accacatcct
5161 gactactaca gtatagttgt ctctcttctt tcatttccct gtccccattt cttttattgta
5221 cataaagtaa ctggtgtatg tgcacacaca tagtgctctc tctttctttt ccttttttaa
5281 actaaatggc cgatgttctg ttctggttgg catcagatgg agatgggtctg ggggaaagta
5341 ctgggtttgt gaaaataccc ccttctccat tagtgcatg ctctttcagc tcttatcttt
5401 atattccagt aagtattttt gctctcattg ttttaacaaa agaaccacaac aacaccaaat
5461 ctttgcatac cttgttcgat tggagaattt taatgttttt catttatcat tgtaaaaccg
5521 aggacaattt tataactttt ttgtacgtgg ctgttacatg tagggcaatc tgcctttaag
5581 tagggataaa ttactcttga ataaaatgat cctagatagt ttcccttca agtcaagcgt
5641 cttgtgtttt aaataaactt cttgttttaa atgaaaaaaa aaaaaacaaa caaacaacaaa
5701 aaagctggga gaaggtatag gagaaacagg ggaaggcacg gcccttcccc aaagcagacg
5761 gacaaatctt tgggtccttc agctcccaac acaagaaagc agagatcttt ctatgctcag
5821 catccttccc agggcaggga gccctcagc ccaccaatgg gtactaacca gatgctctc
5881 tccccacaca gctccaagac caaggtgtct acaaggccat gaatgaattt gacatcttca
5941 tcaactgcat agaagcatac atgatgatca aaatgaaaag ctaaaacacc tgcagtggtg
6001 attgagtctg ctggactcca ggacctagac agagctctct aaatctgatc cagggatctt
6061 agctaaccga aacaactcct tggaaaacct cgtttgtacc tctctccgaa atatttatta
6121 cctctgatac ctacgttccc attctattta ttactgagc ttctctgtga actatttaga
6181 aagaagccca atattataat ttacagtat ttattatttt taacctgtgt ttaagctgtt
6241 tccattgggg acactttata gtattttaaag ggagattata ttatatgatg ggaggggttc
6301 ttcccttgga agcaattgaa gcttctattc taaggctggc cacacttgag agctgcaggg
6361 cctcttgcta tgggtctctt tcaattgtct tcatccctga gtccagagct cctaagagag
6421 ttgtgaagaa actcatgggt cttgggaaga gaaaccaggg agatcctttg atgatcattc
6481 ctgcagcagc tcagaggggt cccctactgt catccccag ccgcttcac cctgaaaact
6541 gtggccagtt tgttatttat aaccacctaa aattagttct aatagaactc atttttaact
6601 agaagtaatg caattcctct gggaaatgtg tattgtttgt ctgcctttgt agcagactct
6661 aattttgaat aaatggatct tattcgaatt acagtgtggg gtctattgag ttctgtctga
6721 tttaaaagaa aaatccctta aaattccaga gggcagaagc agtgaatctt agactccaca
6781 aaaagaatgc cagcaacctc tccaggaagg ggttgagctc ggatcagatc agaggaaggt
6841 cttgcctggc tttcaaagca tcagcataaa ctactgatat cttcaagctc agtcccttaa
6901 aatgtgtcct gaaaccttaa aaggcattct accttccaaa gctagggaag gtgattctaa
6961 gtaaccatcg gaaggaaagt ggaagcatca aagctgaaac tctgagacga aatgttgggg
7021 ttaaaaatgg aagctagggg caggaggggtg gggagatggc tcagcagtta gagtgtgtgc
7081 cggcaccagt gagacaggag ttcatatcct tggaatccaa ccaacacaca accaacacta
7141 ggcaagagat gcctaagtgt tcagtgggtg cttcaagctc cagaggtcct ggggtgaact
7201 tagatcc

```

## (2) INFORMATION FOR SEQ ID NO:70:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3632 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```

1 aaagagctgg aggcgcgcag gccggctccg ctccggcccc ggacgatgcg gcgcgccag
61 gatgctgccg tgcctcgtag tgcgtctggc ggcgctcttc agcctccgtc ttggctcaga
121 cgctcatggg acagagctgc ccagccctcc gtctgtgtgg tttgaagcag aatttttcca
181 ccacatcctc cactggacac ccattccaaa tcagtctgaa agtacctgct atgaagtggc
241 gctcctgagg tatggaatag agtccctgga ctccatctcc aactgtagcc agaccctgtc
301 ctatgacctt accgcagtga ccttggacct gtaccacagc aatggctacc gggccagagt
361 cggggctgtg gacggcagcc ggcactccaa ctggaccgtc accaacaccc gcttctctgt
421 ggatgaagtg actctgacag ttggcagtgt gaacctagag atccacaatg gcttcatcct
481 cgggaagatt cagctaccca ggcccaagat ggcccccgcg aatgacacat atgaaagcat
541 cttcagtcac ttccgagagt atgagattgc cattcgcaag gtgcccggaa acttcacgtt
601 cacacacaag aaagtaaaac atgaaaactt cagcctccta acctctggag aagtgggaga
661 gttctgtgtc caggtgaaac catctgtctc ttcccgaagt aacaagggga tgtgtgttaa
721 agaggagtgc atctccctca ccaggcagta ttaccctgtg accaacgtca tcatcttctt
781 tgcctttgtc ctgctgtctt ccggagccct cgcctactgc ctggccctcc agctgtatgt
841 gcggcgccga aagaagctac ccagtgtcct gctcttcaag aagcccagcc ccttcatctt
901 catcagccag gctccctccc cagagaccca agacaccatc caccctgttg atgaggaggc
961 ctttttgaag gtgtccccag agctgaagaa cttggacctg cacggcagca cagacagtgg
1021 ctttggcagc accaagccat ccctgcagac tgaagagccc cagtctctcc tccctgaccc
1081 tcacccccag gctgacagaa cgctgggaaa cggggagccc cctgtgtctg gggacagctg
1141 cagttagtgg agcagcaata gcacagacag cgggatctgc ctgcaggagc ccagcttagg
1201 cccagcacca gggccacact gggagcaaca ggtggggagc aacagcaggg ccaggatgga
1261 cagtggcatt gacttagttc aaaactctga gggccgggct ggggacacac aggggtggctc
1321 ggccttgggc caccacagtc ccccgagacc tgaggtgcct ggggaagaag acccagctgc
1381 tgtggcattc cagggttacc tgaggcagac cagatgtgct gaagagaagg caaccaagac
1441 aggtgcctg gaggaagaat cgcccttgac agatggcctt ggcccaaat tcgggagatg
1501 cctggttgat gaggcaggct tgcatccacc agccctggcc aagggctatt tgaacagga
1561 tcccttagaa atgactctgg cttcctcagg ggcaccaacg ggacagtgga accagcccac
1621 tgaggaaatg tactcctgg ccttgagcag ctgcagtgac ctgggaatat ctgactggag
1681 ctttggccat gaccttgccc ctctaggctg tgtggcagcc ccagggtggtc tcttgggcag

```

```
1741 ctttaactca gacctggtca cctgccccct catctctagc ctgcagtcaa gtgagtgact
1801 cgggctgaga ggctgctttt gatttttagcc atgcttgcctc ctctgcttgg accaggagga
1861 gggccctggg gcagaagttt ggacagaggg agtctgggca cttttctgca agtccactgg
1921 ggctggccca gccaggctgc agggctggtc aggggtgtctg gggcaggagg aggccaaactc
1981 actgaactag tgcagggtat gtgggtggca ctgacctgtt ctgttgactg gggccctgca
2041 gactctggca gagctgagaa gggcaggggac cttctccctc ctaggaactc tttcctgtat
2101 cataaaggat tatttgctca ggggaacctat ggggctttct ggagtgtgtg tgaggccacc
2161 aggctgaagt cagctcagac ccagacctcc ctgcttaggc cactcgagca tcagagcttc
2221 cagcaggagg aagggtgta ggaatggaag cttcaggggc ttgctgctgg ggtcattttt
2281 aggggaaaaa ggagatatg atggtcacat ggggaacctc ccctcatcgg gcctctgggg
2341 caggaagctt gtcactggaa gatcttaagg tataatattt ctggacactc aaacacatca
2401 taatggattc actgaggga gacaaaggga gccgagacc tggatggggc tccagctca
2461 gaacccatcc ctctgttggg tacctctggc acccatctgc aaatatctcc ctctctccaa
2521 caaatggagt agcatcccc tggggcactt gctgaggcca agccactcac atcctcactt
2581 tgctgcccc ccatcttgc gacaacttcc agagaagcca tggtttttg tatttggtcat
2641 aactcagccc tttggcgcc cttctgggctt gggcaccagc tcatgccagc cccagagggt
2701 cagggttggg ggcctgtgct tgtgtttgct gctaattgtc agctacagac ccagaggata
2761 agccactggg cactgggctg gggccctgc cttgttgggtg ttcagctgtg tgattttgga
2821 ctagccactt gtcagagggc ctcaatctcc catctgtgaa ataaggactc caccttttagg
2881 ggaccctcca tgtttctggt gtattagcca agctggctct gggagaatgc agatactgtc
2941 cgtggactac caagctggct tgtttcttat gccagaggct aacagatcca atgggagtc
3001 atggtgtcat gccaaagacg tatcagacac agccccagaa gggggcatta tgggccccgc
3061 ctccccatag gccatttggg cttctgcctc aaacaaaggc agttcagtc acaggcatgg
3121 aagctgtgag gggacaggcc tgtgcgtgcc atccagagtc atctcagccc tgcctttctc
3181 tggagcattc tgaaaacaga tattctggcc cagggaatcc agccatgacc cccacccctc
3241 tgccaaagta ctcttaggtg ccagtctggt aactgaactc cctctggagg caggcttgag
3301 ggaggattcc tcagggttcc cttgaaagct ttattttatt attttgttca tttatttatt
3361 ggagaggcag cattgcacag tgaaagaatt ctggatatct caggagcccc gaaattctag
3421 ctctgacttt gctgtttcca gtggtatgac cttggagaag tcacttatcc tcttgagacc
3481 tcagtttctc catctgcaga ataagtactg acttgtctaa ttcataggga tgtgaggttc
3541 tgctgaggaa atgggtatga atgtgccttg aacacaaagc tctgtcaata agtgatacat
3601 gttttttatt ccaataaatt gtcaagacca ca
```

## (2) INFORMATION FOR SEQ ID NO:71:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

```
1 gctgtagctg gtgagaggaa gtcctagagg ctatggacac tctgctgctg ggatcaccga
61 gatgagcagc agctgctcag ggctgagcag ggtcctggtg gccgtggcta cagccctggt
121 gtctgcctcc tccccctgcc ccaggcctg gggcccccca ggggtccagt atgggcagcc
181 agggagggtcc gtgaagctgt gttgtcctgg agtgactgcc ggggacccag tgcctctggt
241 tcgggatggg gagccaaagc tgctccaggg acctgactct gggctagggc atgaactggt
301 cctggccccg gcagacagca ctgatgaggg cacctacatc tggcagacc tggatggtgc
361 acttgggggc acagtgaccc tgcagctggg ctaccctcca gcccgccctg ttgtctcctg
421 ccaagcagcc gactatgaga acttctcttg cacttgaggt cccagccaga tcagcggttt
481 acccaccgcg tacctcacct cctacaggaa gaagacagtc ctaggagctg atagccagag
541 gaggagtcca tccacagggc cctggccatg cccacaggat cccctagggt ctgcccgtg
601 tgttgtccac ggggctgagt tctggagcca gtaccggatt aatgtgactg aggtgaaccc
661 actgggtgcc agcacagcc tgctggatgt gagcttgtag agcatcttgc gccctgaccc
721 accccagggc ctgcggttag agtcagtacc aggttaccct cgacgcctgc gagccagctg
781 gacataccct gcctcctggc cgtgccagcc ccacttctg ctcaagttcc gtttgagta
841 ccgtccggcg cagcatccag cctggtccac ggtggagcca gctggactgg aggaggtgat
901 cacagatgct gtggctgggc tgccccatgc tgtacgagtc agtgcccggt actttctaga
961 tgctggcacc tggagcacct ggagcccgga ggcctgggga actccgagca ctgggaccat
1021 accaaaggag ataccagcat ggggcagct acacacgag ccagagggtg agcctcaggt
1081 ggacagccct gctctccaa ggcctccct ccaaccacac cctcggtac ttgatcacag
1141 ggactctgtg gagcaggtag ctgtgctggc gtctttggga atcctttctt tcttgggact
1201 ggtggctggg gccctggcac tggggctctg gctgaggctg agacggggtg ggaaggatgg
1261 atccccaaag cctgggttct tggcctcagt gattccagtg gacaggcgct caggagctcc
1321 aaacctgtag aggaccagg agggcttcgg cagattccac ctataattct gcttctgtg
1381 tgtggataga aaccaggcag gacagtagat ccctatggtt ggatctcagc tggaaagttct
1441 gtttgagacc catttctgtg agaccctgta tttcaaattt gcagctgaaa ggtgcttgta
1501 cctctgattt caccacagag ttggagttct gctcaaggaa cgtgtgtaat gtgtacatct
1561 gtgtccatgt gtgaccatgt gtctgtgaag gccagggaac atgtattcct ctgcatgcat
1621 gtatgtaggt gcctgggagt gtgtgtggtc cttgctctg gcccttccct tgcagggttg
1681 tgcagggtgt aataaaa
```

## (2) INFORMATION FOR SEQ ID NO:72:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1682 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```
1 ggaagatgag cagcagctgc tcagggtga gcagggtcct ggtggccgtg gctacagccc
61 tgggtgtctgc ctctccccc tgcctccagg cctggggccc cccaggggtc cagtatgggc
121 agccaggcag gtcctgtaag ctgtgtgtgc ctggagtga cgcgggggac ccagtgtcct
181 ggttttcgga tggggagcca aagctgtctc agggacctga ctctgggcta gggcatgaac
241 tggctcctgg ccaggcagac agcactgatg agggcaccta catctgccag accctggatg
301 gtgcacttgg gggcacagt accctgcagc tgggctaccc tccagcccgc cctgtgtct
361 cctgccaaag agccgactat gagaacttct cttgcacttg gagtcccagc cagatcagcg
421 gtttaccac cgcctacctc acctcctaca ggaagaagac agtcctagga gctgatagcc
481 agaggaggag tccatccaca gggccctggc catgcccaca ggatccccta ggggtgccc
541 gctgtgtgt ccacggggct gaggctctga gccagtagcg gattaatgtg actgagggtg
601 acccactggg tgccagcaca cgcctgtctg atgtgagctt gcagagcatt ttgcccctg
661 acccacccca gggcctgcgg gtgagtcag taccaggtta ccccgagcg ctgcgagcca
721 gctggacata ccctgcctcc tggcctggcc agcccactt cctgctcaag ttccgtttgc
781 agtaccgtcc ggcgcagcat ccagcctggt ccacggtgga gccagctgga ctggaggagg
841 tgatcacaga tgctgtggct gggctgcccc atgctgtacg agtcagtgcc cgggacttcc
901 tagatgctgg cactggagc acctggagcc cggaggcctg gggaactccg agcactggga
961 ccataccaaa ggagatacca gcatggggcc agctacacac gcagccagag gtggagcctc
1021 aggtggacag ccctgtcctt ccaaggccct ccctccaacc acaccctcgg ctacttgatc
1081 acagggactc tgtggagcag gtatgtgtgc tggcgtcttt gggaatcctt tcttctctgg
1141 gactggtggc tggggccctg gcaactggggc tctggctgag gctgagacgg ggtgggaagg
1201 atggatcccc aaagcctggg ttcttggcct cagtgtatcc agtggacagg cgtccaggag
1261 ctccaaacct gttagagacc caggagggtt tcggcagatt ccacctataa ttctgtcttg
1321 ctggtgtgga tagaaaccag gcaggacagt agatccctat ggttggatct cagctggaag
1381 ttctgtttgg agccatttcc tgtgagaccc tgtatttcaa atttcagct gaaagggtct
1441 tctacctctg atttcacccc agagtgtggg ttctgtctca ggaacgtgtg taatgtgtac
1501 atctgtgtcc atgtgtgacc atgtgtctgt gaggcaggga acatgtattc tctgcatgca
1561 tgatgttagg tgcctgggga gtgtgtgtgg gtccttggct cttggccttt ccttcaggg
1621 gttgtgcagg tgtgaataaa gagaataagg aagttcttgg agattatact cagaaaaaaa
1681 aa
```

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 413 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```
1 tctgtggagc aggtagctgt gctggcgtct ttgggaatcc tttcttctct gggactgggtg
61 gctggggccc tggcactggg gctctggtta gtgactgcca ttggtccctc agcctctgat
121 cctcacacat gctctgatgc ccatagacca cattcatctc cacccttcat gactgcctgc
181 tgaacctgtc tgattctgga actacctccc catacctcca tcccctatgc cccacttgat
241 tttaactgat tctctctctg accttttact aataaacctt ttggcggaga ctgagataac
301 ccacattggt ggagagacag ctgcctttct atgccccagg ctgaggtctg gacggggtgg
361 gaaggatgga tcccaaaagc ctgggttctt ggccctcagt attccagtgg aca
```

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3791 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```
1 gctgtagctg gtgagaggaa gtccatagagg ctatggacac tctgtctgtg ggatcaccga
61 gatgagcagc agctgtctag ggtgagcag ggtcctgggt gccgtggcta cagccctggt
121 gtctgcctcc tccccctgcc cccaggcctg gggcccccca ggggtccagt atgggcagcc
181 agggagggtcc gtgaagctgt gttgtcctgg agtgactgcc ggggaccagc tgcctgtgtt
241 tcgggatggg gagccaaagc tgctccaggg acctgactct gggctagggc atgaactggt
301 cctggcccaag gcagacagca ctgatgaggg cacctacatc tgccagaccc tggatgggtc
361 acttgggggc acagtgacc tgcagctggg ctaccctcca gcccgccctg ttgtctcctg
421 ccaagcagcc gactatgaga acttctcttg cacttggagt cccagccaga tcagcgggtt
481 acccaccgcg tacctcacct cctacaggaa gaagacagtc ctaggagctg atagccagag
541 gaggagtcca tccacagggc cctggccatg cccacaggat cccctagggg ctgcccgtg
601 tgttgtccac ggggtgtagt tctggagcca gtaccggatt aatgtgactg aggtgaacct
661 actgggtgcc agcacagcc tgctggatgt gacttgcag agcatcttc gccctgacct
721 acccagggc ctgcgggtag agtcagtacc aggttaccct cgacgcctgc gagccagctg
781 gacataacct gcctcctggc cgtgccagcc ccaacttctg ctcaagtcc gtttgcagta
841 ccgtccggcg cagcatccag cctgggtccac ggtggagcca gctggactgg aggggtgat
901 cacagatgct gtggctgggc tgccccatgc tgtacgagtc agtgcccggg acttctaga
961 tcttggcacc tggagacct ggagcccagg gccctgggga actccgagca ctgggacct
1021 accaaaggag ataccagcat ggggccagct acacacgcag ccagaggtgg agcctcaggt
1081 ggacagccct gctcctccaa ggcctccct ccaaccacac cctcggctac ttgatcacag
1141 ggactctgtg gagcaggtag ctgtgtgtgg gtctttggga atccttctt tcttgggact
1201 ggtggctggg gccctggcac tggggctctg gctgaggctg agacggggtg ggaaggatgg
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1261 atccccaag cctgggttct tggcctcagt gattccagtg gacaggcgtc caggagctcc
1321 aaacctgtag aggacccagg agggcttcgg cagattccac ctataattct gtcttgctgg
1381 tgtgtagata aaccaggcag gacagtagat ccctatgggt ggatctcagc tggaagtctt
1441 gtttgagacc catttctgtg agacctgtga tttaaattt gcagctgaaa ggtgcttgta
1501 cctctgattt caccacagag ttggagttct gctcaaggaa cgtgtgtaat gtgtacatct
1561 gtgtccatgt gtgaccatgt gtctgtgaag gccagggaac atgtattcct ctgcatgcat
1621 gtatgtaggt gcctgggagt gtgtgtggtc cttgctctgg ccccttccct tgcagggttg
1681 tgcagggtgtg aataaa
1 ggaagatgag cagcagctgc tcagggtcga gcagggtcct ggtggccgtg gctacagccc
61 tgggtgtctgc ctctccccc tgcccccagg cctggggccc cccaggggtc cagtatgggc
121 agccaggcag gtcctgtaag ctgtgtgtgc ctggagtac tgccggggac ccagtgtcct
181 ggtttcggga tggggagcca aagctgtctc agggacctga ctctgggcta gggcatgaac
241 tggctctggc ccaggcagac agcactgatg agggcaccta catctgccag accctggatg
301 gtgcacttgg gggcacagtg accctgcagc tgggctaccc tccagcccgc cctgttgtct
361 cctgccaagc agccgactat gagaacttct cttgcacttg gattccacag cagatcagcg
421 gtttaccac ccgctacctc acctctaca ggaagaagac agtcctagga gctgatagcc
481 agaggaggag tccatccaca gggccctggc catgccaca gggtcctccc
541 gctgtgtgtt ccacggggct gaggttctga gccagtaccg gattaatgtg actgagtgta
601 acccactggg tgccagcaca cgcctgtctg atgtgagctt gcagagcatc ttgcgccttg
661 accaccccca gggcctgcgg gtagagttag taccagggtt ccccgacgc ctgcagacca
721 gctggacata ccctgcctcc tggcctggcc agcccactt cctgtctaac ttccgtttgc
781 agtacgctcc ggcgcagcat ccagcctggt ccacggttga gccagcttga ctggaggagg
841 tgatcacaga tctgtgtgct gggctgcccc atgctgtacg agtcagtggc cgggactttc
901 tagatgctgg cacttgagc acctggagcc cggaggcctg gggaactccg agcactggga
961 ccataccaaa ggagatacca gcatggggcc agctacacac gcagccagag gtggagcctc
1021 aggtggacag ccctgtcctt ccaaggccct ccctccaacc acaccctcgg ctacttgatc
1081 acagggactc tgtggagcag gtagctgtgc tggcgtcttt gggaatcctt tcttctctgg
1141 gactggtggc tggggccctg gcactggggc tctggctgag gctgagacgg ggtgggaagg
1201 atggtatccc aaagcctggg ttcttggcct cagtgtattc agtggacagg cgtccaggag
1261 ctccaaacct gttagggacc caggagggtc tcggcagatt ccacctataa ttctgtcttg
1321 ctgtgttggg tagaaaccag gcaggacagt agatccctat ggttggatct cagctggaag
1381 ttctgtttgg agccccattt tgtgagaccc tgtatttcaa atttgagct gaaaggtgct
1441 tctacctctg atttcacccc agagttggag ttctgtcaa ggaacgtgtg taatgtgtac
1501 atctgtgtcc atgtgtgacc atgtgtctgt gaggcaggga acatgtattc tctgcatgca
1561 tgtatgtagg tgccctggga gtgtgtgtgg gtccttggct cttggccttt ccttgagggg
1621 gttgtgcagg tgtgaataaa gagaataagg aagtctcttg agattatact cagaaaaaaa
1681 aa
1 tctgtggagc aggtagctgt gctggcgtct ttgggaatcc tttctttcct gggactgggtg
61 gctggggccc tggcactggg gctctggtta gtgactgcca ttggtccctc agcctctgat
121 cctcacacat gctctgatgc ccatagacca cattcatctc cacccttctg cactctctgc
181 tgaacctgtc tgattctgga actacctccc catacctcca tcccctatgc cccacttgat
241 ttttaactgat tctctctctg accctttact aataaacctt ttggcgga ctgagataac
301 ccacattggt ggagagacag ctgcctttct atgccccagg ctgaggctga gacggggtgg
361 gaaggatgga tccccaaagc ctgggttctt ggcctcagtg attccagtg aca

```

## (2) INFORMATION FOR SEQ ID NO:75:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 762 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

```

1 atgtggcccc ctgggtcagc ctcccagcca ccgccctcac ctgccgaggc cacaggtctg
61 atcccagcgg ctgcgcctgt gtcctgcagc tgccggctca gcatgtgtcc agcgcgcagc
121 ctctcctctg tggctaccct ggtcctctcg gaccacctca gtttggcag aaacctcccc
181 gtggccactc cagacccagg aatgttccca tgccttcacc actcccaaaa cctgtgagg
241 gccgtcagca acatgctcca gaaggccaga caaactctag aattttacc ttgcacttct
301 gaagagattg atcatgaaga tatcacaaa gataaaaacca gcacagtgga ggctgttta
361 ccattggaat taaccaagaa tgagagtgtc ctaaattcca gagagacctc ttccataact
421 aatgggagtt gcctggcctc cagaaagacc tcttttatga tggccctgtg ccttagtagt
481 atttatgaag acttgaagat gtaccagtg gagttcaaga ccatgaatgc aaagcttctg
541 atggtatccta agaggcagat ctttctagat caaacatgc tggcagttat tgatgagctg
601 atgcaggccc tgaatttcaa cagttagact gtgccacaaa aatcctccct tgaagaaccg
661 gatttttata aaactaaaat caagctctgc atactttctc atgctttcag aattcgggca
721 gtgactattg atagagtgt gagctatctg aatgcttct aa

```

## (2) INFORMATION FOR SEQ ID NO:76:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2056 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```

1 aagcttcttt tgcataactg gcgctggatt ttactgaga ctttacgtta cagttttttt
61 tttttaaatt tcaagggtgt ttacgaaca catgaataaa atatttgtgt cattttgaac

```

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```
121 cttacttgct ttattttatg catgtattta tttatggggg ggcacaagga ctcatctgtg
181 gtgggtgcagc cactgtaaat aaattagtga aactacttca cgtcaatttc tgttcagtac
241 acttttagtga tggatcgag gaaattaata catgtttaca aaaagccccc cccccagttg
301 ttacatatgc ctacagagata ccagttgtga aaagtgcagg tgcacttaca cacatacgca
361 cacacacccc acaaatggta tcatacgaaa aaacatacct gcaatctgat ttgtccactt
421 aattgtatat cttggataga gaacttgttt cactgggaagg ctaaaaggca aagtctgggg
481 aggcctagag gacacagggg atgggaggag gcgctctgag ctggatgtaa ggtctccacc
541 cacggccaga gcacaaggtc ggataaccag tgggctgccc ggcttggtg cctgggccct
601 cccctgccga gacaaacggc tggagggagg aagtgtgcgg ctgggaagct ccgctgctct
661 ggcccgggtt tcccatttcc ccttcccgc gctgagacgg cgaggaaagt tagcccgaa
721 atctgcgccc gcctaaaacc cggcctggtc ccagccaccg cccaggaac tccccccacc
781 gcaggggcgg aggtcgagag cagggatgga gaagtggacc tgcgcggtg gactccgggg
841 cgcggtgga ctccggggcg cggggggact ccgaggagcg ggtggactgt gggcgcggg
901 taccgtctcg cagcgacctc tgcggcgccg tctggggatg gcccgcattc gtctgcgtgt
961 acctggtata cgtgcaggta catgttcttg ttacgtgca gactgggagg gggatgggg
1021 ggtccacacc ggtgtacacc ttgtacatac tcttagcaac ttgaaattcc accacgagag
1081 atattcttat tccgctattc ctgtgcatct gcacggagcc cctagggcca tagatttgtg
1141 tgcaaatgaa atgaggatgt agtctgggtg cccaaggggg ggtgccttga gtgtggtgt
1201 ctgtatgcct ccctgaggtt atttaccttt ctgtcccat ccgcccctat gagcgagtac
1261 ctatgagcac aggatgtgca catatttgag tcttattagt ggtacacgca gttttatcat
1321 ctcccagggt ctgtgtctgt atgaaatgtg catgggtgtg tgtgtgcacg cgtgtgttcc
1381 cactcgggga atgtggggag aggtgcatgg agccaagatg ggtggtaaat agtatgtttc
1441 tgaaattaaa ggactaatgt ggaggaaggg gccccagatg tactaaaccc tttgccttca
1501 tctcatcctc tctgacttgg gaagaaccag gattttgttt ttaagccctt gggcatacag
1561 ttgttccatc ccgacatgaa ctacgctccc cgtctgaccg ccccttgccc ttcctttctc
1621 ctcatctgtt ggaacccagg gaatctgcct agtctgtctt ccaagcacct tggccatgat
1681 gtaaacccag agaaattagc atctccatct ccttccctat tccccacca aaagtcattt
1741 cctcttagtt cattacctgg gattttgatg tctatgttcc ctctcgtta ttgatacaca
1801 cacagagaga gacaaacaaa aaaggaactt cttgaaattc cccagaagg ttttgagagt
1861 tcttttcaat gttgcaacaa gtcagtttct agtttaagtt tccatcagaa aggagtagag
1921 tatataagtt ccagtaccag caacagcagc agaagaaaca acatctgttt caggggccatt
1981 ggactctccg tccctgccag agcaaggtaa gcacttccca agcccctacc tccctccctc
2041 cctgtggggc ctgcag
```

## (2) INFORMATION FOR SEQ ID NO:77:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1703 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```
1 gaattctcag acagcagcat tagaaggggc cttagagatc aaccatttct cttattttac
61 acacacctaa aactccctac agccgtgctt catcagcttc gagcagatga gccaccacaga
121 aggcagctcc agttattagg tectaggggc tgggtgtagt caggcccttt ggaagctcca
181 agtcagagat caaacacatc ctcccacta cccacgccta ggggtactaa tgctgtggg
241 aaaaaaact gaactaaaaa gtcccacagg aacctcaaac ccagcacatc caaaatggaa
301 attctcacca tctcctccaa actcagtcct cttatacagt aatccctgta aagctagaac
361 aatctccatt ccccattctc agggccttcc tctcccgctc acctgaggag ctaccaagcc
421 ttggccaca agcctcttga gagtccctcc tgcccacct gtgttctcca tactgaataa
481 ggacttggcc acaccttgtc aactcttccc tctgtcttac tctgacccc tggatcccc
541 catcatgcaa attctgccc atctcccgc taaaacccag gaagactccc cactactctc
601 agcacagaaa gtacactcct tagtatggca tcccctgccc tcatggcatg gcccatccag
661 cccctcagcc tcacaccctg caaggacacc tagaccccca cctccctcaa ccttcatga
721 ctgcgcttct gatccctgtt tcccctggct agaccctgcg tgccctcccg ctggaagcgg
781 tctaagcctt gcttgttttt aacactcagg ttggggcccc tgcctgctcc cgggagcctt
841 tgctgactcc tggaccccg tgcctccggt gagcgtgggc tcttctcta ggtcttctc
901 ccaggaactc tgtgtattca tctatcggt aaactggatt ctctacaaga gtaataattg
961 cagagtcagc cagctctcat cctttttag gtttcagaaa agacctgta acaaaacgcc
1021 ttgagtctga tttagtgtgg caatgcccga aggtcctgt tctccctggg tgcctgcac
1081 ctggtgcaac gtcggccttg catctagtga gccatctaaa ggaacgatga tgagtgaatg
1141 atttgcttac ccttccagt actaggcttg aggtcgtggg tagggcccat ccctacgcag
1201 gacatgcaaa gtgggaggca ctctctctc tacctcgcca gggggcgctg cacagctgcg
1261 gggcggggta gcttagacac gggcgctccg gctaaggccg gggaccaggt ggtgtggcg
1321 ggggtgccc cccgctgtg gaccccgcg agtaactgcg aacatttcgc tttcattttg
1381 ggccgagctg gagcgggcgg ggccgtccc gaacggctgc ggccgggcac cccgggagtt
1441 aatccgaaag cgccgcaagc ccccgggggc ggccgcaccg cacgtgtcac cgagaagctg
1501 atgtagagag agacacagaa ggagacagaa agcaagagac cagagtcctc ggaaagctc
1561 gccgcgcctc gggacaatta taaaatgtg gcccctggg tcagcctccc agccaccgcc
1621 ctacactgcc gcggccacag gtctgcatcc agcggctcgc cctgtgtccc tgcagtgcg
1681 gctcagcatg tgtccagcgc gca
```

## (2) INFORMATION FOR SEQ ID NO:78:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4521 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```
1 atgtggcccc ctgggtcagc ctcccagcca ccgccctcac ctgccgcggc cacaggtctg
61 catccagcgg ctgcgcctgt gtccctgcag tgcgggtca gcatgtgtcc agcgcgcagc
121 ctccctcttg tggctacctt ggtccctctg gaccacctca gtttgccag aaacctcccc
181 gtggccactc cagaccagg aatgttccca tgccttcacc actcccaaaa cctgctgagg
241 gccgtcagca acatgtccca gaaggccaga caaactctag aattttacc ttgcacttct
301 gaagagattg atcatgaaga tatcacaaaa gataaaacca gcacagtgga ggcctgttta
361 ccattggaat taaccaagaa tgagagttgc cttaaattcca gagagacctc ttccataact
421 aatgggagtt gcctggcctc cagaaagacc tcttttatga tggccctgtg ccttagtagt
481 atttatgaag acttgaagat gtaccagggtg gagttcaaga ccatgaatgc aaagcttctg
541 atggatccta agaggcagat ctttctagat caaaacatgc tggcagttat tgatgagctg
601 atgcaggccc tgaatttcaa cagtgcagac gtgccacaaa aatcctccct tgaagaaccg
661 gatttttata aaactaaaat caagctctgc atacttcttc atgctttcag aattcgggca
721 gtgactattg atagagtgat gagctatctg aatgcttcct aa

1 aagcttcttt tgcataactg gcgctggatt tttactgaga ctttacgtta cagttttttt
61 tttttaaatt tcaagtgct tttacgaaca catgaataaa atatttgtgt cattttgaac
121 cttacttgtc ttattttatg catgtattta tttatggggg ggcacaagga ctcactgtgt
181 gtggtgcagc cactgtaaat aaattagtga aactacttca cgtcaatttc tgttcagtac
241 acttttagtg tggatcggag gaaattaata catgtttaca aaaagccctt cccccagttg
301 ttacatatgc ctacagagata ccagttgtga aaagtgcagg tgcacttaca cacatacgca
361 cacacacccc acaaatggta tcatacgaaa aaacatacct gcaatctgat ttgtccactt
421 aattgtatat cttggataca gaacttgttt cactggaagg ctaaaaggca aagtctgggg
481 aggcctagag gacacagggg atgggaggag gcgctctgag ctggatgtaa ggtctccacc
541 cacggccaga gcacaaggtc ggataaccag tgggcctgcc ggcttggtg cctgggccct
601 cccctgccga gacaaaaggc tggaggggagg aagtgtgcgg ctgggaagct ccgctgctct
661 ggccggggtt tcccatttcc cccttcccgc gctgagacgg cgaggaaagt tagcccgaa
721 atctgcgcc gcctaaaacc cggcctgttc ccagccaccg cccaggaac ttccccacc
781 gcaggggcgg aggtcgagag cagggatgga gaagtggacc tgcgcgggtg gactccgggg
841 cgcggggtga ctccggggcg cggggggact ccgaggagcg ggtggactgt ggggcgcggg
901 taccgtctcg cagcgacctc tgcggcgggc tctggggatg gcccgcact gtctgcgtgt
961 acctggtata cgtgcaggta catgttcctg ttcacgtgca gactggcgcg gggatggggg
1021 ggtccacacc ggtgtacacc tttgcatacc tcttagcaac ttgaaattcc accacgagag
1081 atactcttat tccgctattc ctgtgcatct gcacggagcc cctagggcca tagatttgtg
1141 tgcaaaatgaa atgaggatgt agtctgggtg ccaaaggggg ggtgccttga gtgtggttgt
1201 ctgtatgcct cctgagggtt atttcacttt ctgctcccat ccgccctat gagcgagtac
1261 ctatgagcac aggatgtgca catatttgag tcttattagt ggtacacgca gttttatcat
1321 ctccccaggt ctgtgtctgt atgaaatgtg catgggtgtg tgtgtgcacg cgtgtgttcc
1381 cactcgggga atgtggggag aggtgcatgg agccaagatg ggtggtaaat agtatgtttc
1441 tgaaattaaa ggactaatgt ggaggaaggc gccccagatg tactaaaccc tttgccttca
1501 tctcatcttc tctgacttgg gaagaaccag gattttgttt ttaagccctt gggcatacag
1561 ttgttccatc ccgacatgaa ctacgcctcc cgtctgaccg ccccttgccc tctctcttc
1621 ctcgatctgt ggaaccagg gaatctgcct agtctgtctt ccaagacctt tggccatgat
1681 gtaaacccag agaaattagc atctccatct ccttccctat tccccacca aaagtcattt
1741 cctcttagtt cattacctgg gattttgatg tctatgttcc ctctcgta ttgatacaca
1801 cacagagaga gacaaacaaa aaaggaactt cttgaaattc cccagaaagg ttttgagagt
1861 tgttttcaat gttgcaacaa gtcagtttct agtttaagtt tccatcagaa aggagtagag
1921 tatataagtt ccagtaccag caacagcagc agaagaaaca acatctgttt cagggccatt
1981 ggactctccg tctgcccag agcaaggtaa gcacttccca agccctacc tccctccct
2041 cctgtgggc ctgcag

1 gaattctcag acagcagcat tagaagggc cttagagatc aaccatttct cttattttac
61 acacacctaa aactccctac agcctgtgct catcagcttc gagcagatga gccaccacaga
121 aggcagctcc agttattagg tcttagggcc tgggtgtagt caggcccttt ggaagctcca
181 agtcagagat caaacacatc ctccccacta cccacgccta gggtagctaa tgctgtggg
241 aaaaacaact gaactaaaaa gtcccacagg aacctcaaac ccagcacatc caaaatggaa
301 cttctcacca tctctccaa actcagctct cttatacagt aatccctgta aagctagaac
361 aatctccatt cccattctc agggccttcc tctcccgctc acctgaggag ctaccaagcc
421 ttggcccaca agccctctga gagtccctcc tggccaccct gtgttctcca tactgaataa
481 ggacttggcc acacettgtc aactcttccc tctgctctac tctgacccc tggatcccc
541 catcatgcaa attctgccac atctcccgcc taaaaccag gaagactccc cactactctc
601 agcacagaaa gtacactcct tagtatggca tcccctgccc tcatggcatg gcccatccag
661 cctccagcc tcacaccctg caaggacacc tagaccccca cctccctcaa cccttcatga
721 ctgcgcttct gatccctgtt tcccctggct agaccctgcg tgcctcccg ctggaagcgg
781 tctaatagct gcttgttttt aacactcagg ttggggcccc tgcctgctcc cgggagcctt
841 tgctgactcc tggaccccg tgcctccggt gagcgtgggg tctttctcta ggtcttctct
901 cccaggactc tgtgtattca tctatcggt aaactggatt ctctacaaga gtaataattg
961 cagagtcagc cagctctcat cccttttcag gtttcagaaa agactctgta acaaaacgcc
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```

1021 ttgagtctga tttagtgtgg aaatgccccca aggggtcctgt tctccctggg tgcctctcac
1081 ctgggtgcaac gtcggcctgg catctagtga gccatctaaa ggaacgatga tgagtgaatg
1141 atttgcctac cccttccagt actaggctgg aggtcgtggt tagggcccat ccctacgcag
1201 gacatgcaaa gtgggagggca ctctctctc tacgtcggca gggggcgctg cacagctgcg
1261 gggcggggta gcttagacac ggggcgtccg gctaaggccg gggaccaggt gtgggtggcg
1321 ggggtgtccc cccgcctggg gaccccgccg agtaactgcg aacatttctc ttctattttg
1381 ggccgagctg gaggcgccgg ggccgtcccg gaacggctgc ggcggggcac cccgggagtt
1441 aatccgaaaag cgccgcaagc ccccgggggc ggccgcaccg cacgtgtcac cgagaagctg
1501 atgtagagag agacacagaa ggagacagaa agcaagagac cagagtcccc ggaaagtcct
1561 gccgcgcctc gggacaatta taaaatgtg gccccctggg tcagcctccc agccaccgcc
1621 ctcacctgcc gggccacag gtctgcatcc agcggctcgc cctgtgtccc tgcagtggcg
1681 gctcagcatg tgtccagcgc gca

```

## (2) INFORMATION FOR SEQ ID NO:79:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1742 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

```

1 caagcccgaga gccctgccat ttctgtgggc tcaggtccct actgtcagc cccttctccc
61 ctccggcaagg ccacaatgaa ccggggagtc ccttttaggc acttgcttct ggtgctgcaa
121 ctggcgctcc tcccagcagc cactcaggga aagaaagtgg tgctgggcaa aaaaggggat
181 acagtggaaac tgacctgtac agcttcccag aagaagagca tacaattcca ctggaaaaac
241 tccaaccaga taaagattct gggaaatcag ggctccttct taactaaagg tccatccaag
301 ctgaatgac gcgctgactc aagaagaagc ctttgggacc aaggaaactt cccctgatc
361 atcaagaatc ttaagataga agactcagat acttacatct gtgaagtggg ggaccagaag
421 gaggaggtgc aattgctagt gttcggattg actgccaact ctgacaccca cctgcttcag
481 gggcagagcc tgaccctgac cttggagagc cccctgggta gtgcccctc agtgcaatgt
541 aggagtccaa ggggtaaaaa catacagggg ggaagacccc tctccgtgtc tcagctggag
601 ctccaggata gtggcaccct gacatgcact gtcttgagca accagaagaa ggtggagtcc
661 aaaatagaca tcgtgtgtct agctttccag aaggcctcca gcatagtcta taagaaagag
721 ggggaacagg tggagtcttc ctccaccct gcctttacag ttgaaaagct gacgggcagt
781 ggcgagctgt ggtggcaggg gagaggggct tccctctcca agtcttgat cactttgac
841 ctgaagaaca aggaagtgtc tgtaaaacgg gttaccagg accctaagct ccagatgggc
901 aagaagctcc cgctccacct caccctgccc caggccttgc ctcagtatgc tggctctgga
961 aacctcacc tggcccttga agcgaataca ggaagtgtgc atcaggaagt gaacctggtg
1021 gtgatgagag ccactcagct ccagaaaaat ttgacctgtg aggtgtgggg acccacctcc
1081 cctaagctga tgctgagctt gaaactggag aacaaggagg caaaggctct gaagcgggag
1141 aaggcgggtg ggtgtctgaa ccctgaggcg gggatgtggc agtgtctgct gactgactcg
1201 ggacaggtcc tgctggaatc caacatcaag gttctgcccc catggtccac cccggtgcag
1261 ccaatggccc tgattgtgtg gggggcgctc gccggcctcc tgcttttcat tgggttaggc
1321 atcttcttct gtgtcaggtg ccggcaccca aggcgccaag cagagcgcat gtctcagtc
1381 aagagactcc tcagtgaaga gaagacctgc cagtgccttc accggtttca gaagacatgt
1441 agccccattt gaggcacgag gccaggcaga tcccacttgc agcctcccca ggtgtctgcc
1501 ccgcgtttcc tgcctgcgga ccagatgaat gtagcagatc ccacgctctg gcctcctgtt
1561 cgctcctccc acaatttgc attgtttctc ctgggttagg ccccggttc actggttagg
1621 tgttgccttc tagtttcag aggttaatc acaccgtcct ccacgccatt tccttttctt
1681 tcaagcctag cccttctctc attatttctc tctgacctc tcccactgc tcatttggat
1741 cc

```

## (2) INFORMATION FOR SEQ ID NO:80:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```

1 ctgccaactc tgacaccac ctgcttcagg ggcagagcct gaccctgacc ttggagagcc
61 cccctggtag tagccctca gtgcaatgta ggagtccaag gggtaaaaac atacaggggg
121 ggaagacct ctccgtgtct cagctggagc tccaggatag tggacacctg acatgcactg
181 ttttgcagaa ccagaagaag gtggagtcca aaatagacat cgtggtgcta gctttcc

```

## (2) INFORMATION FOR SEQ ID NO:81:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4040 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```

1 tgcagagac agagaaagga catctgcgag gaaagtcccc tgatggctgt caacaaagtg
61 ccacgtctct atggctgtgt acgtcgagca cagatttta tcgccttat catatcttgg
121 tgcataaacg cacctcacct cggtaacccc ttgtccgtc ttatgagaca ggctttatta
181 tccgcatttt atatgagggg aatctgacgg tggagagaga attatcttgc tcaaggcgac

```



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```

241 acagcagagc ccacaggtgg cagaatccca cccgagcccg cttcgaccgg cggggtggaa
301 accacggggc cccgcccggc tgcgttcca gagctgaact gagaagcgag tcctctccgc
361 cctgcggcca cccgcccagc cccgaccccg ccccgggccc atccctactc gccgccagct
421 ccccgcgccc accccggagt tgggtggcga gagcgggag gcgaggcgag gagggcgggc
481 gctggcaccg ggaacgccc agcgccgcca gagagcgag agagcgcgac acgtgcggcc
541 cagagcaccg gggccaccgg gtcccgcag gcccgggacc gcgcccgtg gcaggcgaca
601 cgtggaagaa tacggagtgc tataccagag ttgattgtg atggcacata cttttagagg
661 atgtcattg gcatattatg ttataatcac gtggtgtgtg attaaagcaa aaatagatgc
721 gtgcaagaga ggcgatgtga ctgtgaagcc ttcccatgta attttacttg gatccactgt
781 caataattaca tgctctttga agcccagaca aggcgtgctt cactattcca gacgtaacaa
841 gttaatcctg tacaagtttg acagaagaat caattttcac catggccact ccctcaattc
901 tcaagtcaca ggtcttcccc ttggtacaac cttgtttgtc tgcaaaactg cctgtatcaa
961 tagtgatgaa attcaaatat gtggagcaga gatcttcgtt ggtgttgctc cagaacagcc
1021 tcaaaattta tcctgcatac agaaggagga acaggggact gtggcctgca cctgggaaag
1081 aggcagagac acccacttat acactgagta tactctacag ctaagtggac caaaaaattt
1141 aacctggcag aagcaatgta aagacattta ttgtgactat ttggactttg gaatcaacct
1201 caccctgaa tcacctgaat ccaatttcac agccaagggt actgctgtca atagtcttgg
1261 aagctcctct tcacttccat ccacattcac attcttggac atagtggagc ctcttctccc
1321 gtgggacatt agaatacaat ttcaaaaggc ttccgtgagc agatgtacc tttattggag
1381 agatgagggg ctggtactgc ttaatcgact cagatatcg cccagtaaca gcaggctctg
1441 gaatatggtt aatgttacia aggccaaagg aagacatgat ttgctggatc tgaaccattt
1501 tacagaatat gaatttcaga tttcctctaa gctacatctt tataagggaa gttggagtga
1561 ttggagtga tcattgagag cacaacaccc agaagaagag cctactggga tgttagatgt
1621 ctggtacatg aaacggcaca ttgactacag tagacaacag atttctcttt tctggaagaa
1681 tctgagtgtc tcagaggcaa gaggaaaaat tctccactat caggtgacct tgcaggagct
1741 gacaggaggg aaagccatga cacagaacat cacaggacac acctcctgga ccacagtcat
1801 tcctagaacc ggaaattggg ctgtggctgt gtctgcagca aattcaaaag gcagttctct
1861 gccactcgt attaacataa tgaacctgtg tgaggcagg ttgctggctc ctggccaggt
1921 ctctgcaaac tcagagggca tggacaacat tctggtgact tggcagcctc ccaggaaaga
1981 tccctctgct gttcaggagt acgtggtgga atggagagag ctccatccag ggggtgacac
2041 acaggtccct ctaaactggc tacggagtgc accctacaat gtgtctgctc tgatttcaga
2101 gaacataaaa tcctacatct gttatgaaat ccgtgtgtat gcactctcag gggatcaagg
2161 aggatgcagc tccatcctgg gtaactctaa gcacaaagca ccactgagtg gcccccacat
2221 taatgccatc acagaggaaa aggggagcat ttaatttca tggaaacagca ttccagtcca
2281 ggagcaaatg ggctgcctcc tccattatag gatatactgg aaggaaacgg actccaactc
2341 ccagcctcag ctctgtgaaa ttccctacag agtctcccaa aattcacatc caataaacag
2401 cctgcagccc cgagtgcac atgtcctgtg gatgacagct ctgacagctg ctggtgaaa
2461 ttcccacgga aatgagaggg aattttgtct gcaaggtaaa gccaattggg tggcgtttgt
2521 ggcaccaagc atttgcattg ctatcatcat ggtgggcatt ttctcaacgc attacttcca
2581 gcaaaagggt tttgttctcc tagcagccct cagacctcag tgggtgtagc gagaaattcc
2641 agatccagca aatagcactt gcgctaagaa atatcccat gcagaggaga agacacagct
2701 gcccttggac aggtcctga tagactggc cagcctgaa gatcctgaac gctgtgcat
2761 cagtgaagtc cttcatcaag tgaccocagt tttcagacat cccctctgct ccaactggcc
2821 acaaaaggaa aaaggaatcc aaggtcatca ggctctgag aaagacatga tgcacagtgc
2881 ctcaagccca ccacctccaa gagctctcca agctgagagc agacaactgg tggatctgta
2941 caaggtgctg gagagcaggg gctccgacc aaagccagaa aaccagcct gtccctggac
3001 ggtgctccca gcaggtgacc ttcccaccca tgatggctac ttacctcca acatagatga
3061 cctccctcca catgaggcac ctctcgctga ctctctggaa gaactggagc ctccagcat
3121 ctccctttct gttttccct caagttctct tcacctactc accttctcct gtggtgataa
3181 gctgactctg gatcagttaa agatgaggtg tgactccctc atgctctgag tgggtgaggt
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3301 tgctccagca gctgtcatct ctgggtgcca ccacgtgctt gggtgcagct agaggacagg
3361 caagccagct ctgggggagt cttaggaact gggagttggt cttactcag atgcctcatc
3421 ttgcttttcc cagggcctta aaattacatc cttactgtg tggacctaga gactccaaact
3481 tgaattccta gtaactttct tggatgtgt gccagaaagg gaaatgagga ggagagtga
3541 aaccacagct cttagtagta atggcataca gtctagagga ccattcatgc aatgactatt
3601 tctaaagcac ctgctacaca gcaggctgta cacagcagat cagtactgtt caacagaact
3661 tcctgagatg atggaaatgt tctacctctg cactcactgt ccagtacatt agacactagg
3721 cacattggct gttaatcact tggatgtgt ttagcttgac tgaggaatta aattttgatt
3781 gtaaatthaa atcgccacac atggctagt gctactgtat tggagtgcac agctctagat
3841 ggtccttaga ttattgagag cctccaaaac aatcaacct agttctatg atgaagacat
3901 aaaagacact ggtaaacacc aatgtaaaag ggcccccaag gtggtcatga ctggtctcat
3961 ttgcagaagt ctaagaatgt acctttttct ggccgggctt ggtagctcat gcctgtaact
4021 ccagcacttt gggaggctga

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## (2) INFORMATION FOR SEQ ID NO:82:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6019 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```

1 caagccaga gccctgccat ttctgtggc tcaggtccct actgctcage ccttccctcc
61 ctgggcaagg ccacaatgaa ccggggagtc ctttttaggc acttgcttct ggtgctgcaa
121 ctggcgctcc tcccagcagc cactcaggga aagaaagtgg tgctgggcaa aaaaggggat

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181 acagtggaaac tgacctgtac agcttcccag aagaagagca tacaattcca ctggaaaaac  
241 tccaaccaga taaagattct gggaaatcag ggctccttct taactaaagg tccatccaag  
301 ctgaatgatc gcgctgactc aagaagaagc ctttgggacc aaggaaactt cccctgac  
361 atcaagaatc ttaagataga agactcagat acttatctct gtgaagtggg ggaccagaag  
421 gaggaggtgc aattgctagt gttcggattg actgccaact ctgacaccca cctgcttcag  
481 gggcagagcc tgacctgtac cttggagagc ccccttggtg ttagcccttc agtgcaatgt  
541 aggaagtccaa ggggtaaaaa catacagggg gggaaagacc tctccgtgtc tcagctggag  
601 ctccaggata ttggcacctg gacatgcaact gtcttgacaga accagaagaa ggtggagttc  
661 aaaatagaca tcgtggtgct agctttccag aaggcctcca gcatagtcta taagaaagag  
721 ggggaacagg tggagttctc cttcccactc gcctttacag ttgaaaagct gacgggcagt  
781 ggagagctgt ggtggcaggg ggagagggct tcctcctcca agtcttggat cacctttgac  
841 ctgaagaaca aggaagtgtc tgtaaaaagg gttaccagg accctaagg ccagatggg  
901 aagaagctcc cgctccacct caccctgccc caggccttgc ctcagtatgc tggctctgga  
961 aacctcacc tggcccttga agcgaataca ggaagtgtc atcaggaagt gaacctggtg  
1021 gtgatgagag cactcagct ccagaaaaat ttgacctgtg aggtgtgggg acccactcc  
1081 cctaagctga tgcgtgagctt gaaactggag aacaaggagg caaaggtctc gaagcgggag  
1141 aaggcgtgtg ggtgtgtgaa cctgtaggcg gggatgtggc agtgtctgtc gagtactc  
1201 ggacaggtcc tgctggaatc caacatcaag gttctgcccc catggtccac cccggtgcag  
1261 ccaatggccc tgattgtgct gggggcgctc gccggtctcc tgcttttcat tgggctaggg  
1321 atcttcttct gtgtcaggtg ccggcaccga agggcccaag cagagcggat gtctcagatc  
1381 aagagactcc tcagtggaga gaagactgc cagtgcctc accggtttca gaagacatgt  
1441 agccccattt gaggcacgag gccaggcaga tcccacttgc agcctcccca ggtgtctgcc  
1501 ccgctgttcc tgctgcgga ccagatgaat gtagcagatc ccacgtctgt gcctcctgtt  
1561 cgtctcctcc acaatttgcc attgtttctc ctgggttagg ccccggttcc actggttgag  
1621 tgtgtctctc tagtttccag aggtttaatc acaccgtcct ccacgccatt tcttttctc  
1681 tcaagcctag ccttctctc attatttctc tctgaccctc tcccactgc tcatttggat  
1741 cc

1 ctgccaactc tgacaccac ctgcttcagg ggcagagcct gaccctgacc ttggagagcc  
61 cccctggtag tagccctca gtgcaatgta ggagtccaag gggtaaaaa atacaggggg  
121 ggaagaccct ctccgtgtct cagctggagc tccaggatag tggcacctgg acatgcactg  
181 ttttgcagaa ccagaagaag gtggagttca aaatagacat cgtggtgcta gctttcc

1 tgcagagaa acagaaaagg catctgcag gaaagtctcc tgatggctgt caacaaagtg  
61 ccacgtctct atggctgtgt acgtgagca cacgatttta tgcgcctat catatcttgg  
121 tgcataaacg cactcacct cggtaacccc ttgctccgtc ttatgagaca ggctttatta  
181 tccgcatttt atatgagggg aatctgacgg tggagagaga attatcttgc tcaaggcgac  
241 acagcagagc ccacaggttg cagaatccca cccagagccg cttcgaccgg cggggtggaa  
301 accaggggag cccgcccggc tgctgttcca gagctgaact gagaagcgag tctctccgc  
361 cctgcccga ccccccagcc ccgacccccc ccccgccccc atcctcactg gccgccagct  
421 ccccgccccc accccggagt tgggtggcga gaggcgggag gcggagggcg gaggggggg  
481 gctggcaccg ggaacgcccg agcgccggca gagagcgagg agagcgggcc acgtgcccgc  
541 cagagcaccg gggccaccgg gtcccgcgag gcccgggacc gcgcccgtg gcaggcgaca  
601 cgtggaagaa tacggagttc tataccagag ttgattgttg atggcacata cttttagagg  
661 atgctcattg gcatttatgt ttataatcac gtggctgttg attaaagcaa aaatagatgc  
721 gtgcaagaga ggcgatgtga ctgtgaagcc ttcccatgta attttacttg gatccactgt  
781 caatattaca tgctctttga agcccagaca aggtgtgttt cactattcca gacgtaacaa  
841 gttaatctcg tacaagtttg acagaagaat caattttcac catggccact cctcaattc  
901 tcaagtcaca ggtcttcccc ttggtacaac cttgtttgtc tgcaaaactgg cctgtatcaa  
961 tagtgatgaa attcaaatat gtggagcaga gatcttctgt ggtgtgtctc cagaacagcc  
1021 tcaaaattta tctgcatac agaagggaga acaggggact gtggcctgca cctgggaaag  
1081 aggcagagac acccacttat acactgagta tactctacag ctaagtggac caaaaaattt  
1141 aacctggcag aagcaatgta aagacattta ttgtgactat ttggactttg gaatcaacct  
1201 caccctgaa tcacctgaat ccaatttcac agccaaggtt actgctgtca atagtcttgg  
1261 aagctcctct tcaattccat ccacattcac attcttggac atagtggagc ctcttctcc  
1321 gtgggacatt agaattcaat ttcaaaaggc ttccgtgagc agatgtaccc tttattggag  
1381 agatgagggg ctggtactgc ttaatcgact cagatatcgg cccagtaaca gcaggctctg  
1441 gaatatggtt aatgttacaa aggccaaggg aagacatgat ttgctggatc tgaaccatt  
1501 tacagaatat gaatttcaga ttctctctaa gctacatctt tataagggaa gttggagtga  
1561 ttggagtga tcattgagag cacaacacc agaagaagag cctactggga tgttagatgt  
1621 ctggtacatg aaacggcaca ttgactacag tagacaacag atttctctt tctggaagaa  
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1861 gccactcgt attaacataa tgaacctgtg tgaggcaggg ttgctggctc ctcgaggt  
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1981 tccctctgct gttcaggagt acgtggtgga atggagagag ctccatccag ggggtgacac  
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2101 gaacataaaa tctacatct gttatgaaat ccgtgtgtat gcactctcag gggatcaagg  
2161 aggatgcagc tccatcctgg gtaactctaa gcacaaagca ccactgagt gccccacat  
2221 taatgccatc acagaggaaa aggggagcat tttaatttca tggaaacagc ttcagttcca  
2281 ggagcaaatg ggtgcctcc tccattatag gatatactgg aaggaaacgg actccaactc  
2341 ccagcctcag ctctgtgaaa ttccctacag agtctcccaa aattcacatc caataaacag  
2401 cctgcagccc cgagtgcac atgtcctgtg gatgacagct ctgacagctg ctggtgaaag  
2461 tccccacgga aatgagaggg aattttgtct gcaaggtaaa gccaatttga tggcgtttgt  
2521 ggcaccaagc atttgcatg ctatcatcat ggtgggcatt ttctcaacgc attacttcca  
2581 gcaaaagggtg tttgttctcc tagcagccct cagacctcag tgggtgtagc gagaaattcc

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2641 agatccagca aatagcactt gcgctaagaa atatccatt gcagaggaga agacacagct  
2701 gcccttgagc aggcctcctga tagactggcc cagcctgaa gatcctgaa cgctggctat  
2761 cagtgaagtc ctccatcaag tgacccagc ttcagacat ccccccctgct ccaactggcc  
2821 acaaaaggaa aaaggaatcc aaggtcatca ggctctgag aaagacatga tgcacagtgc  
2881 ctcaagccca ccacctccaa gagctctcca agctgagagc agacaactgg tggatctgta  
2941 caaggtgctg gagagcaggg gctccgaccc aaagccagaa aaccagcct gtccttgagc  
3001 ggtgctccca gcaggtgacc tcccaccca tgatggctac ttaccctcca acatagatga  
3061 cctcccctca catgaggcac ctctcgctga ctctctggaa gaactggagc ctcagcacat  
3121 ctccctttct gttttccctt caagttctct tcaccactc acctctcct gtggtgataa  
3181 gctgactctg gatcagttaa agatgagggtg tgaactcctc atgctctgag tggtagaggct  
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3301 tgctccagca gctgctatct ctgggtgcca ccacgggtct ggctgcagct agaggacagg  
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3421 ttgcttttcc cagggcctta aaattacatc cttactgtg tggacatga gactccaatc  
3481 tgaattctta gtaactttct tggtagctg gccagaaagg gaaatgagga ggagagtaga  
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3661 tcctgagatg atggaaatgt tctacctctg cactcactgt ccagtacatt agacactagg  
3721 cacattggct gtaatacact tggaaatgtt ttagcttgac tgaggaatta aattttgatt  
3781 gtaaatttta atcgccacac atggctagtg gctactgtat tggagtgcac agctctagat  
3841 ggctcctaga ttattgagag cctccaaaac aaatcaacct agttctatag atgaagacat  
3901 aaaagacact ggtaaacacc aatgtaaaag ggccccaag gtggtcatga ctggtctcat  
3961 ttgcagaagt ctaagaatgt acctttttct ggcgggctg gtagctcat gcctgtaac  
4021 ccagcacttt gggaggctga

## (2) INFORMATION FOR SEQ ID NO:83:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5670 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

1 ggatccccgc tgacaatcta gaaacaagca acagaccctc tgatgtagcc atctgtgccg  
61 cgctctccgc caccgcccgc cagccttggt tccctggaga ccacctcca gggcaggggc  
121 tgccgctcgg ccgggcccgc ggggtccctc ggctgacat ggccggtgct ggagcggcac  
181 gtgcgcgcct cggcccctcg gccgctcccg cccctcgccg gtgcgcaccg gcgctcgggg  
241 agccgctggc ccgggtgtcc agccggccct tgcctgctt ggctgctgga ccgccacctt  
301 tgccgcccc cgcgcagcct ccgagcttcc cagactggcc ggtctgcgcg cccacctctg  
361 cctcccggac cggccaccgc cggaggccgc ggaggagggc ccggccgcgc agatcccgt  
421 tatcggggcc catctcccgt tacataaggc caccacctta tctccgcccg ccacgcccgc  
481 cgcaaccgcc gcgccagcgc cttctccac gcgcgggggc gcccctgccc accgctccc  
541 gcagggtttt tgggtggccat gggggataag gggcgtagc tcaccgggc ggggtcccg  
601 gagttgcaca gaccaaggta gttcccgcct cctccccc cccagggag cctgtgggag  
661 atgcccgtgg ccctctacta cagattagga aacaggcccg tagaggggtc gcgcggccaa  
721 gtagcggcac tcaggcact gggggccctc gagggaagg gcagacttct gggagtcaag  
781 gccagcagct gggctgggaa gcttcgagtg tggacagaga ggggtgggaa gacgttccct  
841 gttgggaagg aggggtggga agcttggtg gcctctgagc gggaatccag catgccttgt  
901 gaggagggtc acaagcacac ccttgtgagg aggttgagcc ccacgagga caggacggag  
961 ggagcctgag caggcagaga gggggcctgg ggaggcgctg gttcggggag gaagtgggta  
1021 ggggagaaat cttgacatca acacccaaca ggcaaatgcc gtggcctctg ctgtgggggt  
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1381 acttccagcc actctggaag ctgaggtggg gggatcgctt gactctggga gttggaggcc  
1441 agcctaggca ggcaacatag tgagaccaca tctccaaaaa aacaaaaaaa aacaaaaaaa  
1501 aaaaacacca aaaaagctcc cagaaagacc tctgaatctt tctggatctc tcagtggaga  
1561 cctggaatc tgaactttga caatccctct cacagtgggg ccaaggagga attaggaag  
1621 ccaaaagaag tgaactttac tcttctattg cctgtttgaa tttgtatcc aagcaagtgt  
1681 tacttaagta atttaagaga ctggttctac gaaaaataaa aactcccaa attccatag  
1741 ctggttagact gtggtcacag ccacagtga ctaagactat ctgctcagca cttctggtga  
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2101 tgggtgtcagg cgtcaccact tgggcttata aaagctgcca caagacgcca aggcacaaag  
2161 ccacccagcc tatgcatccg ctccctcaatc ctctcctgtt ggcaactggc ctcagtgccg  
2221 tttgtgtgac cacggtcatt gctctcactt gccttgccgg ctttgctccc ccaggccctg  
2281 tgctccctc tacagccctc agggagctca ttagaggagc ggtcaacatc accgagaaac  
2341 agaaggtgag tgtcggctag ccagggtcct agctatgagg gctccagggt ggggtgattcc  
2401 caagatgagg tcatgagcag gctgggctcg gtcctaagat gcctgtaggt caggaaaaat  
2461 ctccatggac caaggcccgg cccagccatg agggagagag gactgagggt ggggggctca  
2521 gcactgtgga tggacctatg gagggtgtctg gcagactccc cagggactac ctgctctcct

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2581 ggccctggcct tgtctgccac tgccagctcc tactcagcca ttcttgaaca gaggacagca
2641 gagaagggcc agcacccccc cagaacctatg tggcatttgc caactggatt ttgaccataa
2701 caatgcagcc attctccccc gcacctatcat agggccgccc ttacaggagg attcgtagt
2761 agagtccgct ccttgcccca ctagttaacag ctacacatgic tgagcactgc ttacaccagg
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2881 gatgaaccca ttctgctaag gtccagttag gttaagttag agaggctgga ttcaagccag
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3061 ggcccaggcc actcctactt cactcgtccc caccctggcc ctcccgag gcccctgtcc
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3181 ttttctctca gctccaaagc cctaaacagt gggacctcac ccctatgcct gctgttcaaa
3241 gcagaaaacg aagctcagga atgctgaggg gctgccaggc ctgctctgtt gccacaccag
3301 ggatgcttgt ggggctctgt ctggggcaga cctggcctgg gctgccaggg caggcccaag
3361 acccctgcca gactctgtt cactgtcact ttgctccac aggcctcgct ctgcaatggc
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3481 gatggggcag aggcctccagg ccttgggctt atcttctctg agcctccctt ccatggctgg
3541 ggttccaagc aagcttcaag tgctctctc gccaggcatc tcagcccat ctctctgag actcacaana
3601 caccaccag actcacctgc cccaggcatc tcagcccat ctctctgag actcacaana
3661 ggcagctgcc caagcagggc ctgacccctc ggtgtccctt cccacagta ctgtgcagcc
3721 ctggaatccc tgatcaacgt gtccaggctgc agtgccatcg agaagacca gaggatgtgt
3781 agcggattct gcccgcacaa ggtctcagct ggggtaaggc atccccacc ctctcacacc
3841 caccctgcac cccctcctgc caacctggg ctgctgaag ggaagctggc tgaatatcca
3901 tgggtgtgtt ccacccagg gtggggccat ttgtggcaga gggacgtggc cttcgggatt
3961 tacaggatct gggctcaagg gctcctaact cctacctggg cctcaatttc cacatctgta
4021 cagtagaggt actaacagta cccacctcat ggggacttcc gtgaggactt aatgagacag
4081 tccctggaag gcccttggtt tgtgcgagtc gtcccggcct ctggcgcttc actcacgtgc
4141 tgacctcttt gtcctgcagc agttttccag cttgcatgtc cgagacacca aaatcgaggt
4201 gggccagttt gtaaaaggac tgcctttaca tttaaagaaa ctttttcgag agggacggtt
4261 caactgaac ttcgaaagca tcattatttg cagagacagg acctgactat tgaagtgtca
4321 gattcatttt tctttctgat gtcaaaaatg tcttgggtag ggggaagga gggtaggga
4381 ggggtaaaat tcttagctt agacctcagc ctgtgctgcc cgtcttcagc ctagccgacc
4441 tcagccttcc ccttgcccag ggtcagcctt ggtgggctc ctctgtcag gggcctgagc
4501 tcgggtggacc cagggtatgac atgtccctac accctcccc tgccctagag cacactgtag
4561 cattacagtg ggtgcccccc ttgccagaca ttgtgtggga cagggaccca ctccacacac
4621 aggcaactga ggcagacagc agctcaggca cacttcttct tggctctatt tattattgtg
4681 tgttatttaa atgagtgtgt ttgtcaccgt tggggattgg ggaagactgt ggctgctggc
4741 acttggagcc aagggttcag agactcagg cccagcact aaagcagtg accccaggag
4801 tccctggtaa taagtactgt gtacagaatt ctgctacctc actggggtcc tggggcctcg
4861 gagcctcatc cgaggcaggg tcaggagagg ggcagaacag ccgctcctgt ctgccagcca
4921 gcagccagct ctcagccaac gagtaattta ttgtttttcc tcttatttaa atattaaata
4981 tgttagcaaa gagttaatat atagaagggt acctgaaaca ctgggggagg ggcattgaa
5041 caagttgttt cattgactat caaactgaag ccagaaataa agttggtgac agataggcct
5101 gattgtattt gtctttcatt ttggcctttg gggacactgg tctgtggtct gaagactctg
5161 aggagctctt cgggaggctg gtgggttgga ggggggact gggatggatt acagcgaggg
5221 taggggtcag tgacctgggc tgaatgcaag ctagctccc aggggtggga catggcctga
5281 aggaagcccc accctctgtc tgctgcacca gcaaggacgg agaggcttgg gccagactgt
5341 cagggttcaa ggagggcac aggagcagac ggagaccag gaagtctcac aatcacatct
5401 cctgaggact ggccagctgt gtctggcacc acccacacat ccatgtctcc ctcaaaccc
5461 aggaggccga tgagaactgt gaggtcaga aagcgtgggc ggtttgccta aggtcacgta
5521 gctacttctt cactggggtc ctggggctc agagcctcat ctgaggtaaa ggaagcaagt
5581 tgggattggg gtccaaaatt cactttaact ccaaagccca cacacttaac caccctgctt
5641 atttctgtcc aaatgtcacc tgcctgaat

```

## (2) INFORMATION FOR SEQ ID NO:84:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1282 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```

1 aagccaccca gcctatgcat ccgtcctca atcctctcct gttggcactg ggcctcatgg
61 cgcttttgtt gaccacggtc attgtctca cttgccttg cggctttgcc tcccaggcc
121 ctgtgcctcc ctctacagcc ctacaggagc tcattgagga gctggtcaac atcacccaga
181 accagaaggg tccgctctgc aatggcagca tggtaggag catcaacctg acagctggca
241 tgtactgtgc agccctggaa tccctgatca acgtgtcagg ctgcagtgcc atcgagaaga
301 cccagaggat gctgagcggg ttctgcccgc acaaggctct agctgggcag ttttccagct
361 tgcatgtccg agacaccaa atcgaggtgg cccagtttgt aaaggacctg ctcttacatt
421 taaagaaact ttttcgagag ggacggttca actgaaactt cgaaagcatc attatttgca
481 gagacaggac ctgactattg aagttgcaga ttcatatttc tttctgatgt caaaaatgtc
541 ttgggttagc gggaaggagg gttaggagg ggtaaaattc cttagcttag acctcagcct
601 gtgctgcccg tcttcagcct agccgacctc agccttcccc ttgcccaggg ctacgctgtg
661 tgggctcctt ctgtccaggg cctgagctc ggtggacca gggatgacat gtccctacac
721 cctccctctg ccttagagca cactgtagca ttacagtggg tgccccctt gccagacatg
781 tgggtggaca gggacccact tcacacacag gcaactgagg ctacggcaca ctagggcaga
841 cttcttctgt gtcttattta ttattgtgtg ttattttaa gagtgtgttt gtcacggtg

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1250

```
901 gggattgggg aagactgtgg ctgctggcac ttggagccaa gggttcagag actcagggcc
961 ccagcactaa agcagtggac cccaggagtc cctggtaata agtactgtgt acagaattct
1021 gctacctcac tggggtctct gggcctcgga gcctcatccg aggcagggtc aggagagggg
1081 cagaacagcc gctcctgtct gccagccagc agccagctct cagccaaaga gtaatttatt
1141 gtttttctct gtattttaat attaaatatg ttagcaaaaga gttaatatat agaagggtac
1201 cttgaacact gggggagggg acattgaaca agttgtttca ttgactatca aactgaagcc
1261 agaaataaag ttggtgacag at
```

## (2) INFORMATION FOR SEQ ID NO:85:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6952 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```
1 ggatcccgcg tgacaatcta gaaacaagca acagaccctc tgatgtagcc atctgtgccc
61 cgccctctccg caccgcccgc cagccttggg tccctggaga ccaccctcca gggcaggggc
121 tgcgctctcg cggggcccgc ggggtccctc ggcctgacat ggccggtgct ggagcggcac
181 gtgcgcgcct cggcccctcg gccgctcccg cccctcgccg gtgcgcaccg gcgctcgggg
241 agccgctggc ccgggtgtcc agccggccct tgcctgtcct ggcgctcgga ccgccacctt
301 tgcgcgcccc tcgcagcct ccgcagcttc cagactggcc ggtctgcgcg cccacccttg
361 cctcccggac cggccaccgc cggaggccgc ggaggagggc ccggccgcgc agatcccgtc
421 tatcggggcc catctcccgt tacataaggc cccccctta tctccgcggg ccacgcggcg
481 cgcaaccgcc gcgcccagcg cttctcccac gcgcgggggc gcccctgccc accgctcccg
541 gcagggtctt tgggtggcat gggggataag gggcgctgac tcaccggggc ggggctccgg
601 gaattgcaca gaccaaggta gttcccgtc cttccccca tcacggagac cctgtgggag
661 atgcgctggg cctctacta cagattagga aacaggcccg tagaggggtc gcgcgcccaa
721 gtacgggcac tccaggcact gggggccctc gagggaaagg gcagacttct gggagtccga
781 gccagcagct gggctgggaa gcttcgagtg tggacagaga ggggtgggaa gacgttccct
841 gtgggaagag aggggtggga agcctgggat gcctctgagc gggaatccag catgccttgt
901 gagggagggtc acaagcacac ccttgtgagg aggttgagcc ccacgcagga caggacggag
961 ggagcctgag caggcagaga gggggcctgg ggaggcgctg gttcggggag gaagtgggta
1021 ggggagaaat cttgacatca acaccaaca ggcaaatgcc gtggcctctg ctgtgggggt
1081 ttctggagga cttctaggaa aacgagggaa gagcaggaaa aggcacatg gctgtagggc
1141 caagcccagg agccgcccctc cacagcactc attctgcaga agggaaattt gaggccccca
1201 gacggcaggg gttgatctcg cagagactgg tgagcaaagg ggatcacccc aagccccagt
1261 ggcaactagga acacttaca tctctgacct ggactaaggc tgccagcctg gccaggttaa
1321 gagtttccca gaaggatggc ccatacactt taaattaaag gggccagaca cgtgcacact
1381 acttccagcc actctgggaa ctgaggtggg gggatcgctt gagtctggga gttggaggcc
1441 agcctaggga ggcaacatag ttgagcccca tctcaaaaa acaaaaaaa acaaaaaaa
1501 aaaaacacca aaaaagctcc cagaaagacc tctgaatctt tctggatctc tcagtggaga
1561 cctggaaatc tgaactttga caatccctct cacagtgggg ccaaggagga attagccaag
1621 ccaaaaagaag tgaactttac tcttctattg cctgtttgaa tttgtatcc aagcaagtgt
1681 tacttaagta atttaagaga ctggttcacg gaaaaataa aactcccaa attccatag
1741 ctggtagact gtggtcacag ccacagtga ctaagactat ctgctcagca cttctggtga
1801 cccaaaaggg tctgaggaca ggagctcaga gttgggtcag ctgtccaggt actcaggggt
1861 gtacacaggc aaactgctgg aactcagggc agcattgcaa atgccacgcc gctctcaggg
1921 ccccttgccct gccgctggaa ttaaaccacc ccagatcttg gaaactctgc cctggaccct
1981 tctcaataag tccatgagaa atcaaatctt ttcccttatg cgacactgga tttccacaa
2041 agtaaaatca agatgagtaa agatgtggtt tctagatagt gcctgaaaaa gcagagacca
2101 tgggtgacag cgtcaccact tgggcctata aaagctgcca caagacgcca aggcacaaag
2161 ccaaccagcc tatgcatccg ctccctcaat ctctcctgtt ggcactgggc ctcatggcgc
2221 ttttgtgac cagggtcatt gctctcactt gccttgccgg ctttgccctc ccaggccctg
2281 tgcctccctc tacagccctc agggagctca ttgaggagct ggtcaacatc accgaagacc
2341 agaagggtgag tgcgggctag ccagggtcct agctatgagg gctccagggt ggggtattcc
2401 caagatgagg tcatgagcag gctgggcctg gtcctaagat gcctgtagggt caggaaaaat
2461 ctccatggac caaggcccgc cccagccatg agggagagag gagctgggct ggggggctca
2521 gcactgtgga tggacctatg gaggtgtctg gcagactccc cagggtactc ctgctcctct
2581 ggcttgccct tgtctgccac tgccagctcc tactcagcca ttcctgaaca gaggacagca
2641 gagaagggcc agcaccctcc cagaacctag tggcatttgc caactggatt ttgaccataa
2701 caatgcagcc attctcccca gcaccatcat agggccgccc ttacaggagg attcgttagt
2761 agagtccgct ccttgcccca ctagtaaacg ctacatgtc tgagcactgc ttacaccagg
2821 cctgggtgcac gtgctttatg tgtcatttca tctactgcca ccacctcaag aggcaggtac
2881 gatgaaccca ttctgctaag gttcagttag gttaagttag agaggctgga ttcaagccag
2941 gcctggccaa caccagagtg tccatgtccc taactgcagt gttccctcac catcagaagg
3001 cagggcattt aatacaccag atccccaccg cctcccatct gatttgtctt ggtcaacagt
3061 gggccaggcc actcctactt cactcgtccc caccctggcc cttcccgagc gcccctgtcc
3121 tcttgccctg actatgtgca gccttgctag cagcttgctc cttactagtg gtgtcaattt
3181 ttttctctca gctccaagac cctaaacagt gggacctcac ccctatgcct gctgttcaaa
3241 gcagaaaacg aagctcagga atgctgagg gctgccaggc ctgcctctgt gccacaccag
3301 ggatgcttgt ggggcctgtg ctggggcaga cctggcctgg gctgccaggg caggcccaca
3361 acccctgccca gcactctgct cactgtcact ttgctcccac aggtcccgct ctgcaatggc
3421 agcatgggat ggagcatcaa cctgacagct ggcattgtaa ggaccttggg gtgacgggag
3481 gatggggcag aggtctcagg ccttgggctt atcttctctg agcctccctt ccattggctg
3541 ggttccaagc aagcttcaag tgctctctc cctcccgcca taatctggcc cttcccgcc
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1251

```
3601 caccacccag actcacctgc gccaggcatc tcagcccat cttcctgcag actcacaaaa
3661 ggcagctgcc caagcagggc ctgacccctc ggtgtccctc cccacagta ctgtgcagcc
3721 ctggaatccc tgatcaacgt gtcaggctgc agtgccatcg agaagaccca gaggatgtcg
3781 agcggattct gcccgacaa ggtctcagct ggggtaaggc atccccacdc ctctcacacc
3841 caccctgcac cccctcctgc caaccctggg ctgcgtgaag ggaagctggc tgaatatcca
3901 tgggtgtgtt ccacccaggg gtggggccat tgtggcagca gggacgtggc cttcgggatt
3961 tacaggatct gggctcaagg gctcctaact cctacctggg cctcaatttc cacatctgta
4021 cagtagaggt actaacagta cccacctcat ggggacttcc gtgaggactg aatgagacag
4081 tccctggaaa gcccttggtt tgtgcgagtc gtcccgccct ctggcgcttc actcacgtgc
4141 tgacctcttt gtctgcagc agttttccag cttgcatgtc cgagacacca aaatcgaggt
4201 ggcccagttt gtaaaggacc tgctcttaca tttaaagaaa ctttttcgag agggacggtt
4261 caactgaaac ttcgaaagca tcattatttg cagagacagg acctgactat tgaagtgtca
4321 gattcatttt tctttctgat gtcaaaaatg tcttgggtag gcgggaagga gggtaggga
4381 ggggtaaaat tccttagctt agacctcagc ctgtgctgcc cgtcttcagc ctagccgacc
4441 tcagccttcc ccttgcccag ggctcagcct ggtgggcttc ctctgtccag ggccctgagc
4501 tcggtggacc cagggatgac atgtccctac acccctcccc tgcctagag cacactgtag
4561 cattacagtg ggtgcccccc ttgccagaca tgtggtggga cagggaccca cttcacacac
4621 aggcaactga ggcagacagc agctcaggca cacttcttct tggctttatt tattattgtg
4681 tgttatttaa atgagtgtgt ttgtcacctg tggggattgg ggaagactgt ggctgctggc
4741 acttgagacc aagggttcag agactcaggc cccagcact aaagcagtgg accccaggag
4801 tccctggtaa taagtactgt gtacagaatt ctgctacctc actggggttc tggggcctcg
4861 gcacctcatc cgaggcaggg tcaggagagg ggcagaacag ccgctcctgt ctgccagcca
4921 gcagccagct ctcagccaac gagtaattta ttgttttcc tcgtatttaa atattaaata
4981 tgttagcaaa gatttaatat atagaagggg acctgaaca ctgggggagg ggacattgaa
5041 caagtgtttt cattgactat caaactgaag ccagaaataa agttggtgac agataggcct
5101 gattgtattt gtctttcatt ttggcctttg gggacactgg tctgtggttg gaagactctg
5161 aggagctctt cgggaggctg gtgggttgga ggaggggact gggatggatt acagcgaggg
5221 tagggtgcag tgacctgggc tgaatgcaag ctagctcccg aggggtggga catggcctga
5281 aggaagcccc acctctctgc tgctgcacca gcaaggacgg agaggcttgg gccagactgt
5341 cagggttcaa ggagggcac aggagcagac ggagacccag gaagtctcac aatcacatct
5401 cctgaggact ggccagctgt gtctggcacc acccacacat ccatgtctcc ctcacacacc
5461 aggaggccga tgagaactgt gaggctcaga aagcgtgggc ggtttgccta aggtcacgta
5521 gctacttctt cactgggggc ctggggcctc agagcctcat ctgaggtaaa ggagcaaaat
5581 tgggattggg gtccaaaatt cactttaact ccaaagccca cacacttaac caccctgcct
5641 atttctgtcc aaatgtcacc tgcctgaat
```

```
1 aagccacca gctatgcat ccgtctctca atctctcct gttggcactg ggctcatggg
61 cgcttttgtt gaccacggtc attgctctca cttgccttgg cggttttggc tccccaggcc
121 ctgtgcctcc ctctacagcc ctcaggagac tcattgagga gctggtcaac atcaccacga
181 accagaaggc tccgctctgc aatggcagca tggataggag catcaacctg acagctggca
241 tgtactgtgc agccctggaa tccctgatca acgtgtcagg ctgcagtgc atcgagaaga
301 cccagaggat gctgagcgga ttctgcccgc acaaggctct agctgggagc ttttccagct
361 tgcattgctg agacacaaa atcgaggtgg cccagtttgt aaaggacctg ctcttacatt
421 taaagaaact ttttcgagag ggacggttca actgaaactt cgaaagcctc attatttga
481 gagacaggac ctgactattg aagttgcaga ttcatttttc tttctgatgt caaaaatgtc
541 ttgggtaggc gggaaggagg gttaggaggg ggtaaaaatc cttagcttag acctcagcct
601 gtgctgcccg tcttcagcct agccgacctc agccttcccc ttgcccaggg ctgagcctgg
661 tgggcctcct ctgtccaggg ccctgagctc ggtggaccca gggatgacat gtccctacac
721 cctcccccctg ccctagagca cactgtagca ttacagtggg tgcccccttc gccagacatg
781 tgggtggaca gggaccact tcacacacag gcaactgagg cagacagcag ctcaggcaca
841 cttcttcttg gtcttattta ttattgtgtg ttattttaa atgagtgtgtt gtcaccgttg
901 gggattgggg aagactgtgg ctgctggcac ttggagccaa gggttcagag actcaggggc
961 ccagcactaa agcagtggac cccaggagtc cctggttaata agtactgtgt acagaattct
1021 gctacctcac tggggtcctg gggcctcgga gcctcatccg aggcagggtc aggagagggg
1081 cagaacagcc gctcctgtct gccagccagc agccagctct cagccaacga gtaatttatt
1141 gtttttcttc gtattttaa attaaatatg ttagcaaaga gttaatatat agaagggtac
1201 cttgaacact gggggagggg acattgaaca agttgtttca ttgactatca aactgaagcc
1261 agaaataaag ttggtgacag at
```

## (2) INFORMATION FOR SEQ ID NO:86:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

```
1 ttcggcatcc gctcctcaat cctctcctgt tggcactggg cctcatggcg cttttgttga
61 ccacggctcat tgctctcact tgccttggcg gctttgcctc cccaggccct gtgcctccct
121 ctacagccct caggagctc attgaggagc tggtaacat caccagaac cagaaggctc
181 cgctctgcaa tggcagcatg gtatggagca tcaacctgac agctggcatg tactgtgcag
241 ccttgaatc cctgatcaac gtgtcaggct gcagtgccat cgagaagacc cagaggatgc
301 tgagcggatt ctgcccgcac aaggtctcag ctgggcagtt ttccagcttg catgtccgag
361 acacaaaaat cgaggtggcc cagtttgtaa aggacctgtt cttacattta aagaaacttt
421 ttcgcgaggg acggttcaac tgaaacttcg aaagcatcat tatttcaga gacagacctt
481 gactattgaa gttgcagatt cacttttctt tctgatgtca aaaatgtctt gggtaggcgg
541 gaaggagggt tagggagggg taaaattcct tagcttagac ctcagcctgt gctgcccgtc
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1252

```
601 ttcagcctag ccgacctcag ccttccccct gccagggct cagcctggtg ggccctctct
661 gtccagggcc ctgagctcgg tggaccagg gatgacatgt ccctacaccc ctccctctgc
721 ctagagcaca ctgtagcatt acagtgggtg ccccccttgc cagacatgtg gtgggacagg
781 gaccacttcc acacacaggc aactgaggca gacagcagct caggcacact tcttcttggt
841 cttattttatt attgtgtgtt atttaaata gttgtgttgt caccgttggt gattggggaa
901 gactgtggct gctggcactt ggagccaagg gttcagagac tcagggcccc agcataaag
961 cagtggaccc caggagtccc tggtaataag tactgtgtac agaattctgc tacctcactg
1021 gggtcctggg gcctcggagc ctcatccgag gcaggggtcag gagaggggca gaacagccgc
1081 tcctgtctgc cagccagcag ccagctctca gccaacgagt aattttattgt ttttctctgt
1141 atttaaatat taaatatgtt agcaaagagt taatatatag aagggtacct tgaacactgg
1201 gggaggggac attgaacaag ttgtttcatt gactatcaaa ctgaagccag aaataaagtt
1261 ggtgacagat
```

## (2) INFORMATION FOR SEQ ID NO:87:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3999 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

```
1 tcagccccgc cgggtccga ggcgagaggc tgcattgagt ggccggcgcg gctctgctggg
61 ctgtggggcg tgcgtctctg cggcgggcgcc gggggcgggg gcggggggcg cgccctctacg
121 gaaactcagc cacctgtgac aaatttgagt gtctctgttg aaaacctctg cacagtaata
181 tggacatgga atccaccga gggagccagc tcaaattgta gtctatgta ttttagtcat
241 tttggcgaca aacaagataa gaaaatagct ccggaaactc gtcgttcaat agaagtacct
301 ctgaatgaga ggatttgtct gcaagtgggg tcccagtgtg gcaccaatga gagtgaagaag
361 cctagcattt tgggtgaaaa atgcatctca cccccagaag gtgatcctga gctgctgtg
421 actgagcttc aatgcatttg gcacaacctg agctacatga agtgttcttg gctccctgga
481 aggaatacca gtcccgcac taactatact ctctactatt ggcacagaag cctggaaaaa
541 attcatcaat gtgaaaacat ctttagagaa ggccaatact ttggtgttct cttgatctg
601 accaaagtga aggattccag tttgaacaa cacagtgtcc aaataatggt caaggataat
661 gcaggaaaaa ttaaacatc cttcaatata gtgcctttaa cttcccggtg gaaacctgat
721 cctccacata ttaaaaacct ctccctccac aatgatgacc tatatgtgca atgggagaat
781 ccaagaattt ttattagcag atgcctattt tatgaagtga aagtcaataa cagccaaact
841 gagacacata atgttttcta cgtccaagag gctaaatgtg agaattcaga atttgagaga
901 aatgtggaga atacatcttg tttcatggtc cctgggtgtt ttcctgatac tttgaacaca
961 gtcagaataa gagtcaaaac aaataagtta tgctatgagg atgacaaact ctggagtaat
1021 tggagccaaag aaatgagtat aggttaagaag cgcaattcca cactctacat aacctgtta
1081 ctcatgttcc cagtcacgtg cgcaagtgca atcatagtac tcctgcttta cctaaaaagg
1141 ctcaagatta ttatattccc tccaattcct gatcctggca agatttttaa agaaatgttt
1201 ggagaccaga atgatgatac tctgcaactg aagaagtacg acatctatga gaagcaaac
1261 aaggaggaaa ccgactctgt agtgcgtgata gaaaacctga agaaagcctc tcagtgtagg
1321 agataattta tttttacctt cactgtgacc ttgagaagat tcttccattt cctcatttgt
1381 tatctgggaa cttattaaat ggaaactgaa actactgcac catttaaaaa caggcagctc
1441 ataagagcca caggtcttta tgttgagtcg cgaccgaaa aactaaaaat aatggcgct
1501 ttggagaaga gtgtggagtc attctcattg aattataaaa gccagcaggc ttcaactag
1561 gggacaaagc aaaaagtgtg gatagtgggt gagttaatct tatcaagagt tgtgacaact
1621 tcctgaggga tctatacttg cttgtgttcc tttgtgtcaa catgaacaaa tttatttgt
1681 aggggaactc atttgggggtg caaatgctaa tgtcaaaact gagtcacaaa gaacatgtag
1741 aaaacaaaat ggataaaaatc tgatatgtat tgtttgggat cctattgaac catgtttgtg
1801 gctattaaaa ctcttttaac agtctgggct gggcccggtg gctcacgcct gtaatcccag
1861 caatttggga gtccgaggcg gccggatcac tcgaggtcag gagttccaga ccagcctgac
1921 caaaatggtg aaacctctc tctactaaaa ctacaaaaat taactgggtg tgggtggcg
1981 tgctgtaat cccagctact cgggaagctg aggcaggtga attgttgaa cctgggagg
2041 ggaggttgca gtgagcagag atcacaccac tgcaacttag cctgggtgac agagcaagac
2101 tctgtctaaa aaacaaaaa aaacaaaaa aaacaaaaa acctcttaat attctggagt
2161 catcattccc ttcgacagca ttttctctg ctttgaaagc ccagaaaaatc agtgttggcc
2221 atgatgacaa ctacagaaaa accagaggca gcttctttgc caagaccttt caaagccatt
2281 ttaggtctgtt aggggcagtg gaggtagaat gactccttgg gtattagagt ttcaaccatg
2341 aagtctctaa caatgtattt tcttcacctc tgctactcaa gtagcattta ctgtgtcttt
2401 ggtttgtgct agggccccgg gtgtgaagca cagacccttt ccagggtttt acagtctatt
2461 tgaactcctc cagttcttgc cacttttttt ttaactctcc accagctatt ttcagacct
2521 ttaactcctc caattccaac actgatttcc ccttttgcac tctcctcctt tcccttctt
2581 gtacgttttt gactttcatt ggaatttagg atgtaaatct gctcaggaga cctggaggag
2641 cagaggataa ttagcatctc aggttaagtg tgagtaatct gagaaacaa gactaattct
2701 tgcatatttt gtaacttcca tgtgagggtt ttcagcattg atatttgtgc attttctaaa
2761 cagagatgag gtggtatctt caggtagaac attgggtatt gcttgagaaa aaaagaaatg
2821 ttgaacctat ttctctttct ttacaagatg ggtccaggat tctcttttct tctgccataa
2881 atgattaatt aaatagcttt tgtgtcttac attggtagcc agccagccaa ggctctgttt
2941 atgctttttg ggggcatata ttgggttcca ttctcaccta tccacacaac atatccgtat
3001 atatccccct tactcttact tccccaaat ttaaagaagt atgggaaatg agaggcattt
3061 cccccacccc atttctctcc tcacacacag actcatatta ctggtaggaa cttgagaact
3121 ttattttcaa gttgttcaaa catttaccaa tcatattaat acaatgatgc tatttgcaat
3181 tcctgctcct aggggagggg agataagaaa ccctcactct ctacaggttt gggtacaagt
3241 ggcaacctgc ttccatggcc gtgtagaagc atggtgccct ggcttctctg aggaagctgg
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3301 gggtcatgac aatggcagat gtaaaagttat tcttgaagtc agattgaggg tgggagacag
3361 ccgtagtaga tgttctactt tgttctgctg ttctctagaa agaatttttg gtttctctgt
3421 ataggaatga gattaattcc ttccaggta tttataaatt ctgggaagca aaacctatgc
3481 ctccccctag ccattttttac tgttatccta ttttagatggc catgaagagg atgctgtgaa
3541 attcccaaca aacattgatg ctgacagtca tgcagtctgg gagtggggaa gtgatctttt
3601 gtccccatcc tcttctttta gcagtaaaat agctgagggg aaaggagggg aaaaggaagt
3661 tatgggaata cctgtggtgg ttgtgatccc taggtcttgg gagctcttgg aggtgtctgt
3721 atcagtggtg ttcccatccc ctgtgggaaa ttagtaggct catttactgt tttaggtcta
3781 gcctatgtgg atttttttct aacataccta agcaaaccce gtgtcaggat ggtaatctct
3841 attctttctg tcagtttaagt tttcccttc atctgggcac tgaagggata tgtgaaacaa
3901 tgtaaacatt tttggtagtc ttcaaccagg gattgtttct gtttaacttc ttataggaaa
3961 gcttgagtaa aataaatatt gtctttttgt atgtcacc

```

## (2) INFORMATION FOR SEQ ID NO:88:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4039 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```

1 tgccaaggct ccagcccggc cgggctccga ggcgagaggc tgcattggagt ggccggcgcg
61 gctctgcggg ctgtggggcg tgcgtctctg cgccggcgcg gggggcgggg gggggggcg
121 cgcgccctac gaaactcagc cactgtgac aaatttgagt gtctctgttg aaaacctctg
181 cacagtaata tggacatgga atccaccga gggagccagc tcaaattgta gtctatggta
241 ttttagtcat tttggcgaca aacaagataa gaaaatagct ccggaaactc gtcgttcaat
301 agaagtaccc ctgaatgaga ggatttgtct gcaagtgggg tcccagtgtg gcaccaatga
361 gagtgagaag cctagcattt tggttgaaaa atgcattctca ccccagaag gtgatcctga
421 gtctgtctgt actgagcttc aatgcatttg gcacaacctg agctacatga agtgttcttg
481 gctccctgga aggaatacca gtcccgacac taactatact ctctactatt ggcacagaag
541 cctggaaaaa attcatcaat gtgaaaacat ctttagagaa ggccaatact ttggttggtc
601 ctttgatctg accaaaagtga aggattccag ttttgaacaa cacagtgtcc aaataatggt
661 caaggataat gcaggaaaaa ttaaacctac cttcaatata gtgcctttaa cttcccggtg
721 gaaacctgat cctccacata ttaaaaacct ctcttccac aatgatgacc tatatgtgca
781 atggggagaat ccacagaatt ttattagcag atgcctattt tatgaagtag aagtcaataa
841 cagccaaact gagacacata atgttttcta cgtccaagag gctaaatgtg agaatccaga
901 atttgagaga aatgtggaga atacattctg tttcatgttc cctggtgttc ttctgtatc
961 tttgaacaca gtcagaataa gagtcaaaac aaataagtta tgcattgagg atgacaaact
1021 ctggagtaat tggagccaag aaatgagtat aggttaagaa cgcaattcca cactctacat
1081 aaccatgtta ctcatgttc cagtcattct cgagggtgca atcatagtac tctgtcttta
1141 cctaaaaagg ctcaagatta ttatattccc tccaattcct gatcctggca agatttttaa
1201 agaaaatgtt ggagaccaga atgatgatac tctgcactgg aagaagtacg acatctatga
1261 gaagcaaacc aaggaggaaa ccgactctgt agtgcgtgata gaaaacctga agaaagcctc
1321 tcagtgtatg agataattta tttttacctt cactgtgacc ttgagaagat tcttccatt
1381 ctccatttgt tatctgggaa cttattaaat ggaaactgaa actactgcac catttaaaaa
1441 caggcagctc ataagagcca caggtcctta tgttgagtcg cgcaccgaaa aactaaaaat
1501 aatggggcgt ttggagaaga gtgtggagtc attctcattg aattataaaa gccagcaggc
1561 ttcaaactag gggacaaaag aaaaagtgat gatagtgtg gagttaatct tatcaagagt
1621 tgtgacaact tcctgaggga tctatacttg ctttgtgttc tttgtgtcaa catgaacaaa
1681 ttttatttgt aggggaactc atttgggtg caaatgctaa tgtcaaaact ggtcacaaa
1741 gaacatgtag aaaacaaaaa ggataaaaat tgatatgtat tgtttgggat cctattgaac
1801 catgtttgtg gctattaaaa ctcttttaac agtctgggct ggggtccggtg gctcacgctt
1861 gtaatccag caatttgga gtccgaggcg ggccgatcac tcgaggtcag gattccaga
1921 ccagcctgac caaaatgtgt aaacctctct tctactaaaa ctacaaaaa taactgggtg
1981 tgggtggcgc tgcctgtaat ccagctact cgggaagctg aggcaggtga attgtttgaa
2041 cctgggaggt ggaggttgca gtgagcagag atcacaccac tgcactctag cctgggtgac
2101 agagcaagac tctgtctaaa aaacaaaaa aaacaaaaa acctcttaat
2161 attctggagt catcattccc ttccagagca ttttctctg ctttgaagc ccagaaatc
2221 agtgttggtc atgatgaaa ctacagaaaa accagaggca gcttcttttg caagaccttt
2281 caaagccatt ttaggtgtgt aggggcagtg gaggtagaat gactccttg gtattagat
2341 ttcaaccatg aagtctctaa caatgtatct tcttcacctc tgctactcaa gtatgattta
2401 ctgtgtcttt ggtttgtgct agggcccccg gtgtgaagca cagaccctt ccagggtttt
2461 acagtctatt tgagactcct cagttcttgc cactttttt ttaattctcc accagtcatt
2521 ttccagacct ttaactcct caattccaac actgatttcc ctttttgcat tctccctctt
2581 tcccttctct gtacgtttt gactttcatt ggaaattagg atgtaaatct gctcaggaga
2641 cctggaggag cagaggataa ttagcatctc aggttaagtg tgagtaatct gagaaacaa
2701 gactaattct tgcataattt gtaacttcca tgtgagggtt ttcagcattg atatttgtgc
2761 attttctaaa cagagatgag gtgttatctt cacgtagaac attggtattc gcttgagaaa
2821 aaaaagatag ttgaacctat ttctctttct ttacaagatg ggtccaggat tctcttttc
2881 tctgccataa atgttaattt aaatagcttt tgtgtcttac attggtagcc agccagccaa
2941 ggtctgtttt atgcttttgg ggggcatata ttgggttcca ttctcaccta tccacacaa
3001 atatccgtat atatcccttc tactcttact tccccaaat ttaaagaagt atgggaaatg
3061 agaggcattt cccccacccc atttctctcc tcacacacag actcatatta ctggtaggaa
3121 cttgagaact ttatttccaa gttgttcaaa catttaccaa tcatattaat acaatgagtc
3181 tatttgcaat tctgtctct aggggagggg agataagaaa ccctcactct ctacaggttt
3241 ggttacaagt ggcaacctgc ttccatggcc gtgtagaagc atggtgcccc ggcttctctg

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3301 aggaagctgg ggtcatgac aatggcagat gtaaagttat tcttgaagtc agattgagggc
3361 tgggagacag ccgtagtaga tgttctactt tctcttagaa agaataatttg
3421 gttttcctgt ataggaatga gattaattcc tttccaggta tttataatt ctgggaagca
3481 aaaccctatgc cccccctag ccatttttac tgttatccca ttttagatggc catgaagagg
3541 atgctgtgaa attcccaaca aacattgatg ctgacagtca tgcagtctgg gagtggggaa
3601 gtgatctttt gttcccatcc tcttctttta gcagtaaaat agctgagggg aaaggggagg
3661 aaaaggaagt tatgggaata cctgtgggtg ttgtgatccc taggtcttgg gagctcttgg
3721 aggtgtctgt atcagtggat ttcccatccc ctgtgggaaa ttagtaggct catttactgt
3781 tttaggctcta gcctatgtgg attttttcct aacataccta agcaaaccca gtgtcaggat
3841 ggtaattctt attctttcgt tcagttaagt ttttcccttc atctggggac tgaagggata
3901 tgtgaaacaa tggttaacatt tttggtagtc ttcaaccagg gattgtttct gtttaacttc
3961 ttataggaaa gcttgagtaa aataaatatt gtctttttgt atgtcaagcg ggccgccacc
4021 gcggtggaaa ctccagctt

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## (2) INFORMATION FOR SEQ ID NO:89:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5670 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```

1 ggatccccgc tgacaatcta gaaacaagca acagaccctc tgatgtagcc atctgtgccc
61 cgctctccg caccgcccgc caccgcttgg tccctggaga ccaccctcca gggcagggggc
121 tgccgctcgg ccgggcccgc ggggtccctc ggcctgacat ggccggtgct ggagcggcac
181 gtgcgcgcct cggcccctcg gccgctcccg cccctcgccg gtgcgcaccg gcgctcgggg
241 agccgctggc ccgggtgtcc agccggccct tgccctgcct ggcgctcgga ccgccacctt
301 tgccgcccc tcgccagcct ccgcagcttc cagactggcc ggtctgcgcg cccacccttg
361 cctcccgac cggccaccgc cggaggccgc ggaggagggc ccggccgcgc agatcccgct
421 tatcggggcc catctcccg taccataaggc cccccctta tctccgcggg ccacgcggcg
481 cgcaaccgcc gcgccagcgc cttctccacc gcgcgggggc gccctggccc accgctcccg
541 gcagggtctt tggtggccat gggggataag gggcggtgac tcaccggggc ggggctccgg
601 gatttgacac gaccaaggtg gttccccgct cttccccca tcacggagac cctgtgggag
661 atccgctggg ccctctacta cagattagga aacaggcccg tagaggggtc gcgcggccaa
721 gtacgggcac tccaggcact gggggccctc gaggggaagg gcagacttct gggagtcaga
781 gccagcagct gggctgggaa gcttcgagtg tgacagaga ggtgggaat gacgtccct
841 gtgggaagag aggggtggca agcctgggat gcctctgagc gggaaatccag catgccttgt
901 gaggagggtc acaagcacac cttgtgagg aggttgagcc ccacgagga caggacggag
961 ggagcctgag caggcagaga gggggccttg ggaggcgctg gttcggggag gaagtgggta
1021 ggggagaaat cttgacatca acaccaaca ggcaaatgcc gtggcctctg ctgtgggggt
1081 ttctggagga cttctaggaa aacgagggaa gagcagaaa aggcgacatg cgtgtagggc
1141 caagcccagg agccgcccct caccagactc attctgcaga agggaaattt gaggcccca
1201 gacggcaggg gttgatcctg cagagactgg tgagcaaaag ggatcaccct aagccccagt
1261 ggactagga acacttaca tctctgacct ggactaaggc tgccagcctg gccaggttaa
1321 gatgttccca gaaggatggc ccatacactt taaattaaag gggccagaca cgtgcacct
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1441 agcctaggca ggcaacatag tgagaccca tctccaaaaa aacaaaacaa aacaaaacaa
1501 aaaaacacca aaaaagctcc cagaagacc tctgaatctt tctggatctc tcagtggaga
1561 cctggaaatc tgaactttga caatccctct cacagtgggg ccaaggagga attaggcaag
1621 ccaaaagaag tgaactttac tctctattg cctgtttgaa tttgtatcc aagcaagtgt
1681 tacttaagta atttaagaga ctggttcac gaaaaataa aactcccaa attcccatag
1741 ctggtagact gtggtcacag ccacagtga ctaagactat ctgctcagca cttctggtga
1801 cccaaaaggg tctgaggaca ggagctcaga gttgggtcag ctgtccaggt actcaggggt
1861 gtcacaggca aaactgctgg aactcagggc agcattgcaa atgccacgcc gctctcaggg
1921 cccttgcct cccgctggaa ttaaacccac ccagactctg gaaactctgc cctggacctt
1981 tctcaataag tccatgagaa atcaaaactc ttcctttatg cgacactgga ttttccacaa
2041 agtaaaatca agatgagtaa agatgtggtt tctagatagt gcctgaaaaa gcagagacca
2101 tgggtgcagg cgctcaccact tgggcctata aaagctgcca caagacgcca aggcacaaag
2161 ccacccagcc tatgcatccg ctctcactc ctctctgtt ggcactgggc cctatggcgc
2221 ttttgttgac caccgtcatt gctctcactt gccttggcgg ctttgcctcc ccaggccctg
2281 tgcctccctc tacagccctc agggagctca ttgaggagct ggtcaacatc acccagaacc
2341 agaaggtgag tgtcggctag ccagggtcct agctatgagg gctccagggt ggggtattcc
2401 caagatgagg tcattgagcag gctgggcctg gtcctaagat gctgtagggt caggaataat
2461 ctccatggac caaggcccgc ccagccatg agggagagag gagctgggct ggggggctca
2521 gcactgtgga tggacctatg gaggtgtctg gcagactccc cagggactac ctgctctcct
2581 ggcctggcct tgtctgccac tgccagctcc tactcagcca ttctgaaca gaggacagca
2641 gagaagggcc agcaccctcc cagaaccatg tggcatttgc caactggatt ttgaccataa
2701 caatgcagcc attctcccca gcaccatcat agggccgccc ttacaggagg attcgtagt
2761 aggtccgct ccttgcccca ctagtaacag ctacatgtc tgagcactgc ttacacagg
2821 cctggtgcac gtgctttatg tgcatttca tcaactgcag ccacctcaag aggcaggtac
2881 gatgaaccca ttctgctaag gttcagttag gtttaagtac agaggctgga ttcaagccag
2941 gcctggccaa caccagagtg tccatgctcc taactgcagt gttccctcac catcagaagg
3001 cagggcattt aatacaccag atccccaccg cctcccatct gatttgtctt ggtcaacagt
3061 gcccagggcc actcctactt cactcgctcc caccctggcc cttcccgag cccctgtccc
3121 tctgcccctg actatggcaa gccttgcatt cagcttgtcc cttactagtg gtgtcaattt
3181 tttctctca gctccaagac cctaaacagt gggacctcac ccctatgcct gctgttcaaa

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3241 gcagaaaacg aagctcagga atgctgaggg gctgccaggc ctgcctctgt gccacaccag
3301 ggarctctgt ggggcctgtg ctggggcaga cctggcctgg gctgccaggg caggcccaca
3361 acccctgcca gcaactctgt cactgtcact ttgctccac aggtccgct ctgcaatggc
3421 agcatggtat ggagcatcaa cctgacagct ggcatggtaa ggacctttgg gtgcaggag
3481 gatggggcag aggtctccagg ccttgggctt atcttctctg agcctccctt ccatggctgg
3541 ggttccaagc aagcttcaag tgctctcctc cctcccgcca taatctggcc ccttcccgcc
3601 caccacccag actcacctgc gccaggcatc tcagcccat cttctgcag actcacaana
3661 ggcagctgcc caagcagggc ctgacccctc ggtgtccctt cccacagta ctgtgcagcc
3721 ctggaatccc tgatcaacgt gtcaggctgc agtgccatcg agaagaccca gaggatgctg
3781 agcggattct gcccgacaa ggtctcagct ggggtaaggc atccccacc ctctcacacc
3841 caccctgcac cccctcctgc caaccctggg ctgctgaag ggaagctggc tgaatatcca
3901 tgggtgtgtt ccaccagggt gtggggccat tgtggcagca gggacgtggc cttcgggatt
3961 tacagatctt gggctcaagg gctcctaact cctacctggg cctcaatttc cacatctgta
4021 cagtagaggt actaacagta cccacctcat ggggacttcc gtgaggactg aatgagacag
4081 tccctggaaa gccctgtgtt tgtgcgagtc gtcccgccct ctggcgcttct actcacgtgc
4141 tgacctcttt gtctcgcagc agttttccag cttgcatgtc cgagacacca aaatcgaggt
4201 ggcccagttt gtaaaggacc tgctcttaca tttaaagaaa ctttttcgag agggacgtgt
4261 caactgaaac ttcgaaagca tcattatttg cagagacagg acctgactat tgaagtgcga
4321 gattcatttt tctttctgat gtcaaaaatg tcttgggtag gcgggaagga gggtaggga
4381 ggggtaaaat tcttagctt agacctcagc ctgtgctgcc cgtcttcagc ctgaccgacc
4441 tcagccttcc ccttgcaccg ggctcagcct ggtgggcctc ctctgtccag gccctgagc
4501 tcgggtggacc cagggatgac atgtccctac acccctcccc tgccctagag cacactgtag
4561 cattacagtg ggtgcccccc ttgccagaca tgtggtggga cagggaccca cttcacacac
4621 aggcaactga ggcagacagc agctcaggca cacttcttct tggctctatt tattattgtg
4681 tgttatttaa atgagtgtgt ttgtcaccgt tggggattgg ggaagactgt ggtgctggc
4741 acttggagcc aagggttcag agactcaggg cccagcact aaagcagtg accccaggag
4801 tccctggtaa taagtactgt gtacagaatt ctgctacctc actggggtcc tggggcctcg
4861 gagcctcatc cgaggcaggg tcaggagagg ggcagaaacg ccgctcctgt ctgccagcca
4921 cgagccagct ctacgcaaac gagtaattta ttgttttcc tcgtatttaa atattaaata
4981 tgtagcaaaa gagttaatat atagaagggt acctgaaca ctgggggagg ggacattgaa
5041 caagttgttt cattgactat caaactgaag agttgtgac agataggcct
5101 gattgtattt gtctttcatt ttggcctttg gggacactgg tctgtgtct gaagactctg
5161 aggagctctt cgggaggctg gtgggttggg ggaggggact gggatggatt acagcgaggg
5221 tagggtgcag tgacctgggc tgaatgcaag ctagctcccg aggggtggga catggcctga
5281 aggaagcccc accttctgtc tgctgcacca gcaaggacgg agaggcttg gccagactgt
5341 cagggttcaa gggggcagc aggagcagac ggagaccag gaagtctcac aatcacatct
5401 cctgaggact ggccagctgt gtctggcacc acccacacat ccatgtctcc ctcaaaccc
5461 aggaggccga tgagaactgt gaggctcaga aagcgtgggc ggtttgccta aggtcacgta
5521 gctacttctt cactggggtc ctggggcctc agagcctcat ctgaggtaaa ggagcaaaat
5581 tgggattggg gtccaaaatt cactttaact ccaaagccca cacacttaac caccctgctt
5641 atttctgtcc aaatgtcacc tgcctgaat
```

## (2) INFORMATION FOR SEQ ID NO:90:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14978 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

```
1 ttcggcatcc gctcctcaat cctctcctgt tggcactggg cctcatggcg cttttgttga
61 ccacgggtcat tgctctcact tgccctggcg gctttgcctc cccaggccct gtgcctccct
121 ctacagccct caggagctc attgaggagc tggtaacat caccagaac cagaaggctc
181 cgctctgcaa tggcagcatg gtatggagca tcaacctgac agctggcatg tactgtgcag
241 ccctggaatc cctgatcaac gtgtcaggct gcagtgccat cgagaagacc cagaggatgc
301 tgagcggatt ctgcccgcac aaggctctcag ctgggcagtt ttccagcttg catgtccgag
361 acacaaaaat cgagggtggc cagtttgtaa aggacctgct cttacattta aagaaacttt
421 ttcgagaggg acggttcaac tgaacttcg aaagcatcat tatttgaga gacaggacct
481 gactattgaa gttgcagatt ctttttctt tctgatgtca aaaatgtctt gggtagggcg
541 gaaggagggt tagggagggt taaaattcct tagcttagac ctacagctgt gctgcccgct
601 ttcagcctag ccgacctcag ccttcccctt gccagggtc cagcctgggt ggcctcctct
661 gtccaggggc ctgagctcgg tggaccagg gatgacatgt ccctacacc ctcccctgcc
721 ctagagcaca ctgtagcatt acagtgggtg cccccctgc cagacatgtg gtgggacagg
781 gacccacttc acacacaggc aactgaggca gacagcagct caggcacact tcttcttggt
841 cttatttatt attgtgtgtt atttaaata gtgtgtttgt caccgttggg gattggggaa
901 gactgtggct gctggcactt ggagccaagg gttcagagac tcaggggccc agcataaag
961 cagtggaccc caggagtccc tggtaataag tactgtgtac agaattctgc tacctcactg
1021 ggtgctctgg gcctcggagc ctcatccgag gcagggtcag gagaggggca gaacagccgc
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5221 tagggtgcag tgacctgggc tgaatgcaag ctagctcccc aggggtggga catggcctga  
5281 aggaagcccc accctctgtc tgcctgcacca gcaaggacgg agaggcttgg gccagactgt  
5341 cagggttcaa ggagggcac aggagcagac ggagaccag gaagtctcac aatcacatct  
5401 cctgaggact ggccagctgt gtctggcacc acccacacat ccatgtctcc ctcacaaccc  
5461 aggaggccga tgagaactgt gaggtctcaga aagcgtgggc ggtttgccta aggtcacgta  
5521 gctacttctc cactggggtc ctggggcctc agagcctcat ctgaggtaaa ggagcaaatg  
5581 tgggattggg gtccaaaatt cactttaact ccaaagccca cacacttaac caccctgcct

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5641 atttctgtcc aaatgtcacc tgtcctgaat

## (2) INFORMATION FOR SEQ ID NO:91:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

```
1 caacaccttc agaaataatc ctttgggtga tctcttgta atcatttgtg caggctagag
61 aggcacctgt gaatgataag gctactgaga agcatcattg gcctgggtcct ggcactacca
121 aagggcaggg gaagcgatgc ccaaggggct cctgaccagc acatcatccc acgcaaaaac
181 attctccagg tcccttggtc caggcaggaa atccccagct ctgagcgccc tgccagggct
241 ctgcctaggg acaccttttc caggtctaga gaatcaaagg agcctccaga gcagctagga
301 gggcctgagc tgaccaagca agcctgtctc acaagacaaa tgcagtcaag acctgggtgt
361 attactgttc ttgagctctg aagggcaggg aggggtctga gcctcaaatc agacagagaa
421 atgctcaagt cacttctgcc aactcactgt gatggcagct acagatgaca gcccctctca
481 agactcttca gctcacagac aagccactga cttcatctgt acacaccccc atccccaatg
541 caagcccact gtacacttac aggtataaat gcatttgcaa ggcttgcaa aatgccctat
601 gtacgtaaaa ctgaccacaa aaatccaaaa ttgcaagtgc cagatgccag ccaggtcaga
661 acatcctggc ttcagcaatg ggctgctcag catgggagcc ttttatgggc caggcctggc
721 tgggctgccc ctcccctccc agcatgaccc aacaccaggc tctctaggcc ctggcgagg
781 tgggctcttg aggccagtc tggcctgatg cttctgtgct cgggtgctcct gggtagcaag
841 gcgcttctgt gaccctgggg gagctgggtg cttgagcccc agggccctct ggcctcctct
901 cagggccact gtcagtgagg gagcctggc caccagcact caggtcctgt accctcttgt
961 tcaggtcatt gcgctctgtc tgcagtgcgc ggcacagctt ctccagcctg tggattttta
1021 cctgcaggcc ctccagttct ttatcccgga ctgttttctc ctccagccatc tcaagcaggg
1081 ccttggttgc gctctccac cgggaccggt acatggtggt ttctttctcc agcttcttga
1141 tcttcttagt catcttttcc atctcctgct tgaatgtggt gaatacctcg ctgcttttgg
1201 aaagtgtgtt ctggaactcc tcaaaactct ctgtgtatag ggcaagctgt tgcttcaggt
1261 gggctctctg ctgcttcac agctcacaca tccctctgga ctctactgcc tctttcagga
1321 gaaaatcctt ctcccgttg tgcgctctt ctgcctcctt tagcatctcc tgggctgct
1381 ggagcttggc atccaccagc tgctgttcta ggtccttggt tttgaagact ttgtcgatat
1441 gctcctcgcg cagctcatac tgctcaatca gcttctttag cctctcagcc agctccatgt
1501 tctcttggcg cagcttggag ttgcgctcat tgtgctgttc catctgcagc tgaatgtcat
1561 tcagtgtcac ctggaagtgc gaggtcacct ccttgcgctt ctccctctcc tcccgggccc
1621 gctgcacacc ttcttcttg agggagcggg tgtgcccgtg cagctcacgg cataggctct
1681 caagcttctg gcgggccagg acggcttgcg gtgctcaccg cgcaggtggt ccttctcttg
1741 caccagctgg ctctgctttt tctgtaggag cttcatctgc ttctgtgaat tcc
```

## (2) INFORMATION FOR SEQ ID NO:92:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```
1 caacaccttc agaaataatc ctttgggtga tctcttgta atcatttgtg caggctagag
61 aggcacctgt gaatgataag gctactgaga agcatcattg gcctgggtcct ggcactacca
121 aagggcaggg gaagcgatgc ccaaggggct cctgaccagc acatcatccc acgcaaaaac
181 attctccagg tcccttggtc caggcaggaa atccccagct ctgagcgccc tgccagggct
241 ctgcctaggg acaccttttc caggtctaga gaatcaaagg agcctccaga gcagctagga
301 gggcctgagc tgaccaagca agcctgtctc acaagacaaa tgcagtcaag acctgggtgt
361 attactgttc ttgagctctg aagggcaggg aggggtctga gcctcaaatc agacagagaa
421 atgctcaagt cacttctgcc aactcactgt gatggcagct acagatgaca gcccctctca
481 agactcttca gctcacagac aagccactga cttcatctgt acacaccccc atccccaatg
541 caagcccact gtacacttac aggtataaat gcatttgcaa ggcttgcaa aatgccctat
601 gtacgtaaaa ctgaccacaa aaatccaaaa ttgcaagtgc cagatgccag ccaggtcaga
661 acatcctggc ttcagcaatg ggctgctcag catgggagcc ttttatgggc caggcctggc
721 tgggctgccc ctcccctccc agcatgaccc aacaccaggc tctctaggcc ctggcgagg
781 tgggctcttg aggccagtc tggcctgatg cttctgtgct cgggtgctcct gggtagcaag
841 gcgcttctgt gaccctgggg gagctgggtg cttgagcccc agggccctct ggcctcctct
901 cagggccact gtcagtgagg gagcctggc caccagcact caggtcctgt accctcttgt
961 tcaggtcatt gcgctctgtc tgcagtgcgc ggcacagctt ctccagcctg tggattttta
1021 cctgcaggcc ctccagttct ttatcccgga ctgttttctc ctccagccatc tcaagcaggg
1081 ccttggttgc gctctccac cgggaccggt acatggtggt ttctttctcc agcttcttga
1141 tcttcttagt catcttttcc atctcctgct tgaatgtggt gaatacctcg ctgcttttgg
1201 aaagtgtgtt ctggaactcc tcaaaactct ctgtgtatag ggcaagctgt tgcttcaggt
1261 gggctctctg ctgcttcac agctcacaca tccctctgga ctctactgcc tctttcagga
1321 gaaaatcctt ctcccgttg tgcgctctt ctgcctcctt tagcatctcc tgggctgct
1381 ggagcttggc atccaccagc tgctgttcta ggtccttggt tttgaagact ttgtcgatat
1441 gctcctcgcg cagctcatac tgctcaatca gcttctttag cctctcagcc agctccatgt
```

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1501 tctcttggcg cagcttggag ttgcgctcat tgtgctgttc catctgcagc tgaatgtcat  
1561 tcagtgtcac ctggaagtgc gaggtcacct ccttgcgctt ctccctctcc tcccgggccc  
1621 gctgcacacc ttcttctctg agggagcggg tgtgcccgtg cagctcacgg cataggtctt  
1681 caagcttgct gcggggccagg acggcttgct gtgtcacccg cgcagggtgt ccttctcttg  
1741 caccagctgg ctctgctttt tctgtaggag cttcatctgc ttctgtgaat tcc

## (2) INFORMATION FOR SEQ ID NO:93:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

1 aaatcctggc tgtcatgtac ttgctatggg cctagagtag cttaccta aa tgctactaac  
61 cttcctccat accattattg taaagattaa aggtgatgca tctgttaagt aactaataga  
121 gtgcttatta aaaggttagt gttcaataag tattaattcc ctccctttct ttttcttact  
181 agtgcacttg tgtttttaat ggatcatact ttaccctaga ttgtattgta ggagcatcg  
241 tggatggatg gctgctggaa accccttgcc atagccagct cttcttcaat acttaaggat  
301 ttaccgtggc tttgagtaat gagaatttcg aaaccacatt tgagaagtat ttccatccag  
361 tgctacttgt gtttacttct aaacagtcatt tttctaactg aagctggcat tcatgtcttc  
421 attttgggat gcagctaata taccagttg gcccaaagca cctaacctat agttatataa  
481 tctgactctc agttcagttt tactctacta atgccttcat ggtattggga accatagatt  
541 tgtgcagctg tttcagtgcg gggcttctta aaacagaagc caactgggtg aatgtaataa  
601 gtgatttgaa aaaaattgaa gatcttattc aatctatgca tattgatgct actttatata  
661 cggaaagtga tgttcacccc agttgcaaag taacagcaat gaagtgtctt ctcttgaggt  
721 tacaagttat ttcacttgag tccggagatg caagtattca tgatacagta gaaaatctga  
781 tcatcctagc aaacaacagt ttgtcttcta atgggaatgt aacagaatct ggatgcaaag  
841 aatgtgagga actggagaaa aaaaatatta aagaattttt gcagagtgtt gtacatattg  
901 tccaaatgtt catcaacact tcttgattgc aattgattct ttttaaagtg tttctgttat  
961 taacaaacat cactctgctg cttagacata acaaaacact cggcatttca aatgtgctgt  
1021 caaaacaagt ttttctgtca agaagatgat cagaccttgg atcagatgaa ccttagaaaa  
1081 tgaaggcaga aaaatgtcat tgagtaatat agtgactatg aacttctctc agacttactt  
1141 tactcatttt ttaatttat tattgaaatt gtacatattt gtggaataat gtaaaatgtt  
1201 gaataaaaat atgtacaagt gttgtttttt aaaaaaaaaa aaaaaaaaaa

## (2) INFORMATION FOR SEQ ID NO:94:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

1 tgtccggcgc ccccgaggag ggaactgggt ggccgcaccc tcccggctgc ggtggctgtc  
61 gccccccacc ctgcagccag gactcgatgg agaattccatt ccaatatatg gccatgtggc  
121 tctttggagc aatgttccat catgttccat gctgctgctg acgtcacatg gagcacagaa  
181 atcaatgtta gcagatagcc agccataca agatcgtatt gtattgtagg aggcacgtg  
241 gatggatggc tgctggaaac cccttgccat agccagctct tcttcaatac ttaaggattt  
301 accgtggctt tgagtaatga gaatttcgaa accacatttg agaagtattt ccattccagt  
361 ctacttgtgt ttacttctaa acagtcattt tctaactgaa gctggcattc atgtcttcat  
421 tttgggctgt ttcagtgcag ggcttcctaa aacagaagcc aactgggtga atgtaataag  
481 tgatttgaaa aaaattgaag atcttattca atctatgcat attgatgcta ctttatatac  
541 ggaagtgtat gttcacccca gttgcaaagt aacagcaatg aagtgtttc tcttgaggtt  
601 acaagtattt tcaattgagt ccggagatgc aagtattcat gatacagtat aaaaatctgat  
661 catcctagca aacaacagtt tgccttctaa tgggaatgta acagaatctg gatgcaaaga  
721 atgtgaggaa ctggaggaaa aaaatattaa agaatttttg cagagttttg tacattattg  
781 ccaaagtgtc atcaacactt cttgattgca attgattctt tttaaagtgt tctgtttatt  
841 aacaaacatc actctgctgc ttagacataa caaaacactc ggcattttaa atgtgctgtc  
901 aaaaacaagt tttctgtcaa gaagatgatc agaccttggg tcagatgaac tcttagaaat  
961 gaaggcagaa aaatgtcatt gagtaataa gtgactatga acttctctca gacttacttt  
1021 actcattttt ttaattttat attgaaattg tacatatgtt tggaataatg taaaatgttg  
1081 aataaaaaata tgtacaagtg ttgtttttta agttgcactg atattttacc tcttattgca  
1141 aaatagcatt tgtttaaggg tgatagtcaa attatgtatt ggtggggctg ggtaccaatg  
1201 ct

## (2) INFORMATION FOR SEQ ID NO:95:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14928 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

1 ggcattgtaa tcagacagaa ctggcctcaa atcctggctg tcatgtactt gctatgggcc  
61 tagagtagct tacctaaatg ctactaacct tctccatcac cattattgta aagattaaag  
121 gtgatgcac tgtaagtaa ctaatagagt gcttattaaa aggtagggtg tcaataagta

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181 ttaattccct ttctttcttt ttcttactag tgcacttgtg tttttaatgg atcatacttt  
241 accctagatt gtattgtagg aggcactgtg gatggatggc tgctggaaac cccttggcat  
301 agccagctct tcttcaatac ttaaggattt accgtggcct tgagtaatga gaatttccgg  
361 taagaagaaa aatagatgaa aatatacctat ggaatttccc ttaaagggtcg tctgaatctc  
421 agagtctttg caataagtta catggttatt ctccaaagat cttgagatat cacagatgtc  
481 tgttcacatt tggattgttc ttattttgaa aataaatagg tttttaaaaa ctctattgac  
541 catcttgata ggctcttctt gtcattataa atgtgttatt tcactttatcc cactcttttg  
601 tgttctctaa atgtctttgt actcactaaa ttgtgtagtc ttagaggggca ggggtgtggg  
661 atcattcatc tttttgaaag gaagcatgaa caattagtg ttaagggtggc agttaacact  
721 gctttctgaa actttaaaag cttcgacaac acaaaagagg cagggtgaaag taccaaaact  
781 ctggtaagtt gtaggataaa tgattttcct aaatcaccaa gaaagattat tagtactct  
841 caagatggaa tacagtatct gtaattgtgt ccattttatc caatttttca ccaaataata  
901 ttaatataat tcattttcat aatttacatg aagttaatat aactattgca tctctgttag  
961 taatgcatgt tattaacctg tgctgtataa aatattttga cctattaaaa aagaaagaag  
1021 gatgaggagg aggtcaaaga taatataaaa actttaagtg gtgacattgg tatgtatgta  
1081 aattaacaaa tatgtcaact ttgttaaaatt atctttgaca tgcactgtga gaaatatctg  
1141 ttaagggaact ttgtgcataa gagacagagt tggagggtggg agagaaaagt aaaaaagata  
1201 aattatagtt ttattatttt tgataagggg cagtaattat gaaattatga caaacttaca  
1261 tctttagacc tagaaatatg ttgacatgtt attttaaacc tcacttttta actaaaaaat  
1321 ttaaccattt gtctatgatt atatttttca gaaaccacat ttgagaagta tttccatcca  
1381 gtgctacttg tgtttacttc taaacagtca ttttctaact gaagctggca tctatgtctt  
1441 cattttgggg gtaattttat ctttaggcat aaataacatt atgttcatgg tcatgatgat  
1501 tgtccttgga tatattttcc attaaattag ttacgttca gtttgcttat atctctaggt  
1561 actcagtatc tgggggatag aaggcagact acagagattt agagagggtt ggtaaaccac  
1621 taactgagca tttttctaca ttgtggtaat agtccaaaca agcattatag agctcaata  
1681 aattgggcct tttgatattt aactgaactt ggaagtatac cacttattga ttagctacat  
1741 atttttcatg gcaattaaaa gtagatattt agaatttgct tatgttactt ttttatctgt  
1801 ccctgacact gactcctcct atcccttgat ctttatccta gttcagttta aaacatttct  
1861 ttctttattt aagccttttg ttgtttcctt ctaataaaat tcatatggtt ccatgactat  
1921 taactttttt cttctctctt agatgcagct aatataccca gttggcccaa agcactaac  
1981 ctatagttat ataactctgac tctcagttca gttttactct actaatgcct tcatgggtat  
2041 gggaaaccata gatttgtgca ggtaattcct catcataaga cagattagtg ttgactatca  
2101 tgcttctgtg taagatccat caggaagtga gtgattattt ttcctcaagc tctaagcatc  
2161 attccaatgt tacttgggtc gtataagtgt attttgtctg gatattaaat ttttaatttt  
2221 atgaaatttg tgaaagtga gtagtatatg atcattcagc ctacactgga atgaagtctg  
2281 tactgtttat ggagaaagct gctgcaagca tagtaagagt gtgagcaaca tgaaaggggc  
2341 atgtttaatg tagtgtaaaa aaaatttact atcaaaatca ttacatgaaa atgattatta  
2401 ctcattttaa gaattttacc tatttattag acttcaaagt ctctgtaaat ctctacttaa  
2461 aggaaactag taattcattc aaaatcattt attgagcatt gccacacatc tggcactgat  
2521 tctatttcat tgtgataaat tgagccagtt tatttataaa gtatgcctac agttaggctt  
2581 ttctctaate cgggttgggtg aagcctcaag ttatcataaa atgccaaaat tgtactatat  
2641 gctcaatgtt tatgttcagt tacaaggctg ttgaatgcac agaagcaagg ataacactga  
2701 ttttttcaat ggtcagaata aaaattattg attgctcttt tgcttatagt attcatcaag  
2761 atgaataggc tccttcaaaa tgctttgctc tatggttttt ctttcagctg tttcagtgca  
2821 gggcttccca aaacagaagc caactgggtg aatgtaataa gtgatttgaa aaaaattgaa  
2881 gatcttattc aagtgagtag tcatttttcc ataaaatgcc tgggtataact gctatggagt  
2941 ttgtctctct ctgtgttttt ctgtctgtct taaggaaacc acacttgaaa caataatatt  
3001 ttgttagaaa tttatgatct tataaagctc aaaaagaagt cttttcctta ctgttttaga  
3061 atctaattat ctttaaaacg taatttataa gcggccagga cggatgagt ctgatttgca  
3121 cagggtgagg attctcttcc tctatctgga gaagccagat atcttgggtg cacctgcagg  
3181 gagaatggct tgaccagggt aacagctgtt gttgcttgtg gactaaaggc cctcttctcc  
3241 cacctcaaga aaacagggtg cctgacctaa ggaagtgatt tttgccattc caggtaatac  
3301 cagcttcagt ggaagtctcg atggcaccat gcataccaaa atagcaccac aaagtctga  
3361 aaactaaatt gtcatgggaa tcacagctaa aaaaaatagg ttagaacttg catgctaaat  
3421 ccaaacaacc tgactgcatg ttaaaataga agatttaa ataggaccagag tgccttaaca  
3481 taatagacat gaagccaaga tacaattgga aatcacccat tgaacaaga aataggaaaag  
3541 ttacaactta aatgagaaaa tatagtcaac agattacaaa attgaagtgg atcagatgtt  
3601 ggaatttctc gacatagatt tgaaaagcaga cattataaaa agtgcttgaa aaagcaatta  
3661 caaatgccct tgaagcaaat gaaaaactaa atgccttaac aaagaaatag aagatatgaa  
3721 aggaaccata tagaaattat ataactgaaa atataactga aatataaagc aaactgtaaa  
3781 ggctcattag cagaatgaat gacagaggaa tgatagttaa tttgacaaca gaatactaga  
3841 gagacagttg acttaagaaa aaaaaagcat cactgatctt gacgacagta acaaaagatt  
3901 cagcattcct atggttagta tcacaggaga gtatgagaat acaccaagta aaagagagag  
3961 attggttgaa ttcataacaa aacaccaccc atctatacta tctataagca gttcacttct  
4021 agtacaatga catacatagg ttgaaattta aaaaagacaga aaaagatata gcatactata  
4081 atgggttgaa tagtgtcccc ccaaatttca catcctcttg gaaccttaaa atgtgatctt  
4141 attttgaaat aatatctttg caaatataat taatgaaatt aagatgagat catactagag  
4201 tagggggggc cctaaatcca atgacaagtg tctttattag aaaagggaaa gacacagagt  
4261 aactcactgg gaagaaagcc atgtgaagac agaggaagag atcagagtga tgcggctata  
4321 agccaaggaa ggccagagat tgccaggatc caccagaacc ttgggggaagt caagaaagca  
4381 ttcttctcta gactgatata catgcataca ttaattataa aaagcagaag tggctatatt  
4441 aacatcaaa ttaattgttat taacataaa tagacttcac agaaaataaa gttgctataa  
4501 tccagagggg tattacaaaa tgataaaaaa taaatctgtg aggaaaaaat aatgttctta  
4561 aatgtatata catcaacaa cgaagactca aaatttgtga aacaaaaaat aatagggata  
4621 aaagagaaat agacaaatcc acaattattc ttgaggactt cactgcctcc tcctcagtaa



4681 ctaatgag tactagacag aaaatcagaa agggcataaa aatataatat aaccaacca  
4741 caggatctaa ttaatacat agagcactac acccaacaac agcagaatat actttctttt  
4801 atcaagacta aatatatact gagccataaa agaaacttta aaaatttttt cagaacttaa  
4861 atcatgcaga atttgttctc aaaccacaat ggaatcaaac cagaatcaa gaattaaat  
4921 acaacgggca aatctccaaa tgcttgaaa ttaataacta tacctctata taatccatgg  
4981 gtcaaaaggt aaatctcaaa ggaattcat aatacataga atgaaaaaaa atgaaatata  
5041 gcatatcaag atatatgtga tgtggctaaa gcaatactga caggacattt ttaaaatca  
5101 aatgaatata ttagaaaaaa aggagaatta tcaaatcaaa aatctaagtt actgcttcaa  
5161 gaaactagaa gaagtagagc aaaacaaatt caatacaagc agaacaaaga aaatatttaa  
5221 atataagagc caaaattaat gaagttgaaa tcaagaaaac aatagaaaaa attaatgaaa  
5281 cataaaactg gttatttgga aaatcaatac aattgatctt taattgacag aaataagaga  
5341 gaagacacaa atctcaggaa tgaaatttgg ggctgtcact acagaattctg cagtcaattag  
5401 aaggataata agaaaaacta tgaacaattt tatgctcaca aatctgataa cttagaggaa  
5461 atggaccaat tcttcagaaa ccacaaacta ccaaaacata atgaagatga aatagacaat  
5521 ccaaacactc atataatcac taaatacatt gaattcatca tacacaagct ccaaaaaagg  
5581 gaccttcaag cctgctggtt acactgaatc attctatcaa atatttacag aagcattaac  
5641 aacaattgta cagtctcttc tagaaaaatag aagaggaagg aacattttcc agttgatttt  
5701 aggaggccag tattactgtg atgctaaaac caaataaaga tattactaaa aaagacaact  
5761 acaaaaatat ctccatttaa cttagatatt aaaatgctct ataaaaatatt aacaaatcga  
5821 attcagcaat gtataaaaaa aattatacac catgaccgag tgagatttat ttcagggtaca  
5881 caagtcttgc tcaattattt gaaagtcaag caatgtaatc taccttatca acagggtaaa  
5941 gaagaaaatc atatgtagaa aaggtatctg ataaaaatga acacctctca tggcctgtgt  
6001 ccctccctat gcctcctgga tttatatgtt gaagtactaa ttgccagtat atcaaatgt  
6061 gactgtattt tgagataggg tcagttaaaa tgaggtcatg agggcaggtc ctactgcaat  
6121 atgactggtt tcttttagaaa aacagataag ggtatagata cacagagata gaaaaccatg  
6181 tgaagacact gggagaaaat ggccacctat aagccaaagg gggaggactc caaagaaacc  
6241 aacactgctg gtacctgat ttcagacctc tagcctcctg aattgtgaga aaataaagtt  
6301 ctattattta agtcaccaag tctgtgttac tttttatagc agccctagca gactgatata  
6361 aacacctatt gaagataaaa tttcttagaa agtaggtgtg gagaactgcc tcaacttggt  
6421 acaaaacatg ttcaaaaagt ctagagctac catacttaat ggtgagtaca agactgaatg  
6481 tttttctgct aggactggaa actaagcagg gatattctct ctcaccactt ttactcaaca  
6541 taattgtctg agttttctgt tgcttataac agagtacttg aaatgcataa tttataaaga  
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7621 tccagtataaaa aagaaaata agctatcaag ccatgaaaag aaatggagaa acctcaaaag  
7681 tcatattgtt gagtgaaga tggggacgcc aatctgaaaa ggcttcacac tgtatgatcc  
7741 caactatgac attttgaaaa aggcaaagct atggagacaa taaaaagatc agtgggtgtt  
7801 aggggtttgg agggaaggag aaatggctag gcagagcaca ggctactttt aaagcagtga  
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8341 gtgggtgatgt gaattctatgc aaatgataaa attgcataaa acttcacaca tatgcaagca  
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8521 ttgttgaagg gtacacagga tctctctgta tttactctta cagtttcata tgaattttaa  
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9001 gtttttgtga tgcagtttca tcatggtgca attagatgca aaaatcagat taactgtttc  
9061 aatttaagag tagccaatat atcagttatt tccaatgctg taatgtatca ccatctgcaa  
9121 tcatattttc cataaattgc ttaaaatcat tcatgttctg cattttacat gattctctac



9181 atttgtctt aaaagattctt aattattctc tatgtgagaa aggtatata acccatgaaa  
9241 cttattagaa ctgaaaaatg gtcttgaact tgtttcatta atatacagac atttcctaag  
9301 gaatgtagga tttgtcatgt tgggtgggtg tcttcccttc agtattgtta ctaaaaccaa  
9361 gaaatgaatc cccaacttca cgtcagggaa aacaaactct atgtcctctc tccattattc  
9421 ctcaattaga acttctctta catagatgac tttctaagca ttggaaagaa accatagtc  
9481 gaaactagaa aaaagagata ttactaacc aattgggtca tgctgctgca caaagaaatt  
9541 gtctccctcc tctggtctca gcatggattc tgtttttctt tgcatttttt gtaaaatgga  
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9661 tttgcaaccc atgggttaga gaaacaacct tagatttttag atttttagatt ttagaagttt  
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9781 tctgaagctc atttttatta ttgctgatat ggtgacagta tttgtctttc aatcctaagc  
9841 agtgactggt ggggttaagg aatattacca gtgctgggca catgggtgta ttccttcatt  
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10201 agctaccact atttaaatg ttaacaacac aatttgattc taaaaattct tacaataaaa  
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10321 atgtgctcgg tgagaaaaac tggccactat ttctgcattt tctagtttca tgttctctg  
10381 tacaattattg ccctccttct tgattgtgtt ttgttggttt gttttggttt ttattttaaa  
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10501 tttataaaat atttgattg actttttgaa aatcaaaatt acatcagat gaaaattaat  
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10741 gtgagttttc caacagttgc ttgagattgc atcttatgtt ttgggcttga tttggagaag  
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10861 ggagtgggtg gcaaaagtgg caccatctcc agcatgcaca caatgctaaa ctgttcaatg  
10921 attgattcag tagacaaaca tttacagaat aatgccaggt agtgtgcttc agtgctagaa  
10981 ttatagttgc aaaccagaca gacaggtcac tgacctcaag gtgtttattg tcaggtgcag  
11041 tggatagaca ttaacttaat tacatactca aatgtctaac atcaataata gtaactcaca  
11101 tttattgagt tattactgta tggcagacac tattctttga gctttaaatt gataattcat  
11161 ttaattccta tgataaatct gtgagatagt tatctttatt tctgtttgaa tgttgagaa  
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11281 ccacaactct tacccgagca gtctgtctgc agagtctgtt atctcatgag aagataaatg  
11341 ctttaaaaag ataacaatga aaatattaat gattcgagta taatctggga catcccaggc  
11401 aacttgagca gttagagggt ccaggagagc aaattctagg tactcgtatg ataggctggg  
11461 gaatcagctg tgcaatggcc ctgaagtgc aagaattagg gctttcattg caaaacacca  
11521 gtggccaaaag caaggtagag agaaagcagt tttgcaacaa agaggcataa tcaaatagat  
11581 tcatttcata aatacttttt agccctcagg agacagtatg aaaaaatacc cataatccct  
11641 gctgttaaaag agggaggaaa cagaataaaa ccaagcactc agcaaatgag taataagtta  
11701 gttatttatg aagtccagtg gtgaaaaagg acacagggtg ggggactgag ggctccagtt  
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12001 ctgtccctct ctctgcgtgt cccatatctg gaatatgata tattttatgt aatgggtatt  
12061 gtctgttttt cctactaga atgtcagctt aaaaatggaca agtgtttttg ttttttatta  
12121 gtactatata caaattccca gaacagtgtc tcatatatat taaatacttt acatatgtat  
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12481 tatatgaaat atgacagtgc ttggcataga ggatgtgctt gataaatgtc gctgattctg  
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12601 ggttcagatg atctctaaaa agtttattct taattgctac atttggaaca ttctagttaa  
12661 ccatgagact gtgtttgaag tacaacaatt tgtgttattc acctaatgg ctcagttcaa  
12721 ccaatgggtg attacagtgt gtcaggccct gtgctaaatg ctagggaac aaacactctg  
12781 gctctgacct tctggcagag agcttagaga atagtattac agtataaaa gagtaaaact  
12841 tcataatatg aatagaatac atgacatatt gtgagagagg tctaaataag gggttctgag  
12901 atgtaaagat gggacattga gtccagccct agggagccag gggttcagag aagcctccct  
12961 aaaagagtac ctgaataatc ttaagtgcga gtgacagcag ctaaaatagg aatgaatgta  
13021 acagagagaa aagcaaggc agagaggcat ctaatagtat gctgtgcatt gcaaggaaag  
13081 ccagatgctc actcagtgtt tctagggcac aacattgagg caagggggat atgtgaaata  
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13201 gctagaagca gatgatagga aaccattgaa gggctcaaag caggaaactcc gtggtctgat  
13261 agacacagct tatttttctc aatgtcctta acccattatt ggaaaaataa acatatatca  
13321 aatctccctg ttctctttcc tctgatttct tcctaatatg ctattttatt gctaagctt  
13381 tcatatctca agacctcacc atatggttca aacgatatga tattccattt ccatgaatg  
13441 tatatttaat ttaattataa attgccaatt taatctctct ctatatattt cagaatgtaa  
13501 cagaatctgg atgcaagaa tgtgaggaa tggaggaaaa aaatattaaa gaatttttgc  
13561 agagttttgc acatattgtc caaatgttca tcaacacttc ttgattgcaa ttgattcttt  
13621 ttaaagtgtt tctgttatta acaaacatca cttctgctgt tagacataac aaaacactcg

13681 gcatgaa tgtgctgtca aaacaagttt ttctgtcaag aagatgatca gaccttggat  
13741 cagatgaact cttagaaatg aaggcagaaa aatgtcattg agtaatatag tgactatgaa  
13801 cttctctcag acttacttta ctcatttttt taatttatta ttgaaattgt acatatttgt  
13861 ggaataatgt aaaatgttga ataaaaatat gtacaagtgt tgttttttaa gttgactga  
13921 tattttacct cttattgcaa aatagcattt gtttaagggt gatagtcaaa ttatgtattg  
13981 gtggggctgg gtaccaatgc tgcagtgcaa cagctatgct ggtaggctcc tgccagtgtg  
14041 gaaccactga ctactggctc tcattgactt ccttactaag catagcaaac agaggaagaa  
14101 ttgtttatca gtaagaaaaa gaagaactat atgtgaatcc tcttctttat actgtaattt  
14161 agttattgat gtataaagca actgttatga aataaagaaa ttgcaataac tggcatataa  
14221 ttgccatcag taaatcttgg tgggtgtggc aataataaac ttctactgat aggtagaatg  
14281 gtgtgcaagc ttgtccaatc acggattgca ggccacatgc ggccaggac aactttgaat  
14341 gtggcccaac acaaattcat aaactttcat acatctcgtt tttagctcat cagctatcat  
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14521 catgctttcc caaatacagg tattttattt tcacattctt ttggccatgt ttatataata  
14581 ataaagaaaa accctgttga ttgttggag ccattgttat ctgacagaaa ataattgttt  
14641 atattttttg cactacactg tctaaaatta gcaagctctc ttctaattga actgtaagaa  
14701 agatgaaata tttttgtttt attataaatt tatttcacct taattctggt aatactcact  
14761 gagtgtactgt ggggtgggaa atgatctctt aagaatttga tttctttcta ttccatagta  
14821 caaactcgtt ctctgttgaa acattcttct atcaccctag tgccctatcc atgtacatgt  
14881 gttcttattg ctctagtcaa acggtgctta taaatatctt tcagaaagct taggagaaat  
14941 ctgtatccta tttagcttcc aataatca

## (2) INFORMATION FOR SEQ ID NO:96:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 486 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

1 cggattggga tcggacctac ttgattcact tctgggaaat caaggatcta cgtaccatgg  
61 attttcaggt gcagattttc agcttctctg taatcagtgc ctcagtcata atgtctagag  
121 ccaactgggt gaatgtaata agtgatttga aaaaaattga agatcttatt caatctatgc  
181 atattgatgc tactttatat acggaaagtg atgttcaccc cagttgcaaa gtaacagcaa  
241 tgaagtgcct tctcttggag ttacaagtta ttctacttga gtcgggatg gcaagtattc  
301 atgatacagt agaaaatctg atcatcctag caaacaacag ttgtcttctt aatgggaatg  
361 taacagaatc tggatgcaaa gaatgtgagg aactggagga aaaaaatatt aaagaatttt  
421 tgcagagttt tgtacatatt gtccaaatgt tcatcaacac ttcttgattg caattgattc  
481 ctcgag

## (2) INFORMATION FOR SEQ ID NO:97:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17864 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

1 aaatcctggc tgtcatgtac ttgctatggg cctagagttag cttacctaaa tgctactaac  
61 cttcctccat accattattg taaagattaa aggtgatgca tctgttaagt aactaataga  
121 gtgcttatta aaaggtaggt gttcaataag tattaattcc ctccctttct ttttcttact  
181 agtgcaattg tgtttttaat ggatcatact ttaccctaga ttgtattgta ggaggcatcg  
241 tggatggatg gctgctggaa accccttgcc atagccagct cttcttcaat acttaaggat  
301 ttaccgtggc tttgagtaat gagaatttgc aaaccacatt tgagaagtat ttccatccag  
361 tgtacttctg ttttacttct aaacagtcatt ttctaaactg aagctggcat tcatgtcttc  
421 attttgggat gcagctaata taccagttg gccc aaagca cctaaccat agttatataa  
481 tctgactctc agttcagttt tactctacta atgccttcat ggtattggga accatagatt  
541 tgtgcagctg tttcagtga gggcttccca aaacagaagc caactgggtg aatgtaataa  
601 gtgatttgaa aaaaattgaa gatcttattc aatctatgca tattgatgct actttatata  
661 cggaaaagtga tgttcacccc agttgcaaa taacagcaat gaagtgcctt ctcttggagt  
721 tacaagttat ttcacttgag tccggagatg caagtattca tgatacagta gaaaatctga  
781 tcatcctagc aaacaacagt ttgtcttcta atgggaatgt aacagaatct ggatgcaaa  
841 aatgtgagga actggagaaa aaaaatatta aagaattttt gcagagtttt gtacatattg  
901 tccaaatgtt catcaacact tcttgattgc aattgattct ttttaagtg tttctgttat  
961 taacaaacat cactctgctg cttagacata acaaaacact cggcatttca aatgtgctgt  
1021 caaaacaagt ttttctgtca agaagatgat cagacccttg atcagatgaa ctcttagaaa  
1081 tgaaggcaga aaaatgtcat tgagtaatat agtgactatg aacttctctc agacttactt  
1141 tactcatttt ttttaattat tattgaaatt gtacatattt gtggaataat gtaaaatgtt  
1201 gaataaaaaat atgtacaagt gttgtttttt aaaaaaaaaa aaaaaaaaaa  
1 tgtccggcgc cccccgggag ggaactgggt ggccgcaccc tcccggctgc ggtggctgtc  
61 gccccccacc ctgcagccag cactgatgg agaatccatt ccaatatatg gccatgtggc  
121 tctttggagc aatgttccat catgttccat gctgctgctg acgtcacatg gagcacagaa  
181 atcaatgta gcagatagcc agccataca agatcgtatt gtattgtagg aggcacgtg  
241 gatggatggc tgctggaaac cccttgccat agccagctct tcttcaatac ttaaggattt  
301 accgtggctt tgagtaata gaatttcgaa accacatttg agaagtattt ccatccagtg  
361 ctacttgtgt ttacttctaa acagtcattt tctaactgaa gctggcattc atgtcttcat

421 tttggg ttcagtgcag ggcttccctaa aacagaagcc aac tga atgtaataag  
481 tgatttgaag aaaattgaag atcttattca atctatgcat attgagctta ctttatatac  
541 ggaaagtgat gttcacccca gttgcaaaagt aacagcaatg aagtgcctttc tcttgaggtt  
601 acaagttatt tcaacttgagt ccggagatgc aagtattcat gatacagtag aaaatctgat  
661 catcctagca aacaacagtt tgccttctaa tgggaatgta acagaatctg gatgcaaaaga  
721 atgtgaggaa ctggaggaaa aaaatattaa agaatttttg cagagttttg tacatattgt  
781 ccaaagtgtc atcaacactt ctgattgca attgattcct tttaaagtgt tctctgtatt  
841 aacaacacac actctgctgc tttagacataa caaaacactc ggcattttaa atgtgctgtc  
901 aaaacaagtt tttctgtcaa gaagatgac agaccttga tcagatgaac tcttagaat  
961 gaaggcagaa aaatgtcatt gagtaataa gtgactatga acttctctca gacttacttt  
1021 actcattttt ttaattttatt attgaaattg tacatatttg tggaataatg taaaatgttg  
1081 aataaaaaata tgtacaagtg ttgtttttta agttgcactg atattttacc tcttattgca  
1141 aaatagcatt tgtttaaggg tgatagtc aaattatgtatt ggtgggctg ggtaccaatg  
1201 ct

1 ggcattgtaa tcagacagaa ctggcctcaa atcctggctg tcatgtactt gctatgggccc

61 tagagttagct tacctaaatg ctactaacct tctcccatc cattatttga aagattaaag  
121 gtgatgcatc tgtaaagtaa ctaatagagt gcttattaaa aggtaggtgt tcaataagta  
181 ttaattccct tcttctctt tcttactag tgcactttgt tttttaattg atcatacttt  
241 accctagatt gtattgtagg aggcactgtg gatggatggc tgctggaac cccttgccat  
301 agccagctct tctcaatac ttaaggattt accgtggctt tgagtaatga gaatttccgg  
361 taagaagaaa aatagatgaa aatatcctat ggaatttccc ttaaaggctg tctgaatctc  
421 agagtctttg caataagtta catggttatt ctccaaagat cttgagatat cacagatgtc  
481 tgttcacatt tggattgttc ttattttgaa aataaatagg tttttaaaaa ctctattgac  
541 catcttgata ggctcttctt gtcattataa atgtgttatt tcacttatcc cactcttttg  
601 tgttctctaa atgtctttgt actcactaaa ttgtgtagtc ttagagggca ggtgtgggt  
661 atcattcatc tttttgaaag gaagcatgaa caattagtgg ttaagggtggc agttaacact  
721 gctttctgaa actttaaaag cttcgacaac acaaaagagg caggtgaaag taccaaaact  
781 ctggaagtgt gtaggataaa tgattttcct aaatcaccaa gaaagattat tagtactct  
841 caagatggaa tacagtatct gtaattgggt ccattttatc caatttttca ccaataata  
901 ttaataaat tcattttcat aatttactg aagttaatat aactattgca tctctgttag  
961 taatgcatgt tattaacctg tgcgtataa aatattttga cctattaaaa aagaaagaag  
1021 gatgaggagg aggtcaaaga taataaaaa actttaagtgt gtgacattgg tatgtatgta  
1081 aattaacaaa tatgtcaact ttgttaaatt atctttgaca tgcactgtga gaaatctg  
1141 ttaaggaaact ttgtgcataa gagacagagt tggagggtgg agagaaagt aaaaaagata  
1201 aattatagtt ttatttttt tgataagggg cagtaattat gaaattatga caaacttaca  
1261 tcttttagacc tagaaatatg ttgacatgtt attttaaac tcacttttta actaaaaaat  
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1 cggattggga tcggacctac ttgattcact tctgggaaat caaggatcta cgtaccatgg  
61 attttcagggt gcagattttc agcttccctgc taatcagtgc ctcagtcata atgtctagag  
121 ccaactgggt gaatgtaata agtgatttga aaaaaattga agatcttatt caatctatgc  
181 atattgatgc tactttatat acggaaagtg atgttcacc cagttgcaaa gtaacagcaa  
241 tgaagtgtct tctcttggag ttacaagtta ttctacttga gtccggagat gcaagtattc  
301 atgatacagt agaaaatctg atcatcctag caaacaacag tttgtcttct aatgggaaatg  
361 taacagaatc tggatgcaaa gaatgtgagg aactggagga aaaaaatatt aaagaatttt  
421 tgcagagtgt tgtacatatt gtccaaatgt tcatcaacac ttcttgattg caattgattc  
481 ctcgag

## (2) INFORMATION FOR SEQ ID NO:98:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1610 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

1 cccagagcag cgctcgccac ctcccccg cctgggcagc gctcgccgg ggagtccagc  
61 ggtgtctctg ggagctgccg ccatggcccc gcggcgggcg cgcggtctgc ggacctcgg  
121 tctcccgcg cgctactgc tgtgtgtgt cccggcccg gcgacgagg gcatcacgtg  
181 cctccccc atgtccgtg aacacgcaga catctgggtc aagagctaca gcttgactc  
241 caggagcgg tacatttga actctggtt caagcgtaaa gccggcacgt ccagcctgac  
301 ggagtgcgtg ttgaacaagg ccacgaatgt cgccactgg acaacccca gtctcaaatg  
361 cattagagac cctgccctgg ttaccaaag gccagcgcca ccctccacag taacgacggc  
421 aggggtgacc ccacagccag agagcctctc cccttctgga aaagagccc cagcttcatc  
481 tcccagctca aacaacacag cggccacaac agcagctatt gtcccgggt cccagctgat  
541 gccttcaaaa tcaccttcca caggaaaccac agagataagc agtcatgagt cctcccacgg  
601 cccccctct cagacaacag ccaagaactg ggaactcaca gcatccgct cccaccagcc  
661 gccaggtgtg tatccacagg gccacagcga caccactgtg gctatctcca cgtccactgt  
721 cctgctgtgt gggctgagcg ctgtgtctct cctggcatgc tacctcaagt caaggcaaac  
781 tcccccgctg gccagcgtt aaatggaagc catggaggct ctgcccgtga cttgggggac  
841 cccagcaga gatgaagact tggaaaaactg ctctcaccac ctatgaaact cggggaatac  
901 agcccagcta agtccggagt gaaggagcct ctctgcttta gctaaagac actgagaaga  
961 ggtgcaagga agcgggctcc aggagcaagc tcaccaggcc tctcagaagt cccagcagga  
1021 tctcacggac tgccgggtcg gcgcctcctg cgcgaggag caggttctcc gcattcccat  
1081 gggcaccacc tgctgcctg tcgtgccttg gaccagggc ccagcttccc aggagagacc

1141 aaaggc gagcaggatt tttatttcat tacagtgtga gct gga ataatgttg  
1201 taatgaaata aaaaccctgc cccgaatctt ccgtccctca tcttacttg cagtccacag  
1261 agaaaagtga catacccaaa gctctctgtc aattacaagg cttctcctgg cgtgggagac  
1321 gtctacaggg aagacaccag cgtttgggct tctaaccacc ctgtctccag ctgtctgtca  
1381 cacatggaca gggaccctggg aaaggtggga gagatgctga gccagcgaa tctctccat  
1441 tgaaggattc aggaagaaga aaactcaact cagtgccatt ttacgaatat atgcgtttat  
1501 atttatactt cctgtctat tatactata cattatatat tatttgtatt ttgacattgt  
1561 acctgtgata aacaaaataa aacatctatt ttcaatattt ttaaaatgca

## (2) INFORMATION FOR SEQ ID NO:99:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

1 atgcttgacc tcaactctc cactgactct gcagcctcag cctctgcagc cagtgtgtt  
61 tctgtagaat ctacagcaga ggcacagtc tgcacgtga cactggagaa gatgtcggca  
121 gggctgggct tcagcctgga aggaggggag ggctccctac acggagacaa gccctcacc  
181 attaacagga ttttcaaagg agcagcctca gaacaaagt agacagtcca gcctggagat  
241 gaaatcttgc agctgggtgg cactgccatg cagggcctca caggtttga agcctggaac  
301 atcatcaagg cactgcctga tggacctgtc acgattgtca tcaggagaaa aagcctccag  
361 tccaaggaaa ccacagctgc tggagactcc tag

## (2) INFORMATION FOR SEQ ID NO:100:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

1 tgcttaaaaa aacacaacag gattttcgaa gaatccttc ttagaaaaa aacaaaaaa  
61 ccaaacaaaa acgtactttc tccccactag tttacaccac aggaagcgag agagctgctg  
121 ccactgctgc taccacagga agacacagca gggagaagcc ctagtgcctc tgccggctgc  
181 ccaggacctg gtatcgggcc acagaccaag tcttccacag agggcgagcc aggttgagga  
241 agagccagcc cagtgaacca aacatccccg ataaaacacc cactgcttaa gaggcaggct  
301 cggatggact atagctttga taccacagcc gaagaccctt gggtaggat ttctgactgc  
361 atcaaaaaact tatttagccc catcatgagt gagaacctg gccacatgcc tctacagccc  
421 aatgccagcc tgaatgaaga agaagggaca cagggccacc cagatgggag cccaccaaa  
481 ctggacaccg ccaatggcac tccaaaagt tacaagtac cagacagcag cactgtgaag  
541 aaaggtcctc ctgtggctcc caagccagcc tggtttcgcc aaagcttgaa aggtttgagg  
601 aatcgtgctt cagagccaag agggctccct gatcctgcct tgtccacca gccagcacct  
661 gcttccaggg agcacctagg atcacacatc cgggcctcct cctcctcctc ctccatcagg  
721 cagagaatca gctcctttga aacctttggc tctctcaac tgctgacaa aggagcccag  
781 agactgagcc tccagccctc ctctggggag gcagcaaaac ctcttgggaa gcatgaggaa  
841 ggacggtttt ctggactctt gggggcaggg gctgcacca ctcttgtgcc ccagcagcct  
901 gagcaagtac tgcctcggg gtccctgca gcctccgagg ccagagaccc aggtgtgtct  
961 gagtccctc cccagggcg gcagcccaat cagaaaact tccccctgg cccggaccg  
1021 ctctaaaggc tgctgtcaac acaggctgag gaatctcaag gccagtgct caagatgcct  
1081 agccagcgag cacggagctt ccccctgacc aggtcccagt cctgtgagc gaagctactt  
1141 gacgaaaaga ccagcaaaact ctattctatc agcagccaag tgtcatcgcc gaagttctg  
1201 tcttctgtgt gccttccatc ttctatctcc tgtgcccaga ctccctgcat cccaaggca  
1261 ggggcatctc caacatcatc atccaacgaa gactcagctg caaatggttc tgctgaaaca  
1321 tctgccttgg acacgggggt ctcgctcaac ctttcagagc tgagagaata tacagagggt  
1381 ctcacggaag ccaagggaaga cgatgatggg gaccacagtt cccttcagtc tggctagctc  
1441 gttatctccc tgctgagctc agaagaatta aaaaaactca tcgaggaggt gaaggttctg  
1501 gatgaagcaa cattaaagca attagacggc atccatgtca ccatcttaca caaggaggaa  
1561 ggtgctggtc ttgggttcag ctgggcagga ggagcagatc tagaaaacaa ggtgattacg  
1621 gttcacagag tggtttccaaa tgggctggcc tcccaggaa ggaactattca gaagggaat  
1681 gaaggttctt ccatcaacgg caagtctctc aaggggacca cgcaccatga tgcttggcc  
1741 atcctccgcc aagctcgaga gccagggcaa gctgtgattg tcacaaggaa gctgactcca  
1801 gaggccatgc ccgacctcaa ctctccact gactctgcag cctcagcctc tgcagccagt  
1861 gatgtttctg tagaatctac agcagaggcc acagtctgca cggtagact ggagaagatg  
1921 tggcaggggc tgggcttcag cctggaagga ggggaaggct ccctacacgg agacaagcct  
1981 ctcaccatta acaggatttt caaaggagca gcctcagaac aaagtgaagc agtccagcct  
2041 gggatgaaa tcttgagct gggtggcact gccatgcagg gcctcacagc gtttgaagcc  
2101 tggaaatca tcaaggcact gcctgatgga cctgtcacga ttgtcatcag gaaaaaagc  
2161 ctccagtcga aggaaccac agctgctgga gactcctagg caggacatgc tgaagccaaa  
2221 gccaaataca cacagctaac acacagctcc cataaccgct gattctcagg gtctctgtg  
2281 ccgccccacc cagatggggg aaagcacagg tgggcttccc agtggctgct gccaggccc  
2341 agaccttcta ggagcccacc cagcaaaagg ttgttcttaa aataagggca gactcacact  
2401 gggcgagctg atacaaattg cagactgtgt aaaaagagag cttaattgata atattgtgt  
2461 gccacaaata aaatggattt attagaattc catatgacat tcatgcctgg cttcgcaaaa  
2521 tgtttcaagt actgtaactg tgtcatgatt ccccccaaa cagtgcattt ttttttctc  
2581 atgaatctgc aatgtgggca gagattggaa tgggcagctc atctctgtcc cacttggcat



2641 cagctggt catgcaaagt catgcaaagg ctgggaccac ctgagatcat tcactcatal  
2701 atctggccgt tgaatgtggc tgggaactca cctggggctg ctggcctgaa tgcttatagg  
2761 tggcctctcc ttgtggcctg ggctcctcac aacatgggtg ctggattccc aggatgagca  
2821 tcccaggatc gcaagagcca cgtagaagct gcatcttgtt tatacctttg ccttggaggt  
2881 tgcattggcat cacctccacc atactccatc agtttagagct gacacaaacc tgcctgggtt  
2941 taaggggaga ggaatatatt ctgggggtcat ttatgaaaaa tacagtttgt cacatgaac  
3001 atttgcacaaa ttgtttttgg ttggatttga gaagtaatcc tagggaaggc tgggtggagcc  
3061 agtaaataga ggagtacagg tgaagcacca agctcaaagc gtggacaggt gtgccgacag  
3121 aaggaaccag cgtgtatatg aggttatcaa ataaaattgc tactacttac ctacc

## (2) INFORMATION FOR SEQ ID NO:101:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3568 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

1 atgctgacc tcaactctc cactgactct gcagcctcag cctctgcagc cagtgtatgtt  
61 tctgtagaat ctacagcaga ggccacagtc tgcacgggtga cactggagaa gatgtcggca  
121 gggctgggct tcagcctgga aggagggag ggctccctac acggagacaa gccctcacc  
181 attaacagga ttttcaaagg agcagcctca gaacaaagt agacagtcca gcctggagat  
241 gaaatcttgc agctgggtgg cactgcatg cagggcctca cagggttga agcctggaac  
301 atcatcaagg cactgcctga tggactgtc acgattgtca tcaggagaaa aagcctccag  
361 tccaaggaaa ccacagctgc tggagactcc tag  
1 tgcttaaaaa aacacaacag gattttcgaa gaatccttc ttgaaaaaca acaaaaaaaa  
61 ccaacaaaa acgtactttc tccccactag ttacaccac aggaagcgag agagctgctg  
121 ccactgctgc taccacagga agacacagca gggagaagcc ctagtgcctc tgccggctgc  
181 ccaggacctg gtatcgccc acagaccaag tctccacag agggcgagcc aggggtgaga  
241 agagccagcc cagtgaacca aacatccccg ataaaaacac cactgcttaa gaggcagct  
301 cgatggact atagctttga taccacagcc gaagaccctt gggtaggat ttctgactgc  
361 atcaaaaact tatttagccc catcatgagt gagaacctat gccacatgcc tctacagccc  
421 aatgccagcc tgaatgaaga agaagggaca caggggcacc cagatgggac cccaccaaa  
481 ctgtacaccg ccaatggcac tccaaaagt tacaagtca cagacagtag cactgtgaag  
541 aaaggtcctc ctgtggctcc caagccagcc tggtttcgcc aaagcttgaa aggtttgagg  
601 aatcgtgctt cagagccaag agggctccct gatcctgctt tgtccacca gccagcact  
661 gcttcaggag agcacctagg atcacacatc cgggctcctc cctcctcctc tccatcagg  
721 cagagaatca gctcctttga aacctttggc tctctcaac tgctgacaa aggagcccag  
781 agactgagcc tccagccctc ctctggggag gcagcaaaac ctcttgggaa gcatgaggaa  
841 ggacggtttt ctggactctt ggggagagg gctgcaccca ctctgtgccc ccagcagcct  
901 gagcaagtac tgcctcggg gtcccttgca gcctccgagg ccagagaccc aggtgtgtct  
961 gagtccctc cccagggcg gcagcccaat cagaaaact tcccccttg cccgagccg  
1021 ctccaaaggc tgcgtgcaac acaggtgag gaatctcaag gccagtgct caagatgcct  
1081 agccagcgag caggagctt cccctgacc aggtccagt cctgtgagc gaagctactt  
1141 gacgaaaaga ccagcaaaact ctattctatc agcagccaag tgcacgcgc tgcattgaaa  
1201 tcttctgtgt gccttccatc ttctatctcc tgtgccaga ctccctgcat cccaaggca  
1261 ggggcatctc caacatcatc atccaacgaa gactcagctg caaatgggtc tgctgaaaca  
1321 tctgccttgg acacgggggt ctgcgtcaac ctttcagagc tgagagaata tacagaggtt  
1381 ctcacggaag ccaaggaaga cgtatgtgg gaccacagt ccttcagtc tggctagtc  
1441 gttatctccc tgcgtgctc agaagaatta aaaaaactca tcgaggaggt gaaggtctg  
1501 gatgaagcaa cattaagca attagacggc atccatgtca ccatcttaca caaggaggaa  
1561 ggtgctggtc ttgggttcag cttggcagga ggagcagatc tagaaaaaa ggtgattacg  
1621 gttcacagag tgtttccaaa tgggctggcc tcccaggaag ggactattca gaagggaat  
1681 gaggttcttt ccatcaacgg caagtctctc aaggggacca cgcacatga tgccttggcc  
1741 atcctccgce aagctcgaga gccagggcaa gctgtgattg tcacaaggaa gctgactcca  
1801 gagggcatgc ccgacctcaa ctccctcact gactctgcag cctcagcctc tgcagcagt  
1861 gatgtttctg tagaatctac agcagaggcc acagtctgca cggtagactt ggagaagatg  
1921 tcggcagggc tgggcttcag cctggaagga gggagggct cctacacgg agacaagcct  
1981 ctcaccatta acaggatttt caaaggagca gcctcagaac aaagttagac agtccagcct  
2041 ggagtagaaa tcttgagct ggttgagcact gccatgcagg gcctcacag gtttgagcc  
2101 ttgaacatca tcaaggcact gcctgtgga cctgtcacga ttgtcatcag gagaaaaagc  
2161 ctccagtcga aggaaccac agctgctgga gactcctagg caggacatgc tgaagccaaa  
2221 gccaataaca cacagctaac acacagctcc cataaccgct gattctcagg gtctctgctg  
2281 ccgccccacc cagatggggg aaagcacagg tgggcttccc agtggctgct gccagggccc  
2341 agaccttcta ggacggcacc cagcaaaagg ttgttcctaa aataaggga gagtacact  
2401 ggggcagctg atacaaattg cagactgtgt aaaaagagag cttaatgata atattgtgtg  
2461 gccacaaata aaatggattt attagaattc catatgacat tcatgcctgg cttcgcaaaa  
2521 tgtttcaagt actgtaactg tgcattgatt ccccccaaa cagtacatt tatttttctc  
2581 atgaatctgc aatgtgggca gagattggaa tgggcagctc atctctgtcc cacttggcat  
2641 cagctggcgt catgcaaagt catgcaaagg ctgggaccac ctgagatcat tcactcatal  
2701 atctggccgt tgaatgtggc tgggaactca cctggggctg ctggcctgaa tgcttatagg  
2761 tggcctctcc ttgtggcctg ggctcctcac aacatgggtg ctggattccc aggatgagca  
2821 tcccaggatc gcaagagcca cgtagaagct gcatcttgtt tatacctttg ccttggaggt  
2881 tgcattggcat cacctccacc atactccatc agtttagagct gacacaaacc tgcctgggtt  
2941 taaggggaga ggaatatatt ctgggggtcat ttatgaaaaa tacagtttgt cacatgaac  
3001 atttgcacaaa ttgtttttgg ttggatttga gaagtaatcc tagggaaggg tgggtggagcc



3061 agtaaatgaggtacagg tgaagcacca agctcaaagc gtgagggt gtgccgacag  
3121 aaggaaccag cgtgtatatg agggatatcaa ataaaattgc tacttattac ctacc

## (2) INFORMATION FOR SEQ ID NO:102:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9203 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

1 gaattcatgc cacaactgag tgattttttt ttctcacaac ccaattccac aaagtaaaag  
61 cctgatgaaa tacagtgaag gctgatgctt attactgtg ttcccaaat ccagagctct  
121 aaaaagggtc tgcatacagt cattcattca atgcttaacg actgagcatt aattccatgc  
181 taagtactga actcagcact aggaataaga aggcgacctg gaggcatact ctctctctaa  
241 agatgcatag agcctcattg gaatgatcag ccgtgtctcc agagagctac aaggcagttt  
301 tcaattggta aatgccctga gagtgatggg ctgtgtggcat gtgtaagggt tagacagacc  
361 tgggacctag acatgacacc actcctgacg aattatgtga gtgtgggtgt ttcacaacca  
421 caatgagatg caatgcctgc acttgtaaca tggaaatagt gatggcatgc cccgcagatt  
481 gctgtgagaa gtcagcggca gagacatgca acattctcag cacagtgcct gccatgtagt  
541 aagggcctag tcagtgttag tgattccttt caatattcct aagatgcaga taagggaaca  
601 gccagagga gggggagcac ttccagaggg aggaatgcgg tgagacttcc ttcagcaggg  
661 tagcactgga gctgggtgtt aaggagttag tgagctttgg gcttatggat ttaacagagg  
721 aaaccaagaa aagaggaggc ggtgttgtag gaacagttag cagttgatga tttttatttt  
781 gttctctggt ctgcttgga acatttttgg ggcaaagaca gcatgaagg tagcgaagaa  
841 ttaatactga agagataggc cagggcaggt tatgaaggat tttgaatacc gggctaagaa  
901 atgtgggctt aatttcaaag acattatgga cactcctaaa atgttacgtt gtagataagg  
961 gaaaagtatt cttccagaag attaaattgg ggctgggcac ggtggctcac gcctgtgatc  
1021 ccagcacttt gggaggcgaa gtgggcagat cacctgaggt caggagtttg agatcagcct  
1081 ggccaacgtg gtgaagcccc atctctactg aaaaaaaaaa ttagccgggc atgtgggtgg  
1141 gtgcctgtaa tctcagctac ttgggaggtt gaagcaggag aatcacatga acctgagagg  
1201 cagaggttgc agtgagccaa gattgcacca ctgcattcca gtgggcgaca gagcaagact  
1261 cagtcaaaaa aaaaaaaga ttaactgga agcaatgggt aagaatggtg gagtggagag  
1321 acacatttga gtgagggaa ccagctgaaa agctgtacag acgtctagac aaaatgtgac  
1381 acaagcatgc cttcacctcc ctgcaaagac cacagaccac tgagctccaa agggggtttg  
1441 gaatccttgt cctgggcgcg catttggttaac tcatcagtgc tggcttgaga gataaactct  
1501 attatccatc cctgaactaa aatcatgaca gaagtggcca gggagctttg ctgctatccc  
1561 ccaggaac acgtcctcca ctcaaattga aagaggacct tctgacaaca tctgtgggac  
1621 ccaacagcac tggtcaccac aagccacaaa atgttaacaa agtcagtttt caattgttag  
1681 ggagggagga ctcagttcat gattcataca aaccaactgt tctctccag tgtttcttgg  
1741 gtggcacaac ccacaagtca acagtggcct gggaactaga catttgagta gagtgggtt  
1801 atttgattca tagtggattt tggttttcca cgggaccctt gtgcccttgt ctagtgaat  
1861 ctggtgaaa ttacaaactg cagaaattca actcagtgcc gcaataacag gatgcacctg  
1921 tagatttcgt agaattagca gcagcattct ttcaatacca gtttgagaga aataaccttg  
1981 tttgcatagt gccaaactgg gcagaatctg aagtgtcttg cctgcctctc ggccatggga  
2041 ggcacgcgat tcagcaacat ctatcccaacc gccatccact taacaagcaa agatggagg  
2101 cctcgtgct ccaggctatc ctgcaatggt tcatttgctt ttgatgggat tatcactttg  
2161 acagatgtgc ttgcaattaa ctgggggctt tctgcttcca atccaaattc ccacaggtgg  
2221 atcactggct cttggggagc aaaaaccctt ctttgtttgt ttttgcttct ccagagcct  
2281 gggcagagct ccccatctct ggatcctacg ttgatatgca ctgaattgaa ttatactaaa  
2341 ggggtgcccc aagagtgcac gagctaagta aaatgtaatt tgtgggacct catgtggaca  
2401 tttcaggtcc atgtgtacaa gataaaggag agaaaatcct gggggacacc acagggctgg  
2461 gaaaatgacc tctactaag cctaacaaga acatccagta cataaacagc aggtctctctg  
2521 caaccgttc ggtccttcca ctgccacgct ccagaaaagc aaagggttat ctctgtctg  
2581 gattttggct ctgagaccac agctcagcac atcactcctc tagagaaaag aaagtctaag  
2641 atgagagagt gaggtgctt tcatgtgggt ccagcgtata gtgcagggca ggcctgattg  
2701 ctgaaccgat ccctgcagac gtgagcggtc acttcccctt ttgagggcca attcttttct  
2761 ctctttgagg agactgtgag cgtcctcagt gcagggctat gttttagctt cttggctctc  
2821 ctacaggtt ctacataat tctttgatta attgcagtca acgtttattg atggattatg  
2881 tgacagaggt gaaattcttt gatctgggtt tcagcttttc ctttccccca ctccctcctt  
2941 tttctttttt tttttttttt ttttttagag cgaggtcttg ctctgtggcc ctggctggag  
3001 tgcagtgtg caatcatagc tcattgcagc cttgacctcc tggggctcaa cgaacctcaa  
3061 cgtcttgccc tctgagtag ctgggactat aggcattgcg caccacgctc agcttcacct  
3121 tttcctttcc ttgtgctccc ctggcagata tgctggtaaa caatgaacca gtcaagagga  
3181 cagcaacagg aggaaaatgg gagaaccccc attattcgtg gactaaacag gcttcccact  
3241 agtccctggct cacagaggaa gtcattgctc atgtttcaaa tgtcctcaaa gctcgttcaa  
3301 ctccaaaatg catgaagaca aaatgggaat tttactcaag atttttgtgg gctgttgggg  
3361 agaagagtta acattgcaaa gcatattgca aactcttatc ttcaaatgat tttaaaattt  
3421 tcttccaagc tctttattat ttctccagag ctgccctgct cttccactc tgggtccttt  
3481 ctctgccaact ctctcagca tgacttctcc ctaatcggcc agcatttctt ttattctata  
3541 gagcaagttt tcttgccctg ggcacctctc atttgcatgt tataccacca caccaagtga  
3601 gcctcagagc accagtgttt taatccctga aaacagtcct tacgggatc agcacagagg  
3661 tctcttggc agcctgtagt ctccagatg acacgtcctc aacagtcaaa gtgagcaagc  
3721 tatggtgccc atcccaagt ggggtcacc atttccctct gcgttcactt ctctcctacc  
3781 ttcttcttta tccatcctt cctccttctt ttttttttct gcattcaatt attcatggtt  
3841 attcatttca tacgggcac tgtgccactt ggttctacag gcattttttt ttttgagaca

3901 gacttttccc cttgtccccc aggttgccgt gcagcgggtg gatcttggct cactgcaatc  
3961 tccacctcct aggttcaagc aagtctctcg ccttagcctc ccaagtagct ggaattacag  
4021 gcatgtgcc acaagcccg ccaatttttg tatttttagt agagacaggg tttcaccatg  
4081 ttggccaggc tggctcctaa ctctgacct caggtgatct gcctgcctcg gcctcccaaa  
4141 gtgctgggat aacaggcggt agccatcgtg ctccggccgtg tctatgggca ttgtggaagt  
4201 gaccgttaac aagccccaag ggtaagtaa ggaaaatgaa aggtgattga ttcctcacca  
4261 cctctcccct ttttctctct actctttgct cctgctcccc aatctagact ctaataaaca  
4321 gaaatgattt ttgttgcaag ctgaaaactc gttcttggg ttggggctag ggggggtggc  
4381 agtcaagctt tagagttgtc tggataataa argctgtctt caaggactgt ccaacattgt  
4441 aggaacaaga gaacaaccca agtgaacaac taactcctgt tcacaaatgc tactgcctct  
4501 ctgccatccc ctaacctcag cctcacacac ttgaatttcg ccaatccatt tgatgagctc  
4561 aaatcagtg aatttctcct cgccaaagct cacaaattct gttccccgtt tcttgcccca  
4621 catccaggca ttaccaactg cttttccct ttgctgata ttctggcctc aagcctcctt  
4681 gccattccaa tttatttcac cttctccag tcttatgat tctctcctg aagagtattt  
4741 cagcatctct atgcctcaat ctccctgca caccacacca gctcggcctc atcatcacat  
4801 tacttggcta tgtcccgctt gggtagaca gcttcagtgg ctgaagtcca tagatcttat  
4861 tctgtttttc gaggtccacc tgactctgaa tccagctgac atttctgccc ttagcttcta  
4921 cccctctcta ctctgggta actatggacc acactctgct tccctaggaa ccactacca  
4981 aggccgtatc catccttcaa ggacaatacg tgggcctttc ctgatcacat cagctcaaca  
5041 acttttccct cctacatttc aattgctctt cttaccataa tcattagtat tcacccact  
5101 gtacgtctag aaagaaagt gtcttaaac taagggaagg cagtctaggt cagaaatttg  
5161 ttgtccgctg ttctgagcag tttcttctag gaagtacca acatttctga taatagaatt  
5221 gagcaatttc ctgatgaagt gagactcagc ttgcaactgt gaccggctgt cctggatgaa  
5281 cctagttact ttaacaaaa tgttcttctc ttgaacttgt tcttctctg aacttaactt  
5341 atcaatgtta tctagataac tttctcctc aaaaaaaaa aaaaaaaaaa cctctacta  
5401 ggaagaaat ctttgaaccg gacttatttg aaattacctc cttgcagcag gtttgaaca  
5461 aaactttgaa tttgcctcac aaagaatttg tctgaaactg ctttagtata tgctagttat  
5521 attgtatgc acatgtggct tcatacatag ttggttgaca cccatagtgt ttatgcactt  
5581 tgttaggtga cgtaagtcca cagataaact ggaacatagg gctatcctct agaggccac  
5641 agtttgacac cttaacctga gatccttggc ctttgaagt tcagagtgc cacaaccgct  
5701 ggtgtgtgtg gctcacactt gtaatccag tactctgcag ggctgaggtg ggaggtcgc  
5761 ttgagtcag gagtctgaga ccagcctggg caacatgaca aaaccccatc tctcaaaaa  
5821 ttacaaaaaa aattagccag gcctgggtgt gcatgcctgt ggtcccagt acttgagagg  
5881 ctgaagtggg aggatcactt gactcaagg ggtagaggct gcagtgaagt gagatggcaa  
5941 cactgcactc cagaaacccc atctcaaaaa aaacagagca aaacaaaaa aactgcccac  
6001 aatgctcctg aaacttccca cggatttatc cagagtatgt gctgatgtgc attttttcca  
6061 agggagggaaa ccaagggttc tatcaaatat agaaaagagt ttttaccatt gtggaagaca  
6121 gtagggcgat tctcaagca tctaaaatca gaaataccat ttgaccagc aatcctatta  
6181 ctgggtatat acccaaggga atagaaatca ttctactata aagtacatg caaccgtatg  
6241 tttattgcag cactatttac aatagcaaaa tggaaaccaac tgaaatgccc atcaatgaga  
6301 ctagataaag aaaatgtgat acatatacac catggaatac tatgcagcca tgaaaaggaa  
6361 tgagatcacg tcttggcag ggacatggat gaagctggaa gccattatcc tcagcaaaact  
6421 aacacaggaa cagaaaaacca aatgcccgat gttctcactc ataagtggga gttgaacaat  
6481 gacagcacat agacatagg aggggaacat cacacgccag ggcctgctgc aggggtgggg  
6541 gtgggggtgt aggggagggg acttagaaga caggtgagta ggtgcagcag accaccatgg  
6601 cacacttata cctatgtaac caacctgcac gttctacaca tgtatcctgg aacttaaat  
6661 aaaaaaaaaa aagagttttt aatccaagaa agattaacag caactagaag aaagaaagag  
6721 atataaacag tgaattgcaa tgcagcacgg caggtgttat gatggagtag aaaggactgg  
6781 aaaaaggcctc ctggaggaag ggacactcaa gtgtctttcc atttcactg taactcatt  
6841 aagggcaaaa gctttgtac agcttcagta tgagatcctg ggcaatccgt gacaaaattg  
6901 gtctgctttt gcacccccaa cttcttctca catcctgca tctgtccatg cagcatcaac  
6961 tggaaacctc agcgtcagca aacgacgaca gagcgttcat ccgtaagggtg aaccagaaaa  
7021 gccagttcaa tgacttgttt aacctgtgtc catctcagaa ccaagagtgt ggcctcttat  
7081 ttaccagaaa aattgtgggg gctttgtgat atggctttaa aaaaatctgt taattgccag  
7141 gcgtgggtgg tcacacctgt aatcccgaca ctttgggagg ccgaggtggg tgaatcgctt  
7201 aaggtcagga gttcgagacc agcctgacca acatgggtgaa actcctgctc tactaaaaat  
7261 acaaaaaacta gctggatgtg gtgacgcgtg cctgtaatcc tagctactca ggaggtgac  
7321 gcaggagaat cacttgaacc tgggaggcag aggttgagat gagccaagt tggtccattg  
7381 cgctccaaaa aaaaaaaaa aatacattaa cataaattta aatattttat aatgacaatc  
7441 cacatttaact acttaagca taagctattt tccaggagag gcagcaagt cttctactc  
7501 ccagcccaa gaagaaagga gcgtgacttt ggtgggagta ctaggagttt ctactggagc  
7561 acttgcccg agagtgaaga acgttcctag agaggaagtt atacctgctg ttggaatttaa  
7621 gagaatcttg tcatattttg acaagttttt tgagatggaa gtctcactct gtcgcccagg  
7681 ctggagtga gtggcgcaat ctcagctcac tgcagcctgc acctcctcgg ttcagctat  
7741 tctctgtct cagcctcct agtaactggg attacaggcg cccgcaacta cgcctggcta  
7801 atttttgtat ttttagtaga aatggggttt tactatgttg gccagactgg tctcaaaact  
7861 ccgacctcag gtgatctgcc tgccctcagc tcccaaagtg ctggaattac aggcgtgtgc  
7921 cactgcgcct ggctaatttt tttttttttt ttttttttagt agagacgggtg gtttaccat  
7981 gtcattccagg ctggtctcaa actcctgacc tcaggtgatc caccacactt ggtctaccaa  
8041 agtgctcga ttacaggcat gagccaccag gccagtcgaa cgtgatgtgt tttggaaccc  
8101 tgaattcctt ggcttgccgg aggtttttct ttttggtaat atctttgtt gctttctagt  
8161 atttaaaaaa ttgtgttttg ctctaactat gcaatggctt taagtcttag acaattttcc  
8221 agggagcaaa acacactcaa ccaatttcat aataatcaga agagagctct gatcaataaa  
8281 taagcaagac tgaattttac aaaataatcc aaagttaaaa accaaagccc actttttgca  
8341 tgatccttta agagaaagaa atctggaagc aaaacacctt ataaaatgac aatgcacttt

8401 caggagc gggcactgtg gtgaaatgat gatggctagt acata agccttgggg  
8461 aattatttat gaattctcag gatccttcag ttcgccgcat cttttccat tatttgaata  
8521 ttggaggctg cctgaccaga atcttgtcag gactttgtc cttcatccca ggtgggtccc  
8581 gctgactcct gaggacgtta cagccctgag gggaggactc agcttatgaa gtgctgggtg  
8641 agaccactgc caagaagtgc ttgctcacc taccttcaac ggcaggggaa tctcctctc  
8701 cttttatggg cgtagctgaa gaaaggattc ataatgaag ttcaatcctt ctcatacaac  
8761 ccagcccaca cctccagcaa ttgaacttga aaaaaaaaac ctggtttgaa aaattaccgc  
8821 aaactatatt gtcataaaaa aaaaaaaaaa aaaaacactt cctatatttg agatgagaga  
8881 agagagtgtc aggcagtttc ctggctgaac acgccagccc aatacttaaa gagagcaact  
8941 cctgactccg atagagactg gatggaccca caaggggtgac agcccaggcg gaccgatctt  
9001 cccatcccac atcctccggc gcgatgccaa aaagaggctg acggcaactg ggccttctgc  
9061 agagaaaagac ctccgcttca ctgcccggc tggcccaag ggtcaggaag atggattcat  
9121 acctgctgat gtggggactg ctcacgttca tcatggtgcc tggctgccag gcaggttaag  
9181 gcctgtgggt gccccggaa ttc

## (2) INFORMATION FOR SEQ ID NO:103:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2335 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

1 gaattccccc ccccccccc cgagagactg gatggaccca caaggggtgac agcccaggcg  
61 gaccgatctt cccatcccac atcctccggc gcgatgccaa aaagaggctg acggcaactg  
121 ggccttctgc agagaaaagac ctccgcttca ctgcccggc tggcccaag ggtcaggaag  
181 atggattcat acctgctgat gtggggactg ctcacgttca tcatggtgcc tggctgccag  
241 gcagagctct gtgacgatga cccgccagag atcccacacg ccacattcaa agccatggcc  
301 tacaaggaag gaacctgtt gaactgtgaa tgcaagagag gtttcccgag aataaaaagc  
361 gggtcactct atatgtctg tacagaaac tctagccact cgtcctggga caaccaatgt  
421 caatgcacaa gctctgccac tcggaacaca acgaaacaag tgacacctca acctgaagaa  
481 cagaaagaaa ggaaaaccac agaaatgcaa agtccaatgc agccagtggc ccaagcgagc  
541 cttccaggtc actgcaggga acctccacca tgggaaaatg aagccacaga gagaatttat  
601 catttcgtg tggggcagat ggtttattat cagtgcgtcc agggatacag ggctctacac  
661 agaggctctg ctgagagcgt ctgcaaaatg acccacggga agacaagggt gacccagccc  
721 cagctcatat gcacagtgga aatggagacc agtcagtttc caggtgaaga gaagcctcag  
781 gcaagccccg aaggccgtcc tgagagtga acttctgccc tcgtcacac aacagatttt  
841 caaatacaga cagaaatggc tgcaaccatg gagacgtcca tatttacaac agagtaccag  
901 gtagcagtgg ccggctgtgt ttctctgctg atcagcgtcc tctcctgag tgggctcacc  
961 tggcagcggg gacagaggaa gagtagaaga acaatctaga aaacccaaa aacaagaatt  
1021 tcttggttaag aagccgggaa cagacaacag aagtcatgaa gcccaagtga aatcaaaggt  
1081 gctaaatggt cgtccaggag acatccgttg tgcttgctg cgttttgaa gctctgaagt  
1141 cacatcacag gacacggggc agtggaacc ttgtctctat gccagctcag tcccatcaga  
1201 gagcgagcgc taccacttcc taaatagcaa ttctccggtt gaagaggaag ggcaaaacca  
1261 ctagaactct ccatcttatt ttcatgtata tgtgttcatt aaagcatgaa tggatatgaa  
1321 ctctctccac cgtatatgta gtataaagaa aagttaggtt acattcatct cattccaact  
1381 tcccagttca ggagtcocaa ggaaagcccc agcactaacg taaatacaca acacacacac  
1441 tctaccctat acaactggac attgtctgct tggttccttt ctcagccgct tctgactgct  
1501 gattctcccg ttcacgttgc ctaataaaca tccttcaaga actctgggct gctaccacga  
1561 aatcatttta cccttggtc aatcctctaa gctaaccctt ttctactgag ccttcagtct  
1621 tgaatttcta aaaaacagag gccatggcag aataatcttt gggtaacttc aaaacggggc  
1681 agccaaaccc atgaggcaat gtcaggaaca gaaggatgaa tgaggtccca ggcagagaat  
1741 catacttagc aaagttttac ctgtgcgtta ctaattggcc tctttaagag ttagtttctt  
1801 tgggattgct atgaatgata ccctgaattt ggcctgcact aatttgatgt ttacaggtgg  
1861 acacacaagg tgcaaatcaa tgcgtacgtt tcctgagaag tgtctaaaaa caccaaaaag  
1921 ggatccgtac attcaatgtt tatgcaagga aggaagaaa gaaggaagtg aagagggaga  
1981 agggatggag gtcacactgg tagaacgtaa ccacggaaaa gagcgcatca ggcttggcac  
2041 ggttggtcag gcctataacc ccagctccct agggagacca ggcgggagca tctcttgagg  
2101 ccaggagttt gagaccagcc tgggcagcat agcaagacac atccctacaa aaaattagaa  
2161 attggctgga tgtggtggca tacgctgta gtcctagcca ctgaggaggc tgaggcagga  
2221 ggattgcttg agcccaggag ttcgaggctg cagtcagtca tgatggcacc actgcactcc  
2281 agcctgggca acagagcaag atcctgtctt taaggaaaaa aagacaaggg aatttc

## (2) INFORMATION FOR SEQ ID NO:104:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1092 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

1 gaattcatgg aaatgggaag ggcagtgatg gagatgggaa ggcagtggg ggttgaggg  
61 gtggggattg ttgttgggta cgaaaacaga attagatcga atgaataaga tctagtattt  
121 gatagcataa cagggtgact ttagtcaaca ataatttatt gtacatttaa aataactaa  
181 aagagtatac ttggatttta acacaaagaa aggataaata cttgaggtga tggatacccc  
241 atttaccctg atgtgattat tatacattgt atgctgtat caaaatagct catgtgcctc

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301 atgaatatag acacctacca catgccacaa aaattaaaaa ctaaaaaaaa cagtcattctc
361 tgaatgctaa acggagtaag gggcttcttg gaaggctggg tgaatggga gtctcgaaa
421 gatggtgtgt tgcaggctgg gaggggggtg agacgctggg gtcacctaga gggacctgct
481 tgtgtgaagc ctacgtatta gtgggtatgt gtgtgaccgg atggaggcgt cagagggtgtt
541 gggtagcctg tgtgagttgg cgtgggggtg atgtaggagg ggagagaggg agggcctgcg
601 ttcccttggc tcctgtgtgc agctaggccc ctatttgaca atgtgtgtct gtgtgtgtgt
661 gtgtgtgtgt gtgtgtgtgt gtgtgcccgc ccagcgtag gaggcagatc tttatctggc
721 cctgggtgct tgaggagttt caggctttct cataagcctc gtctcccgc ctctccacc
781 caggccttgc ccctctatcc tctgcacagg aagtgggctg gctctgggct tttagtcttt
841 gcggccccag cagccagagc tcagcagggc cctggagaga tggccacggg cccagcaccg
901 gggaggactg gagagcgcgc gctgccaccg ccccatgtct cagccagggtg atgtcccctt
961 gcctccctcc cggccctgtg ggaccagcca gagggctggg agtgaaagtc acagagaaga
1021 ctttcagctc tgactcagtt cccccagcag tttctgcctg aactcccatc ccccaacttt
1081 gtcttagaat tc

```

## (2) INFORMATION FOR SEQ ID NO:105:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

```

1 gaagagcaag cgccatgttg aagccatcat taccattcac atccctctta ttctgcagc
61 tgcccctgct gggagtgggg ctgaacacga caattctgac gccaatggg atgaagacaa
121 ccacagctga tttcttcttg accactatgc cactgactc cctcagtgtt tccactctgc
181 ccctcccaga ggttcagtgt tttgtgttca atgtcgagta catgaattgc acttgaacaa
241 gcagctctga gccccagcct accaactca ctctgcatta ttgtacaag aactcggata
301 atgataaagt ccagaagtgc agccactatc tattctctga agaaatcact tctggctgtc
361 agttgcaaaa aaaggagatc cactctacc aaacatttgt tgttcagctc caggaccac
421 gggaaaccag gagacaggcc acacagatgc taaaactgca gaatctgtg atccccggg
481 ctccagagaa cctaactctt cacaactga gtgaatccca gctagaactg aactggaaca
541 acagattctt gaaccactgt ttggagcact tgggtcagta ccggactgac tgggaccaca
601 gctggactga acaatcagtg gattatagac ataagtctc ctgacctagt gtggatggg
661 agaaacgcta caggttctgt gttcggagcc gctttaacc actctgtgga agtgctcagc
721 attggagtga atggagccac ccaatccact gggggagcaa tacttcaaaa gagaatcctt
781 tctgttttgc attggaagcc gtggttatct ctgttggctc catgggattg attatcagcc
841 ttctctgtgt gtatttctgg ctggaacgga cgatgccccg aattcccacc ctgaagaacc
901 tagaggatct tgttactgaa taccacggga acttttcggc ctggagtggg gtgtctaagg
961 gactggctga gagtctgcag ccagactaca gtgaacgact ctgcctcgtc agtgagattc
1021 ccccaaaagg agggggcctt ggggaggggc ctggggcctc cccatgcaac cagcatagcc
1081 cctactgggc ccccccattg tacacctaa agcctgaaac ctgaaccca atcctctgac
1141 agaagaacc cagggtcctg tagccctaag tggtaactac tttccttcat tcaaccacc
1201 tgcgtctcat actcacctca cccactgtg gctgatttgg aattttgtge ccccatgtaa
1261 gaccccttc atttggcatt cccacttga gaattaccct tttgccccga acatgttttt
1321 cttctccctc agtctggccc ttcttttctg caggattctt cctccctccc tcttccctc
1381 ccttctctct tccatctacc ctccgattgt tctgaaccg atgagaaata aagtttctgt
1441 tgataatcat c

```

## (2) INFORMATION FOR SEQ ID NO:106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

```

1 gagagactgg atggaccac aagggtgaca gccaggcgg accgatcttc ccatccaca
61 tcttcgggct cgatgcaaaa aagaggctga cggcaactgg gccttctgca gagaaagacc
121 tccgtttcac tgccccggct ggtcccaagg gtcaggaaga tggattcata cctgctgatg
181 tggggactgc tcacgttcat catggtgcct ggctgccagg cagagctctg tgacgatgac
241 ccgcccagaga tcccacacgc cacattcaaa gccatggcct acaaggaagg aacctgtgtg
301 aactgtgaat gcaagagagg tttccgcaga ataaaaagcg ggtcactcta tatgtctgtt
361 acaggaaact ctagccactc gtcctgggac aaccaatgtc aatgcacaag ctctgccact
421 cggaacacaa cgaaacaagt gacacctcaa cctgaagaac agaaagaaag gaaaaccaca
481 gaaatgcaaa gtccaatgca gccagtggac caagcgagcc ttccagggtg agagaagcct
541 caggcaagcc ccgaaggcgg tcctgagagt gagacttctt gcctcgtcac aacaacagat
601 tttcaaatat agacagaaat ggctgcaacc atggagacgt ccatatttac aacagagyac
661 caggtagcag tggcgggctg tgttttctg ctgatcagcg tctctcctg gagtgggctc
721 acctggcagc ggagacagag gaagagtaga agaacaatct agaaaaccaa aagaacaaga
781 atttcttggg aagaagccgg gaacagacaa cagaagtcac gaagcccaag tgaatcaaa
841 ggtgctaaat ggtcgcccag gagacatccg ttgtgcttgc ctgcttttgg gaagctctga
901 agtcacatca caggacacgg ggcagtggca accttgtctc tatgccagct cagtcccac
961 agagagcgag cgctacccac ttctaataag caatttcgcc gttgaagagg aagggcaaaa
1021 ccaactagaac tctccattct attttcatgt atatgtgttc attaaagcat gaatggtagt
1081 gaactctctc caccctatat gtagtataaa gaaaagtagg tttacattca tctcattcca
1141 acttcccagt tcaggagtcc caaggaaaag cccagcacta acgtaaatac acaacacaca

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1201 cactcta tatacaactg gacattgtct gcgtggttcc tttggcc gcttctgact  
 1261 gctgattctc ccgttcacgt tgcctaataa acatccttca agaactctgg gctgctaccc  
 1321 agaaatcatt ttacccttgg ctcaatcctc taagctaacc cccttccact gagccttcag  
 1381 tcttgaattt ctaaaaaaca gaggccatgg cagaataatc tttgggtaac ttcaaaacgg  
 1441 ggcagccaaa cccatgaggc aatgtcagga acagaaggat gaatgaggtc ccaggcagag  
 1501 aatcatactt agcaaagtgt tacctgtgcg ttactaattg gcctctttaa gaggtagttt  
 1561 ctt

## (2) INFORMATION FOR SEQ ID NO:107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 733 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

1 gaattctcag gaccttcag ttcgcccgcac ccttctccat tatttgaata ttggaggctg  
 61 cctgaccaga atcttgtcag gactttgtct cttcatccca ggtggtcccg gctgactcct  
 121 gaggacgtta cagccctgag gggaggactc agccttatga agtgctgggt gagaccactg  
 181 ccaagaagtg cttgctcacc ctaccttcaa cggcagggga atctcctct ccttttatgg  
 241 gcgtagttaa gaaaggattc ataatgaag ttcaatcctt ctcataacc ccagcccaca  
 301 cctccagcaa ttgaacttga aaaaaaaaaa aaaaacactt cctatatattg agatgagaga agagagtgtt  
 361 gtcatcaaaa aaaaaaaaaa aaaaacactt cctatatattg agatgagaga agagagtgtt  
 421 aggcagtttc ctggtgaac acgccagccc aatactaaa gagagcaact cctgactccg  
 481 atagagactg gatggaccca caaggggtgac agcccaggcg gaccgatctt cccatccccc  
 541 atcctccggc gcgatgcaa aaagaggctg acggcaactg ggccttctgc agagaaagac  
 601 ctccgcttca ctgcccggc tgggtcccaag ggtcaggaag atggattcat acctgtgat  
 661 gtggggactg ctacggttca tcattggtgc tgggtgccag gcaggtaagg gcctgtgggt  
 721 gcccccgaa ttc

## (2) INFORMATION FOR SEQ ID NO:108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

1 gagctctgtg acgatgacc gccagagatc ccacacgcca cattcaaagc catggcctac  
 61 aaggaaggaa ccatgttgaa ctgtgaatgc aagagaggtt tccgcagaat aaaaagcggg  
 121 tcaacttata tgctctgtac aggaactct agccactcgt cctgggacaa ccaatgtcaa  
 181 tgcacaagct ctgacctcg gaacacaacg aaacaagtga cactcaacc tgaagaacag  
 241 aaagaaagga aaaccacaga aatgcaaagt ccaatgcagc cagtggacca agcgagcctt  
 301 ccaggtcact gcaaggaacc tccaccatgg gaaaatgaag ccacagagag aatttatcat  
 361 ttcgtgtgtg ggcagatggg ttattatcag tgcgtccagg gatacagggc tctacacaga  
 421 ggtcctgctg agagcgtctg caaaatgacc cacgggaaga caaggtggac ccagccccag  
 481 ctcatatgca caggtgaaat ggagaccagt cagtttccag gtgaagagaa gcctcaggga  
 541 agccccgaag gccgtctga gagtgaact tctgcctcg tcacaacaa agattttcaa  
 601 atacagacag aatggctgc aaccatggag acgtccatat ttacaacaga gtaccagga  
 661 gcagtgccg gctgtgttt cctgctgac agcgtcctc tctgagtgg gctcacctgg  
 721 cagcagagac agaggaagag tagaagaaca atctag

## (2) INFORMATION FOR SEQ ID NO:109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

1 gaattctcag gaccttcag ttcgcccgcac ccttctccat tatttgaata ttggaggctg  
 61 cctgaccaga atcttgtcag gactttgtct cttcatccca ggtggtcccg gctgactcct  
 121 gaggacgtta cagccctgag ggaggactca gcttatgaag tgctgggtga gaccactgcc  
 181 aagaagtgtc tgctcaccta ccttcaacgg caggggaatc tccctctcct tttatgggag  
 241 tagctgaaga aaggattcat aatgaagt ttcaatcctt catcaccaca gcccacctc  
 301 cagcaattga acttgaaaaa aaaaacttgg tttgaaaaat taccgcaaac tatattgtca  
 361 tcaaaaaaaa aaaaaaaa aaaaacttcc tatatttgag atgagagaag agagtgttag  
 421 gcagtttctt ggctgaacac gccagcccaa tacttaaga gagcaactcc tgactccgat  
 481 agagactgga tggaccaca aggtgacag cccaggcggg ccgatcttcc catccacat  
 541 cctccggcgc gatgcaaaa agaggctgac ggcaactggg ccttctgcag agaaagacct  
 601 ccgcttcaact gcccggctg gtcccaaggg tcaggaagat ggattcatac ctgctgatgt  
 661 ggggactgct cacgttcac atggtgcctg gctgccaggc aggtgaaggcg c

## (2) INFORMATION FOR SEQ ID NO:110:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

```
1 gaattcatgc cacaactgag tgattttttt tttctcaaac ccaattccac aaagtaaaag
  61 cctgatgaaa tacagtgaag gctgatgctt attaactgtg tttcccaaat ccagagctct
 121 aaaaagggtt tgcatacagt cattcattca atgcttaacg actgagcatt aattccatgc
 181 taagtactga actcagcact aggaataaga aggcgaccta gaggcatact ctctctctaa
 241 agatgcatag agcctcattg gaatgatcag ccgtgtctcc agagagctac aaggcagttt
 301 tcaattggta aatgccctga gagtgatggg cttgtggcat gtgtaagggt tagacagacc
 361 tgggacctag acatgacacc actcctgacg aattatgtga gtgtgggtgt ttcacaacca
 421 caatgagatg caatgcctgc acttgtaaca tggaaatagt gatggcatgc cccgcagatt
 481 gctgtgagaa gtcagcggca gagacatgca acattctcag cacagtgtct gccatgtagt
 541 aagggcctag tcagtgtctg tgattccttt caatattcct aagatgcaga taagggaaca
 601 gcccagagga gggggagcac ttccagaggg aggaatgcgg tgagacttcc ttcagcaggg
 661 tagcactgga gctgggtgtt aaggagttag tgagctttgg gcttatggat ttaacagagg
 721 aaaccaagaa aagaggaggc ggtgttgtag gaacagttag cagttgatga tttttatttt
 781 gtctcttggt ctgcttgagg acatttttgt ggcaaagaca gcatgaagga tagcgaagaa
 841 ttaatactga agagataggc cagggcaggt tatgaaggat tttgaatacc gggctaagaa
 901 atgtgggctt aatttcaaag acattatgga cactcctaaa atgttacgtt gtagataagg
 961 gaaaagtatt cttccagaag attaaattgg ggctgggcac ggtggctcac gcctgtgatc
1021 ccagcacttt gggaggcgaa gtgggcagat cacctgaggt caggagtgtg agatcagcct
1081 ggccaacgtg gtgaagcccc atctctactg aaaaaaaaaa ttagccgggc atggtggtgg
1141 gtgcctgtaa tctcagctac ttgggaggct gaagcaggag aatcacatga acctgggagg
1201 cagagggtgc agtgagccaa gattgcacca ctgcattcca gtgggcgaca gagcaagact
1261 cagtcaaaaa aaaaaaaga ttaaactgga agcaatgggt aagaatgggt gagtggagag
1321 acacatttga gtgagggaag ccagctgaaa agctgtacag acgtctagac aaaatgtgac
1381 acaagcatgc cttcacctcc ctgcaaagac cacagaccac tgagctccaa aggggggttg
1441 gaatccttgt cctgggccgc cattggtaac tcactcagtc tggcttgaga gataaactct
1501 attatccatc cctgaactaa aatcatgaca gaagtggcca gggagctttg ctgctatccc
1561 cccagggaac acgtctctca ctcaaatgga aagaggaccc tctgacaaca tctgtgggac
1621 ccaacagcac tggtcaccac aagccacaaa atgttaacaa agtcagtttt caattgttag
1681 ggacggagga ctcagttcat gattcataca aaccaactgt tctctcccag tgttttctgg
1741 gtggcacaac ccacaagtca acagtggctt gggaaactaga catttgagta gatttgggtt
1801 atttgattca tagtggattt tggttttcca cgggaccctt gtgccttgtt ctagttagat
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2041 ggcaccgatc tcagcaacat ctatccaacc gccatccact taacaagcaa agatgggaag
2101 ccctcgtgct ccaggctatc ctgcaatggt tcatttgctt ttgatgggat tatcactttg
2161 acagatgtgc ttgcaattaa ctgggggctt tctgcttcca atccaaattc ccacaggttg
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2341 ggggtcaccc aagagtgcac gagctaagta aaatgtaatt tgtgggacct catgtggaca
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2461 gaaaatgacc tcctactaag cctaacaaga acatccagta cataaacagc aggtctctctg
2521 caaccgcttc ggtccttcca ctgccacgct cccagaaagc aaagggttat ctccgtgtcg
2581 gatattggct ctgagaccac agctcagcac atcactcctc tagagaaaag aaagtctaag
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3841 attcatttca tacgggcata tgtgccactt ggttctacag gcattttttt tttgagaca
3901 gacttttgcc cttgtcccc aggtcggcgt gcagcgggtg gatcttggct cactgcaatc
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3961 tccacct aggttcaagc aagtctcctg ccttagcctc cca gct ggaattacag  
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4201 gaccgttaac aagccccaag ggtaagttaa ggaaaatgaa aggtgattga ttccctaccā  
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5161 ttgtccgctg ttctgagcag tttcttctag gaagtaccaa acatttctga taatagaatt  
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5341 atcaatgcta tctagataac tttctcaaa aaaaaaaaaa aaaaaaaaaa cctctacta  
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6061 aggagggaaa ccaaaggttc tatcaaatā agaaaagagt tttaccatt gtggaagaca  
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7321 gcaggagaat cacttgaacc tgggaggcag aggttgagat gagccaagat tgtgccattg  
7381 cgctccaaaa aaaaaaaaaa aatacattaa cataaattta aatattttat aatgacaatc  
7441 cacattaact acttaaagca taagctattt tccaggagag gcagcaagt cacttactc  
7501 ccatgcccaa gaagaaaaggā gcgtgacttt ggtgggagta ctaggagttt ctactgagc  
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8041 agtgcttga ttacaggcat gagccaccag gccaggtcaa cgtgatgtgt tttggaaccc  
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8221 agggagcaaa acacactcaa ccaatttcat aataatcaga agagagctct gatcaataaa  
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8881 agagagtgtc aggcagtttc ctggtgtaac acgccagccc aatattttaa gagagcaact  
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1 gaattcccc ccccccccc cgagagactg gatggaccca caagggtgac agcccaggcg  
61 gaccgatctt cccatcccac atcctccggc gcgatgccaa aaagaggctg acggcaactg  
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181 atggattcat acctgctgat gtggggactg ctacagttca tcatggtgcc tggctgccag  
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301 tacaaggaag gaaccatgtt gaactgtgaa tgcaagagag gtttcccgag aataaaaaagc  
361 gggctactct atatgctctg tacaggaaac tctagccact cgtcctggga caaccaatgt  
421 caatgcacaa gctctgccac tcggaacaca acgaaacaag tgacacctca acctgaagaa  
481 cagaaagaaa ggaaaaccac agaaatgcaa agtccaatgc agccagtga ccaagcgagc  
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1081 gctaaatggg cgcccaggag acatccgttg tgcttgctg cgttttgaa gctctgaagt  
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1261 ctagaactct ccatcttatt ttcattgata tgtgttcatt aaagcatgaa tggatggaa  
1321 ctctctccac cctatatgta gtataaagaa aagtaggttt acattcatct cattccaact  
1381 tcccagttca ggagtcccaa ggaaagcccc agcactaacg taaatacaca acacacacac  
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1621 tgaatttcta aaaaacagag gccatggcag aataatcttt gggttaacttc aaaacggggc  
1681 agccaaaccc atgaggcaat gtcaggaaca gaaggatgaa tgagggtcca ggcagagaat  
1741 catacttagc aaagttttac ctgtgcgtta ctaattggcc tctttaagag ttagtttctt  
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1861 acacacaagg tgcaaatcaa tgcgtacgtt tcctgagaag tgtctaaaaa caccaaaaag  
1921 ggatccgtac attcaatgtt tatgcaagga aggaaagaaa gaagggaagt aagagggaga  
1981 agggatggag gtcacactgg tagaacgtaa ccacggaaaa gagcgcatca ggcctggcac  
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2161 attggctgga tgtggtgga tacgctgtga gtcctagcca ctcaggaggc tgaggcagga  
2221 ggattgcttg agcccaggag ttcgaggctg cagtcagtca tgatggcacc actgcactcc  
2281 agcctgggca acagagcaag atcctgtctt taaggaaaaa aagacaagg aattc  
1 gaattcatgg aaatgggaag ggcagtgatg gagatgggaa gggcagtggg ggttggaggg  
61 gtggggattg ttgttgggta cgaaaacaga attagatcga atgaataaga tctagtattt  
121 gatagcataa cagggtgact ttagtcaaca ataatttatt gtacatttaa aaataactaa  
181 aagagtatac ttggatttta acacaaagaa aggataaata cttgagggtg tggatacccc  
241 atttaccctg atgtgattat tatacattgt atgcctgtat caaaatagct catgtgcctc  
301 atgaatatag acacctacca catgccaca aaattaaaaa ctaaaaaaaa cagtcactc  
361 tgaatgctaa acggagtaag gggcttccgt gaaggctggg tgaatggga gtctcgaaa  
421 tgtgtgtaag ctacgtatta gtgggtatgt gtgtgaccgg atggaggcgt cagaggtgtt



541 gggtag tgtgagttgg cgtgggggtg atgtaggagg gga ggg agggcctgcg  
601 ttccttggc tctgtgtgc agctaggccc ctatttgaca atgtgtgtct gtgtgtgtgt  
661 gtgtgtgtgt gtgtgtgtgt gtgtgcccgc cccagcgtag gaggcagatc tttatctggc  
721 cctgggtgct tgaggagttt caggctttct cataagcctc gtctcccgc tctccaccc  
781 caggccttgc ccctctatcc tctgcacagg aagtgggctg gctctgggct tttagtcttt  
841 ggggcccag cagccagagc tcagcagggc cctggagaga tggccacggt cccagcaccg  
901 gggaggactg gagagcgcgc gctgccaccg ccccatgtct cagccaggtg atgtccccct  
961 gcctccctcc cggccctgt ggaccagcca gagggtggg agtgaaagtc acagagaaga  
1021 ctttcagctc tgactcagtt cccccagcag tttctgcctg aactcccatc ccccaacttt  
1081 gtcttagaat tc

1 gaagagcaag cgccatgtt aagccatcat taccattcac atccctctta ttcctgcagc

61 tgccctgct gggagtggg ctgaacacga caattctgac gcccaatggg aatgaagaca  
121 ccacagctga tttcttctg accactatgc cactgactc cctcagtgtt tccactctgc  
181 cctccccaga ggttcagtg tttgtgttca atgtcgagta catgaattgc acttggaaaca  
241 gcagctctga gcccagcct accaacttca ctctgcatta ttggtacaag aactcggata  
301 atgataaagt ccagaagtgc agccactatc tattctctga agaatcact tctggctgtc  
361 agttgcaaaa aaaggagatc cacctctacc aaacatttgt tgttcagctc caggaccac  
421 gggaaaccag gagacaggcc acacagatgc taaaactgca gaactctgtg atccccggg  
481 ctccagagaa cctaactct cacaactga gtgaatccca gctagaactg aactggaaca  
541 acagattctt gaaccactgt ttggagcact tgggtcgata cggactgac tgggaccaca  
601 gctggactga acaatcagtg gattatagac ataagtctc ctgacctagt gtggatggg  
661 agaaagccta cagtttctg gtccggagcc gctttaacc actctgtgga agtgctcagc  
721 attggagtga atggagccac ccaatccact gggggagcaa tacttcaaaa gagaatcctt  
781 tctgtttgc attggaagcc gtggttatct ctgttggtc catgggattg attatcagcc  
841 ttctctgtgt gtatttctg ctggaacgga cgatgcccgc aattcccacc ctgaagaacc  
901 tagaggatct tgttactgaa taccacggga acttttcggc ctggagtgtg gtgtctaagg  
961 gactggctga gactctgcag ccagactaca gtgaacgact ctgcctctc agtgagattc  
1021 ccccaaaagg aggggccctt gggggggggc ctggggcctc cccatgcaac cagcatagcc  
1081 cctactgggc cccccatgt tacaccctaa agcctgaaac ctgaacccca atcctctgac  
1141 agaagaacc cagggtcctg tagccctaag tggactaac tttccttcat tcaaccacc  
1201 tgcctctcat actcacctca cccactgtg gctgatttg aattttgtgc cccatgttaa  
1261 gcacccttc atttggcatt cccacttga gaattaccct tttgcccgc acatgtttt  
1321 cttctccctc agtctggccc ttccttttgc caggattctt cctccctccc tcttccctc  
1381 ccttctctt tccatctacc ctccgattgt tctgaaccg atgagaaata aagtttctgt  
1441 tgataatcat c

1 gagagactgg atggaccac aagggtgaca gccaggcgg accgatcttc ccattccaca

61 tctccggcg cgatgccaaa aagaggctga cggcaactgg gccttctgca gagaaagacc  
121 tccgcttcc tgccccggct ggtcccaagg gtcaggaaga tggattcata cctgctgatg  
181 tgggactgc tcacgttcat catggtgcct ggctgccagg cagagctctg tgacgatgac  
241 cggccagaga tcccacagc cacattcaaa gccatggcct acaaggagg aaccatgtt  
301 aactgtgaat gcaagagagg tttccgcaga ataaaaagcg ggtcactcta tatgtctgt  
361 acaggaaact ctagccactc gtccctgggac aaccaatgtc aatgcacaag ctctgccact  
421 cggaaacaaa cgaacaagt gacacctcaa cctgaagaac agaaagaaag gaaaaccaca  
481 gaaatgcaaa gtccaatgca gccagtggac caagcgagcc tccaggtga agagaagcct  
541 caggcaagcc ccgaaggccg tctgagagt gagacttct gcctcgtac aacaacagat  
601 tttcaaatc agacagaaat ggctgcaacc atggagacgt ccatatttac aacagagyac  
661 caggtagcag tggccggctg tgttttctg ctgatcagcg tctcctctc gactgggctc  
721 acctggcagc ggagacagag gaagagtaga agaacaatct agaaaacaa aagaacaaga  
781 atttcttgg aagaagccg gaacagacaa cagaagtcac gaagccaaag tgaattcaaa  
841 ggtgctaaat ggtcggccag gagacatccg ttgtgcttgc ctgcttttgc gaagctctga  
901 agtcacatca caggacacgg ggcagtggca acctgtctc tatgccagct cagtcccatc  
961 agagagcgag cgctaccac ttctaaatag caatttcgcc gttgaagagg aagggcaaaa  
1021 ccactagaac tctccatctt attttcatgt atatgtgtc attaaagcat gaatggtatg  
1081 gaactctctc caccctatat gtagtataaa gaaaagtagg tttacattca tctcattcca  
1141 acttccagc tcaggagctc caaggaaagc cccagcacta acgtaaaatc acaacacaca  
1201 cactctaccc tatacaactg gacattgtct gcgtgggtcc tttctcagcc gcttctgact  
1261 gctgattctc ccgttcacgt tgccataata acatccttca agaactctgg gctgctaccc  
1321 agaaatcatt ttacccttgg ctcaatcctc taagctaacc ccttccact gagccttcag  
1381 tcttgaattt ctaaaaaaca gaggccatgg cagaataatc tttgggtaac ttcaaaacgg  
1441 gtcagccaaa cccatgaggc aatgtcagga acagaaggat gaatgagtc cagtcagag  
1501 aatcatactt agcaaagttt tacctgtgag ttactaattg gcctctttaa gacttagttt  
1561 ctt

1 gaattctcag gatcctcag ttcgcccag ccttctccat tatttgaata ttggaggctg

61 cctgaccaga atcttctcag gactttgtc cttcatccca ggtgggtccc gctgactcct  
121 gaggagctta cagccctgag gggaggactc agccttatga agtgctgggt gagaccactg  
181 ccaagaagtgt cttgctcacc ctaccttcaa cggcagggga atctccctct ccttttatgg  
241 gcgtagtga gaaaggattc ataaatgaag ttcaatcctt ctcatcaacc ccagcccaca  
301 cctccagcaa ttgaacttga aaaaaaaac ctggtttgaa aaattaccgc aaactatatt  
361 gtcataaaaa aaaaaaaaaa aaaaacactt cctatatttg agatgagaga agagagtgt  
421 aggcagtctc ctggctgaac acgccagccc aatactttaa gagagcaact cctgactccg  
481 atagagactg gatggaccca caagggtgac agcccaggcg gaccgatctt cccatccac  
541 atcctccggc gcgatgccaa aaaggaggctg acggcaactg ggccttctgc agagaaagac

601 ctccgcccga ctgccccggc tggccccaa ggtcaggaag atggattcat acctgtgtat  
661 gtggggactg ctacagttca tcatggtgcc tggctgccag gcaggtaaag gcctgtgggt  
721 gcccccgaa ttc  
1 gagctctgtg acgatgacc gccagagatc ccacagccca cattcaaagc catggcctac  
61 aaggaaggaa ccatgttgaa ctgtgaatgc aagagagggt tccgcagaat aaaaagcggg  
121 tcaactctata tgctctgtac aggaactct agccactcgt cctgggaca ccaatgtcaa  
181 tgacaaagct ctgccactcg gaacacaagc aaacaagtga cacctcaac tgaagaacag  
241 aaagaaagga aaaccacaga aatgcaaatg ccaatgcagc cagtggacca agcagcctt  
301 ccaggtcact gcaaggaacc tccaccatgg gaaaatgaag ccacagagag aatttatcat  
361 ttcgtgggtg ggcagatggt ttattatcag tgcgtccagg gatacagggc tctacacaga  
421 ggtcctgtct agagcgtctg caaaatgacc cacgggaaga caaggtggac ccagccccag  
481 tcatatgca caggtgaaat ggagaccagt cagtttccag gtgaagagaa gcctcaggca  
541 agccccgaag gccgtcctga gagtgcagct tcctgcctcg tcacaacaac agattttcaa  
601 atacagacag aaatggctgc aaccatggag acgtccatat ttacaacaga gtaccaggta  
661 gcagtggccg gctgtgtttt cctgtgtatc agcgtcctcc tcctgagtgg gctcacctgg  
721 cagcagagac agaggaagag tagaagaaca atctag  
1 gaattctcag gatccttcag ttgcgcgcat ccttctccat tattgaata ttggaggctg  
61 cctgaccaga atcttgtcag gactttgctc cttcatccca ggtggtccg gctgactcct  
121 gaggacgtta cagccctgag ggaggactca gcttatgaag tgctgggtga gaccactgcc  
181 aagaagtgtg tgctcaccta ctttcaacgg caggggaatc tccctctcct tttatggcg  
241 tagctgaaga aaggattcat aaatgaagt caatccttct catcacccca gcccaacctc  
301 cagcaattga acttgaaaaa aaaaacctgg ttgaaaaat taccgcaac tatattgtca  
361 tcaaaaaaaa aaaaaaaa aaacacttcc tatatttgag atgagagaag agagtgtcag  
421 gcagtttctt ggctgaacac gccagcccaa tacttaaaaga gagcaactcc tgactccgat  
481 agagactgga tggaccaca aggggtgacag cccaggcgga ccgatcttcc catcccat  
541 cctccggcgc gatgccaaaa agaggctgac ggcaactggg ccttctgcag agaaagacct  
601 ccgcttctact gccccggctg gtcccaaggg tcaggaagat ggattcatat ctgtgtatgt  
661 ggggactgct cacgttcatc atggtgcctg gctgccaggc aggttaagggc c

## (2) INFORMATION FOR SEQ ID NO:111:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 544 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

1 aagcttaata taaacaagtt tcttgtcact gccaccacca cgacaaaaa aagctaataca  
61 atcactatat ataatacata tatatactat atataataaa tatatatact atatataata  
121 catatataca ctatatataa tacatatata ctatatatac actatatact atatatacac  
181 atatatatta tgaatgtata tatatagtat atatagtata tatactatgt atgtatatat  
241 agtatatata gtatatatac tatgtatgat atatagtata tatagtatat atactatgta  
301 tgtgtatata tagtatatat agtatatata gtatatatac tatgtatgta tatatatagt  
361 atatatagta tatatactgt gtatgtatat atatagtata tatatactat atatgcatac  
421 atagtatata tgcatatata ctatatatac tatatatatta tatatactat atactatata  
481 tactatatac tgtatatata ctatatatgt atgtatacga tatatatata tactatatat  
541 gtac

## (2) INFORMATION FOR SEQ ID NO:112:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2002 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

1 cagagaagct ctatctccc tccaggagcc cagctatgaa ctcttctcc acaagcgctt  
61 tgggtccagt tgcttctcc ctggggctgc tccgtgtgtt gcctgtgcc ttccctgccc  
121 cagtaccccc aggagaagat tccaaagatg tagccgcccc acacagacag ccaactcacct  
181 cttcagaacg aattgacaaa caaatcgggt acatcctcga cggcatctca gccctgagaa  
241 aggagacatg taacaagagt aacatgtgtg aaagcagcaa agaggcactg gcagaaaaca  
301 acctgaacct tccaaagatg gctgaaaaag atggatgctt ccaatctgga ttcaatgagg  
361 agacttgctt ggtgaaaatc atcactggctc ttttggagtt tgaggatac cttaggtacc  
421 tccagaacag atttgagagt agtgaggaac aagccagagc tgtgcagatg agtacaaaag  
481 tcctgatcca gttcctgcag aaaaaggcaa agaactctaga tgcaataacc acccctgacc  
541 caaccacaaa tgccagcctg ctgacgaagc tgcaggcaca gaaccagtgg ctgcaggaca  
601 tgacaactca tctcattctg cgcagcttta aggagtccct gcagtccagc ctgagggctc  
661 ttcggcaaat gtagcatggg cacctcagat tgttgtgtgt aatgggcatt ccttcttctg  
721 gtcagaaacc tgtccactgg gcacagaact tatgttgttc tctatggaga actaaaagta  
781 tgagcgttag gacactatct taattatctt taatttatta atatttaaat atgtgaagct  
841 gagttaattt atgtaagtga tatttatatt ttaagaagta ccacttgaaa cattttatgt  
901 attagttttg aaataataat ggaaagtggc tatgcagttt gaatatcctt tgtttcagag  
961 ccagatcatt tcttgaaaag tgtacgctta cctcaaataa atggctaact tatacatatt  
1021 tttaaagaaa tatttatatt gtatttatat aatgtataaa atggttttta tacciaataa  
1081 tggcatttta aaaaattcag ca

## (2) INFORMATION FOR SEQ ID NO:113:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

```
1 gaattccggg aacgaaagag aagctctatc tccctccag gagccagct atgaactcct
61 tctccacaag cgccttcggt ccagttgect tctccctggg gctgctcctg gtgttgccctg
121 ctgccttccc tgccccagta cccccaggag aagattccaa agatgtagcc gccccacaca
181 gacagccact cactcttcca gaacgaattg acaaacaaat tcggtacatc ctgcacggca
241 tctcagccct gagaaaggag acatgtaaca agagtaacat gtgtgaaagc agcaaaggag
301 cactggcgaga aaacaacctg aaccttccaa agatggctga aaaagatgga tgcttccaat
361 ctggattcaa tgaggagact tgcctgggtga aaatcatcac tgggtctttg gagtttgagg
421 tatacctaga gtacctccag aacagatttg agagtatga ggaacaagcc agagctgtgc
481 agatgagtagc aaaagtcctg atccagttcc tgcagaaaaa ggcaaagaat ctagatgcaa
541 taaccacccc tgaccaacc acaaatgccg cctgctgac gaagctgcag gcacagaacc
601 agtggctgca ggacatgaca actcatctca ttctgcgcag ctttaaggag ttccctgcagt
661 ccagcctgag ggctcttcg ccaatgtagc atgggcacct cagattgttg ttgttaattg
721 gcattccttc ttctggctcag aaacctgtcc actgggcaca gaacttatgt tgttctctat
781 ggagaactaa aagtatgagc gttaggacac tattttaatt atttttaatt tattaatatt
841 taaatatgtg aagctgagtt aatttatgta agtcatattt atatttttaa gaagtaccac
901 ttgaacatt ttatgtatta gttttgaaat aataatggaa agtggctatg cagtttgaat
961 atcctttgtt tcagagccag atcatttctt ggaaagtgtg ggcttacctc aaataaatgg
1021 ctaacttata catattttta aagaaatatt tatattgtat ttatataatg tataaatggg
1081 ttttatacca ataaatggca ttttaaaaaa ttc
```

## (2) INFORMATION FOR SEQ ID NO:114:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3659 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

```
1 aagcttaata taaacaagtt tcttgtcact gccaccacca cgacaaaaaa aagctaataca
61 atcactatat ataatacata tatatactat atataataaa tatataact atataataa
121 catatataca ctatatataa tacatatata ctatatatac actataact atataacac
181 atatatatta tgaatgtata tatatagtat atatagtata tatactatgt atgtatatat
241 agtatatata gtatatatac tatgtatgat atatagtata tatagtatat atactatgta
301 tgtgtatata tagtatatat agtatatata gtatatatac tatgtatgta tatatatagt
361 atatatagta tatatactgt gtatgtatat atatagtata tatatactat atatgcatac
421 atagtatata tgcataatata ctatatatac tatataatta tatatactat atactatata
481 tactatatac tgtatatata ctatatatgt atgtatacga tatatatata tactatatat
541 gtac
161 cagagaagct ctatctccc tccaggagcc cagctatgaa ctcttctcc acaagcgect
61 tcggtccagt tgccttctcc ctggggctgc tctgtgtgtt gcctgtgcc ttccctgccc
121 cagtaccccc aggagaagat tccaaagatg tagccgcccc acacagacag ccactcacct
181 cttcagaacg aattgacaaa caaattcggg acatcctcga cggcatctca gccctgagaa
241 aggagacatg taacaagagt aacatgtgtg aaagcagcaa agaggcactg gcagaaaaca
301 acctgaacct tccaaagatg gctgaaaaag atggatgctt ccaatctgga ttcaatgagg
361 agacttgctt ggtgaaaaatc atcactggtc ttttggagtt tgagggtatac ctagagtacc
421 tccagaacag atttgagagt agtgaggaaac aagccagagc tgtgcagatg agtacaaaag
481 tcttgatcca gttcctgcag aaaaaggcaa agaacttaga tgcaataacc acccctgacc
541 caaccacaaa tgccagcctg ctgacgaagc tgcaggcaca gaaccagtgg ctgcaggaca
601 tgacaactca tctcattctg cgcagcttta aggagttcct gcagtccagc ctgagggtc
661 ttcggcaaat gtatcatggg cacctcagat tgttgtgtt aatgggcatt ccttctctg
721 gtcagaaacc tgtccactgg gcacagaact tatgttgttc tctatggaga actaaaagta
781 tgagcggttag gacactatgt taatttattt taatttatta atattttaat atgtgaagct
841 gagttaattt atgtaagtga tatttatatt ttaagaagta ccacttgaaa cattttatgt
901 attagttttg aaataataat ggaaagtggc tatgcagttt gaatatcctt tgtttcagag
961 ccagatcatt tcttggaag tgtacgctta cctcaaataa atggctaact tatacatatt
1021 tttaaagaaa tatttatatt gtatttatat aatgtataaa atggttttta taccaataaa
1081 tggcatttta aaaaattcag ca
161 gaattccggg aacgaaagag aagctctatc tccctccag gagccagct atgaactcct
61 tctccacaag cgccttcggt ccagttgect tctccctggg gctgctcctg gtgttgccctg
121 ctgccttccc tgccccagta cccccaggag aagattccaa agatgtagcc gccccacaca
181 gacagccact cactcttcca gaacgaattg acaaacaaat tcggtacatc ctgcacggca
241 tctcagccct gagaaaggag acatgtaaca agagtaacat gtgtgaaagc agcaaaggag
301 cactggcgaga aaacaacctg aaccttccaa agatggctga aaaagatgga tgcttccaat
361 ctggattcaa tgaggagact tgcctgggtga aaatcatcac tgggtctttg gagtttgagg
421 tatacctaga gtacctccag aacagatttg agagtatga ggaacaagcc agagctgtgc
481 agatgagtagc aaaagtcctg atccagttcc tgcagaaaaa ggcaaagaat ctagatgcaa
541 taaccacccc tgaccaacc acaaatgccg cctgctgac gaagctgcag gcacagaacc
601 agtggctgca ggacatgaca actcatctca ttctgcgcag ctttaaggag ttctgcagct
661 ccagcctgag ggctcttcg ccaatgtagc atgggcacct cagattgttg ttgttaattg
721 gcattccttc ttctggctcag aaacctgtcc actgggcaca gaacttatgt tgttctctat
```

781 ggagaaacaa aagtatgagc gttaggacac tattttaatt attttaatt tattaatatt  
841 taaatatgtg aagctgagtt aatttatgta agtcatattt atatttttaa gaagtaccac  
901 ttgaaacatt ttatgtatta gttttgaaat aataatggaa agtggctatg cagtttgaat  
961 atcctttgtt tcagagccag atcatttctt ggaaagtgtg ggcttacctc aaataaatgg  
1021 ctaacttata catattttta aagaaatatt tatattgtat ttatataatg tataaatggt  
1081 ttttatacca ataaatggca ttttaaaaaa ttc

## (2) INFORMATION FOR SEQ ID NO:115:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1194 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

1 ggatcctcct gcaagagaca ccacctctgag gggaagaggg ctctgaacc agcttgaccc  
61 aataagaaat tcttggtgac cgacggggac agcagattca gacgctagag cctgacctgc  
121 gtccgtagtt tccttctagc ttctttttga tttcaaatca agacttacag ggagagggag  
181 cgataaacac aaactctgca agatgccaca aggtcctcct ttgacatccc caacaagaa  
241 ggtgagtagt aatctccccc tttctgcctt gaaccaagtg gcttcagtaa gtttcagggc  
301 tccaggagac ctgggcatgc aggtgccgat gaaacagtgg tgaagagact cagtggcagt  
361 ggcagtgggg agagcactcg cagcacaggc aaacctctgg cacaagagca aagtcctcac  
421 tggaggattc ccaaggggtc cttgggagag ggcaggcagc agccaacctc ctctaagtgg  
481 gctgaagcag gtgaagaaat ggcagaagac gcggtgggtg caaaaaggag tcacacactc  
541 cacctggaga cgccttgaa gtaactgcag aaatttgagg gtggccaggc agttctacaa  
601 cagccgctc acagggagag ccagaacaca gcaagaactc agatgactgg tagtattacc  
661 ttcttcataa tcccaggctt ggggggctgc gatggagtca gaggaaactc agttcagaac  
721 atctttggtt tttacaatac aaattaactg gaacgctaaa ttctagcctg ttaatctggt  
781 cactgaaaaa aaaaaaattt ttttttttca aaaaaacata gctttagctt atttttttt  
841 tctctttgta aaacttcgtg catgacttca gctttactct tgccaagaca tgccaagtgc  
901 tgagtcacta ataaagaaaa aagaagttaa ggaagagtgg ttctgcttct tagcgctagc  
961 ctcaatgacg acctaaagctg cacttttccc cctagtgtgt tcttgcatg ctaaggagc  
1021 tcattgcaca atcttaataa ggtttccaat cagccccacc cgctctggcc ccacctcac  
1081 cctccaacaa agatttatca aatgtgggat tttcccatga gtctcaatat tagagtctca  
1141 accccaata aatataggac tggagatgtc tctgaggctc attctgcctc cgag

## (2) INFORMATION FOR SEQ ID NO:116:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3319 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

1 ggcggtcccc tggttcccc gctcaggtgc ggcgctgtgg caggaagcca cccctcggt  
61 cgcccggtgc ggggggtgt tgcgccatcc gctccggctt tcgtaaccgc accctgggac  
121 ggcccagaga cgctccagcg cgagttcctc aaatgttttc ctgctgtgcc aggacggtcc  
181 gccgctctga gtcattgtcg agtgggaagt cgactgaca ctgagccggg ccagagggag  
241 aggagccgag cgccggcgcg ggcgagggga ctgcagtggt gtgtagagag ccgggctcct  
301 gcggtatggg gctgcccccg gggcctgagc ccgctgccc gccaccggcc ccgccccgcc  
361 cctgccaccc ctgccgccc gttcccatta gectgtccgc ctctgcggga ccatggagtg  
421 gtgcccagag aggaagcatg ctggccgctg gctgcgcgct gctggctgcc ctgctggccg  
481 gcgcccagag ggcgctggcc ccaaggcgct gccctgcgca ggaggtggca agaggcggtc  
541 tgaccagtct gccaggagac agcgtgactc tgacctgcc gggggtagag ccggaagaca  
601 atgccactgt tcaactgggtg ctccaggaag cggtgcagag ctcccacccc agcagatggg  
661 ctggcatggg aaggaggctg ctgctgaggt cgggtgcagct ccacgactct ggaactatt  
721 catgtaccg ggccggccgc ccagctggga ctgtgcaatt gctgtgtggt gttcccccg  
781 agagccccca gctctcctgc ttccggaaga gccccctcag caatgttgtt tgtgagtggt  
841 gtcctcggag caccatcc ctgacgacaa aggtgtgtgt cttggtgagg aagtttcaga  
901 acagtccggc cgaagacttc caggagcgt gccagtattc ccaggagtcc cagaagttct  
961 cctgccagtt agcagtcctg gaggagaca gctctttcta catagtgtcc atgtgcgtcg  
1021 ccagtgtgt cgaggagcaag ttacgaaaa ctcaaacctt tcagggtgtg ggaatcttgc  
1081 agcctgatcc gcctgccaac atcacagtca ctgccgtggc cagaaacccc cgctggctca  
1141 gtgtcacctg gcaagacccc cactcctgga actcatctt ctacagacta cggtttgagc  
1201 tcagatatcg ggctgaacgg tcaaagacat tcacaacatg gatgtcaag gacctccagc  
1261 atcactgtgt catccacgac gcctggagcg gcctgaggca cgtgtgtag cttcgtgccc  
1321 aggaggagtt cgggcaaggc gagtggagcg agtggagccc ggaggccatg ggcacgcctt  
1381 ggacagaatc caggagtcct ccagctgaga acgaggtgtc caccoccatg caggcactta  
1441 ctactaataa agacgatgat aatattctct tcagagattc tgcaaatgag acaagcctcc  
1501 cagtgaaga ttcttcttca gtaccactgc ccacattcct ggttgctgga gggagcctgg  
1561 cttcgggaac gctcctctgc attgccattg ttctgaggtt caagaagacg tggaagctgc  
1621 gggctctgaa ggaaggcaag acaagcatgc atccgcccga ctctttgggg cagctggtcc  
1681 cggagaggcc tcgacccacc ccagtgtgtt ttctctcat ctcaccaccg gtgtccccc  
1741 cgagcctggg gcttgacaat acctcgagcc acaaccgacc agatgccagg gacccagga  
1801 gcccttatga catcagcaat acagactact tcttccccag atagctggct ggggtggacc  
1861 agcagcctgg acctgtgga tgacaaaaca caaacgggct cagcaaaaga tgcttctcac  
1921 tgccatgcca gcttatctca ggggtgtgct gcctttggct tcacggaaga gccttgccga

1981 aggtttct ccaggggaaa atcagcctgc tccagctgtt cagctgtg aggtttcaaa  
2041 cctccctttc caaatgcccc gcttaaagg gttagagtga acttggtgga ctgtgaagag  
2101 aaccatatca agactctttg gacactcaca cggacactca aaagctgggc aggttggtgg  
2161 gggcctcggg gtggagaagc ggctggcagc ccacccctca acacctctgc acaagctgca  
2221 ccctcaggca ggtgggatgg atttcagcc aaagcctcct ccagccgcca tgctcctggc  
2281 ccaactgcac gtttcatctt ccaactcaaa ctcttaaaac ccaagtggcc ttagcaaat  
2341 ctgtttttct aggcctgggg acggctttta cttaaagcc aaggcctggg ggaagaagct  
2401 ctctctccc tttcttccc acagttcaaa aacagctgag ggtgagtggg tgaataatac  
2461 agtatgtcag ggcctggctg ttttcaacag aattataatt agttcctcat tagcagttt  
2521 gcctaaatgt gaatgatgat cctaggcatt tgctgaatac agaggcaact gcattggctt  
2581 tgggtgtcag gacctcaggt gagaagcaga ggaaggagag gagaggggca cagggtctct  
2641 accatcccct gttagagtgg agctgagtgg gggatcacag cctctgaaaa ccaatgttct  
2701 ctcttctcca cctcccacaa aggagagcta gcagcaggga gggcttctgc catttctgag  
2761 atcaaaacgg ttttactgca gctttgtttg ttgtcagctg aacctgggta actagggag  
2821 ataataatga ggaagacaat gtgaaaagaa aaatgagcct ggcaagaatg cgtttaaact  
2881 tggtttttaa aaaactgctg actgttttct cttagagagg tggaatatcc aatattcgct  
2941 gtgtcagcat agaagtaact tacttaggtg tgggggagc accataactt tgtttagccc  
3001 aaaaccaagt caagtgaaaa aggaggaaga gaaaaaatat tttcctgcca ggcatggagg  
3061 ccacgcact tcgggaggtc gaggcaggag gatcacttga gtccagaagt ttgagatcac  
3121 cctgggcaat gtgataaaac cccatctcta caaaaagcat aaaaattagc caagtgtggt  
3181 agagtgtgcc tgaagtccca gatacttggg gggctgaggt gggaggatct cttagcctg  
3241 ggaggtcaag gctgcagtga gccgagattg caccactgca ctccagcctg ggggtacaga  
3301 gcaagtgaga ccctgtctc

## (2) INFORMATION FOR SEQ ID NO:117:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4413 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

1 ggatcctcct gcaagagaca ccacctctgag gggaagaggg cttctgaacc agcttgaccc  
61 aataagaaat tcttgggtgc cgacggggac agcagattca gagcctagag ccgtgcctgc  
121 gtccttagtt tccttctagc ttctttttga ttcaaatca agacttacag ggagagggag  
181 cgataaacac aaactctgca agatgccaca aggtcctcct ttgacatccc caacaaagaa  
241 ggtgagtagt aatctcccc tttctgcct gaaccaagt gcttcagtaa gtttcagggc  
301 tccaggagac ctgggcatgc aggtgccgat gaaacagtgg tgaagagact cagtggcagt  
361 ggcaagtggg agagcactcg cagcacaggc aaacctctgg cacaagagca aagtcctcac  
421 tggaggattc ccaagggtca cttgggagag ggcaggcagc agccaacctc ctctaagtgg  
481 gctgaagcag gtgaagaaat ggcagaagac gcggtgggtg caaaaaggag tcacacactc  
541 cacttgagga cgccttgaag taactgcacg aaatttgagg gtggccaggc agttctacaa  
601 cagccgcctc acagggagag ccagaacaca gcaagaactc agatgactgg tagtattacc  
661 ttcttcataa tcccaggctt ggggggctgc gatggagtca gaggaaactc agttcagaac  
721 atctttggtt tttaacaatac aaattaactg gaacgctaaa ttctagcctg ttaattcgtg  
781 cactgaaaaa aaaaaaattt tttttttt aaacaaacata gctttagctt attttttt  
841 tctctttgta aaacttctg catgacttca gctttactct tgtcaagaca ttgccaaagtgc  
901 tgagtacta ataaagaaaa aagaagtaaa ggaagagtgg ttctgcttct tagcgctagc  
961 ctcaatgacg acctaagctg cacttttccc cctagttgtg tcttgcgatg cttaaggagc  
1021 tcattgcaca atcttaataa ggtttccaat cagccccacc cgctctggcc ccacctcac  
1081 cctccaacaa agatttatca aatgtgggat tttcccatga gtctcaatat tagagtctca  
1141 accccaata aatataggac tggagatgtc tctgaggctc attctgcctc cgag  
1 ggcggtccc tgttctccc gctcaggtgc ggcgtgtgg caggaaagcca cccctcgtg  
61 cgccgggtgc gcggggctgt tgcgccatcc gctcgggtt tcgtaaccgc accctgggac  
121 ggccagaga cgctccagcg cgagtctcct aaatgttttc ctgctgtgcc aggaccgtcc  
181 gccgtctga gtcagtgtcg agtgggaagt cgcactgaca ctgagccggg ccagagggag  
241 aggaagcagg cgccgagcgg ggcagaggga ctgcagtggt gtgtagagag ccgggtcctc  
301 gcggtgggg gctgcccccg gggcctgagc ccgctgccc gccaccgcc ccgccccgcc  
361 cctgccaccc ctgcgcgccg gttcccatta gctgtccgc ctctgcggga ccatggagtg  
421 gtacccgagg aggaagcatg ctggccgtcg gctgcgcgt gctggctgcc ctgctggccg  
481 cgccgggagc ggcgtggcc ccaaggcgct gccctgcgca ggaggtggca agaggcgtgc  
541 tgaccagtct gccaggagac agcgtgactc tgacctgcc ggggtagag ccggaagaca  
601 atgccactgt tcactgggtg ctcaagagc cggtgcagc cccaccacc agcagatggg  
661 ctggcatggg aaggaggctg ctgctgaggt cggtgcagct ccacgactct ggaaactatt  
721 catgtaccg ggcggccgc ccagctggga ctgtgcactt gctggtgat gttcccccg  
781 aggaagccca gctctcctgc ttccggaaga gccccctcag caatgtgtt tgtgagtggg  
841 gtcctcggag caccatcc ctgacgaca aggtgtgtct ctggtgag aagtttcaga  
901 acagtccggc cgaagacttc caggagcgt gccagtatt ccaggagtcc cagaagtct  
961 cctgccagtt agcagtcagg gaggagaca gctctttcta catagtgtcc atgtgcgtcg  
1021 ccagtgtgt cgaggcaag ttacagaaaa ctcaaactt tcagggtgtt ggaatcttgc  
1081 agcctgatcc gcctgccaac atcacagtca ctgccgtggc cagaaacccc cgctggctca  
1141 gtgtcacctg gcaagacccc cactcctgga actcatctt ctacagacta cggtttgagc  
1201 tcagatatcg ggtgaacgg tcacaacatg gatggtcaa gacctccagc  
1261 atcactgtgt catccacgac gcttgaggc cgtggtgag cgtggtgag cttcgtgcc  
1321 aggaagagtt cgggcaaggc gagtggagcg agtggagccc ggaggccatg ggcacgcctt  
1381 ggacagaatc caggagtctc ccagctgaga acgaggtgtc caccacctat caggcactta

1441 ctactaataa agacgatgat aatatttctt ttagagattc tgcaaatgag acaagcctcc  
1501 cagtgaaga ttcttcttca gtaccattgc ccacattcct ggttgctgga gggagcctgg  
1561 ccttcggaac gctcctctgc attgccattg ttctgaggtt caagaagacg tggagctgce  
1621 gggctctgaa ggaaggcaag acaagcatgc atccgccgta ctctttgggg cagctggctc  
1681 cggagaggcc tcgacccacc ccagtgcctg ttctctcat ctcccccacc gtgtcccca  
1741 gcagcctggg gtctgacaat acctcgagcc acaaccgacc agatgccagg gaccacgga  
1801 gcccttatga catcagcaat acagactact tcttccccag atagctgggt ggggtggacc  
1861 agcagcctgg accctgtgga tgacaaaaca caaacgggct cagcaaaaga tgcttctcac  
1921 tgccatgcca gcttatctca ggggtgtgag gcctttgggt tcacggaaga gccttgcgga  
1981 aggttctacg ccaggggaaa atcagcctgc tccagctgtt cagctggttg aggtttcaaa  
2041 cctccctttc caaatgcccc gcttaaaggg gtttagtgta acttgggcca ctgtgaagag  
2101 aaccatatca agactctttg gacactcaca cggacactca aaagctgggc aggttggtg  
2161 gggcctcggt gtggagaagc ggctggcagc ccaccctca acacctctgc acaagctgca  
2221 ccctcaggca ggtgggatgg atttcagcc aaagcctcct ccagccgcca tgctcctggc  
2281 ccactgcacg gtttcatctt ccaactcaaa ctcttaaaac ccaagtgcct ttagcaaat  
2341 ctgtttttct aggcctgggg acggctttta cttaaacgcc aaggcctggg ggaagaagct  
2401 ctctcctccc tttcttccct acagttcaaa aacagctgag ggtgagtggt tgaataatac  
2461 agtagtcag ggctggctcg ttttcaacag aattataatt agttcctcat tagcagtttt  
2521 gcctaaatgt gaatgatgat cctaggcatt tgctgaatac agaggcaact gcattggctt  
2581 tgggttcgag gacctcaggt gagaagcaga ggaaggagag gagaggggca cagggtctct  
2641 accatccctt gttaggtggg agctgagtg gggatcacag cctctgaaaa ccaatgttct  
2701 ctcttctcca cctccacaaa aggagagcta gcagcaggga gggcttctgc catttctgag  
2761 atcaaaacgg ttttactgca gctttgtttg ttgtcagctg aacctgggta actagggag  
2821 ataataataa ggaagacaat gtgaaaagaa aaatgagcct ggcaagaatg cgtttaaact  
2881 tggtttttaa aaaactgctg actgttttct cttgagaggg tggaaatatc aatattcgct  
2941 gtgtcagcat agaagtaact tacttaggtg tgggggaaag accataactt tgtttagccc  
3001 aaaaccaagt caagtgaaga aggaggaaga gaaaaaatat tttcctgcca ggcatggagg  
3061 ccacgcact tcgggaggtc gaggcaggag gatcacttga gtccagaagt ttgagatcag  
3121 cctgggcaat gtgataaaac cccatctcta caaaaagcat aaaaattagc caagtgtggt  
3181 agagtgtgcc tgaagtccca gatacttggg gggctgaggt gggaggatct cttgagcctg  
3241 ggaggtcaag gctgcagtga gccgagattg caccactgca ctccagcctg gggtagacaga  
3301 gcaagtgaga cctgtctc

## (2) INFORMATION FOR SEQ ID NO:118:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1533 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

1 ataccctaggc actaatatg ttccatagt actatgtgta cctgaaaagt tgtgtggcaa  
61 tcaaattttc acaaatagaa tctgttttta aatacactaa gaaagtacct actttatcct  
121 ttaaaacaaga ggtcagcaga ctttttctac aaagggtcag atagtaaga ttttacacct  
181 ttgttacaat acaatctcta tctcatctac ttagctctgc cattgttgca taaaagcagc  
241 tgtagatgat acacaaatgg gtgagctgtg attccaaatg aaacgttatt tgcaaaaaca  
301 ggtggtagat taaatttggg cccaaggctt acttgggaaa aaaaaagatc ttttggaaaa  
361 gaaaaaataa atgaataatt tttttaaaaa attgttcctt aggtcatagt ttgccagccc  
421 ctgccctaaa caaataattc ttgaatgcct actgtggtgt gtaagatag agtaataacc  
481 agggatacac agagaacaaa agagaaaaac tgctattctt gtgaaacttg gaagttggag  
541 gtaagctatt taaaataaac ccacaataaa gtacttcaca tagtgcagac tgtttcttta  
601 aatcaaaact cactccaaac aaccaattga ttactttgt aagtttgaat tttgtcttc  
661 agattctttt aaagtgggcc cttagtcagg agcgggtggct catgcctgta gtccatgac  
721 tttgggaggc tgaggcaggc agatcacttg aggtcaggag ttcgagacaa gcctggccaa  
781 catggcgaaa ccccgctctc actgaaaaca caaaaattag gctggcatag tggcatttgc  
841 ctgtagtctt agtactcag gaggtgagg caggagaatt gcttgaacct gggaggtgaa  
901 aattgcagtg agccgagatc atgctattgt actccagcct gggcaacaaa gcaagactcg  
961 tctcaaaaaa ataaaaatta aaaaaataaa gttagcctcta gcctaagata gcttgagcct  
1021 aggtgtgaat ctactgcctt actctgatgt aagcacagta agtgtggggg ctgcagggaa  
1081 tatccaggag gaacaataat ttcagaggct ctgtctcttc atgtccttga cctctgctta  
1141 cagcagcaat acttttactc agacttctgt tttctggaac ttgccttctt tttgtctgtg  
1201 tttatacttc ccttgtctgt ggttagataa gtataaagcc ctgagatcaa gcttctctgt  
1261 ctctctccct cctcccttc ctcttactct cattcatttc atacacactg gctcacacat  
1321 ctactctctc tctctatctc tctcagaatg acaattctag gtacaacttt tggcatgggt  
1381 ttttctttac ttcaagtcgt ttctggagaa agtggctatg ctcaaaatgg tgagtcattt  
1441 ctaacttttc ttatggattt tggattatct gtagcatggt ttcaggttat tcagttccct  
1501 aagagacctg agtcaggcac tgggtttgag tgc

## (2) INFORMATION FOR SEQ ID NO:119:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1658 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

1 cttctctctt atctctctca gaatgacaat tctaggtaca acttttggca tggttttttc

61 tttacttctgctgtttctg gagaaagtgg ctatgctcaa aatgact tgggaagatgc  
121 agaactggat gactactcat tctcatgcta tagccagttg gaagtgaatg gatcgagca  
181 ttcactgacc tgtgcttttg aggacccaga tgtcaacacc accaatctgg aatttgaaat  
241 atgtggggcc ctctgtggagg taaagtgcct gaatttcagg aaactacaag agatatattt  
301 catcgagaca aagaaattct tactgattgg aaagagcaat atatgtgtga aggttgga  
361 aaagagtcta acctgcaaaa aaatagacct aaccactata gttaaactcg aggtcctttt  
421 tgacctgagt gtcactctatc gggaaggagc caatgacttt gtggtgacat ttaatacatc  
481 acacttgcaa aagaagtatg taaaagtttt aatgcatgat gtagcttacc gccaggaaaa  
541 ggatgaaac aaatggacgc atgtgaattt atccagcaca aagctgacac tctgcagag  
601 aaagctccaa ccggcagcaa tgtatgagat taaagttcga tccatccctg atcactattt  
661 taaaggcttc tggagtgaat ggagtcgaag ttattacttc agaactccag agatcaataa  
721 tagctcaggg gagatggatc ctatcttact aaccatcagc attttgagtt ttttctctgt  
781 cgctctgttg gtcactcttg cctgtgtgtt atggaaaaaa aggattaagc ctatcgtatg  
841 gccactctc cccgatcata agaagactct ggaacatctt tgtaagaaac caagaaaaaa  
901 tttaaatgtg agtttcaatc ctgaaagttt cctggactgc cagattcata ggggtgatga  
961 cattcaagct agagatgaag tggaaagttt tctgcaagat acgtttcttc agcaactaga  
1021 agaactctgag aagcagaggc ttggagggga tgtgcagagc cccaactgcc catctgagga  
1081 tgtagtctgc actccagaaa gctttggaag agattcatcc ctacatgcc tggctgggaa  
1141 tgtcagtcca tgtgacgccc ctattctctc ctcttcagg tccctagatc gcaggagag  
1201 tggcaagaat gggcctcatg tgtaccagga cctcctgctt agccttggga ctacaacag  
1261 cacgctgccc cctccatttt ctctccaatc tggaaatcctg acattgaacc cagttgtcca  
1321 gggctagccc attcttactt cctgggagc aaatcaagaa gaagcatatg tcaccatgtc  
1381 cagcttctac caaaaccagt gaagtgtgaag aaaccagac tgaacttacc gtgagcgaca  
1441 aagatgattt aaaaggaag tctagagttc ctagtctccc tcacagcaca gagaagacaa  
1501 aattagcaaa accccactac acagtctgca agattctgaa acattgctt gaccactctt  
1561 cctgagttca gtggcactca acatgagtca agagcatcct gcttctacca tgtggatttg  
1621 gtcacaaggt ttaaggtgac ccaatgattc agctattt

## (2) INFORMATION FOR SEQ ID NO:120:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3191 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

1 atacctaggg actaatttag ttccatatgt actatgtgta cctgaaaagt tgtgtggcaa  
61 tcaaattttc acaaatagaa tctgttttta aatacactaa gaaagtacct actttatcct  
121 ttaacaaga ggtcagcaga ctttttctac aaagggtcag atagtaaaga ttttacacct  
181 tttgtacaat acaatctcta tctcatctac ttagctctgc cattgttgca taaaagcagc  
241 tgtgatgat acacaaatgg gtgaggctgt attccaaatg aaacgttatt tgcaaaaaa  
301 ggtgttagat taaatttggg ccgaaggctt acttgggaaa aaaaagatc ttttgaaaa  
361 gaaaaataa atgaataatt tttttaaaaa attgttccct aggtcatagt ttgccagccc  
421 ctgccctaaa caaataattc ttgaatgcct actgtggtgt gtaagatag agtaaatacc  
481 agggatacac agagaacaaa agagaaaaac tgctattctt gtgaaacttg gaagttggag  
541 gtaagctatt taaaaataac ccacaataaa gtacttcaca tagtcagac tgtttcttta  
601 aatcaaaaact cactccaaac aaccaattga ttcactttgt aagtttgat ttttgccttc  
661 agattctttt aaagtgggccc cttagtcagg agcgggtggc catgcctgta gtcctagcac  
721 tttgggaggg tgaggcaggc agatcacttg aggtcaggag ttcgagacaa gcctggccaa  
781 catggcgaaa ccccgctctc actgaaaaa caaaaattag gctggcatag tggcatttgc  
841 ctgtagtctt agctactcag gaggttgagg caggagaatt gcttgaacct gggaggtgaa  
901 aattgcagtg agccgagatc atgctattgt actccagcct gggcaacaaa gcaagactcg  
961 tctcaaaaaa ataaaaatta aaaaaataaa gtacgtctta gcctaagata gcttgagcct  
1021 aggtgtgaat ctactgcctt actctgatgt aagcacagta agtgtggggg ctgcagggaa  
1081 tatccaggag gaacaataat ttcagaggct ctgtctcttc atgtccttga cctctgctta  
1141 cagcagcaat acttttactc agacttccctg tttctggaac ttgccttctt ttttgcctgt  
1201 tttatacttc ccttgcctgt ggttagataa gtataaagcc ctatagctaa gcttctctgt  
1261 tttctccctt cctccctctc ctcttactct cattcatttc atacacactg gctcacacat  
1321 ctactctctc tctctatctc tctcagaatg acaattctag gtacaacttt tggcatggtt  
1381 ttttctttac ttcaagtcgt ttctggagaa agtggctatg ctcaaaatgg tgagtcattt  
1441 ctaacttttc ttatggattt tggattatct gtagcatggt ttcaggttat tcagttccct  
1501 aagagacctg agtcaggcac tgggtttgag tgc  
1 ctctctctct atctctctca gaatgacaat tctaggtaca acttttgga tggtttttct  
61 tttacttcaa gtcgtttctg gagaaagtgg ctatgctcaa aatggagact tgggaagatgc  
121 agaactggat gactactcat tctcatgcta tagccagttg gaagtgaatg gatcgagca  
181 ttcactgacc tgtgcttttg aggacccaga tgtcaacacc accaatctgg aatttgaaat  
241 atgtggggcc ctctgtggagg taaagtgcct gaatttcagg aaactacaag agatatattt  
301 catcgagaca aagaaattct tactgattgg aaagagcaat atatgtgtga aggttgga  
361 aaagagtcta acctgcaaaa aaatagacct aaccactata gttaaactcg aggtcctttt  
421 tgacctgagt gtcactctatc gggaaggagc caatgacttt gtggtgacat ttaatacatc  
481 acacttgcaa aagaagtatg taaaagtttt aatgcatgat gtagcttacc gccaggaaaa  
541 ggatgaaac aaatggacgc atgtgaattt atccagcaca aagctgacac tctgcagag  
601 aaagctccaa ccggcagcaa tgtatgagat taaagttcga tccatccctg atcactattt  
661 taaaggcttc tggagtgaat ggagtcgaag ttattacttc agaactccag agatcaataa  
721 tagctcaggg gagatggatc ctatcttact aaccatcagc attttgagtt ttttctctgt  
781 cgctctgttg gtcactcttg cctgtgtgtt atggaaaaaa aggattaagc ctatcgtatg



841 gccagcttc cccgatcata agaagactct ggaacatctt tgtaagaac caagaaaaa  
901 tttaaatgtg agtttcaatc ctgaaagtgt cctggactgc cagattcata ggggtgatga  
961 cattcaagct agagatgaag tggagggttt tctgcaagat acgtttcctc agcaactaga  
1021 agaactctgag aagcagagggc ttggagggtg tgtgcagagc cccaactgcc catctgagga  
1081 tgtagtctgc actccagaaa gctttggaag agattcatcc ctcacatgac tggctgggaa  
1141 tgtcagtcca tgtgacgccc ctattctctc ctcttccagg tccctagact gcaggagag  
1201 tggcaagaat gggcctcatg tgtaccagga cctcctgctt agccttggga ctacaacag  
1261 cacgtgcccc cctccatttt ctctccaatc tggaaatcctg acattgaacc cagttgctca  
1321 gggtcagccc attcttactt ccttggggtc aaatcaagaa gaagcatatg tcaccatgtc  
1381 cagcttctac caaaaccagt gaagtgtaa aaaccagac tgaacttacc gtgagcgaca  
1441 aagatgattt aaaagggaag tctagagttc ctagtctccc tcacagcaca gagaagacaa  
1501 aattagcaaa accccactac acagtctgca agattctgaa acattgcttt gaccactctt  
1561 cctgagttca gtggcactca acatgagttc agagcatcct gcttctacca tgtggatttg  
1621 gtcacaaggt ttaagggtgac ccaatgatcc agctattt

## (2) INFORMATION FOR SEQ ID NO:121:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1846 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

1 ctcagctctg ctatggtctc cagcagcccc cgcccgcgc tgcccgcact cctggtcctg  
61 ctcggggctc tgttcccagg acctggcaat gccagacat ctgtgtcccc ctcaaaagtc  
121 atcctgcccc ggggaggtct cgtgctggtg acatgcagca cctcctgtga ccagcccaag  
181 ttgttgggca tagagacccc gttgcctaaa aaggagttgc tctgcctgg gaacaaccgg  
241 aagggttatg aactgagcaa tgtcaagaa gatagccaac caatgtgcta ttcaaaactgc  
301 cctgatgggc agtcaacagc taaaaccttc ctcaccgtgt actggactcc agaacgggtg  
361 gaactggcac cctcccctc ttggcagcca gtgggcaaga acctaccct acgtgcccag  
421 gtggaggggt gggcaccccc ggcaacctc accgtggtgc tgcctcgtgg ggagaaggag  
481 ctgaaacggg agccagctgt gggggagccc gctgaggtca cgaccaggt gctggtgagg  
541 agagatcacc atggagccaa tttctcgtgc cgcactgaac tggacctgcg gccccaaggg  
601 ctggagctgt ttgagaacac ctcggccccc taccagctcc agaccttgt cctgccagcg  
661 actcccccac aactgtcag ccccgggtc cttagaggtg acacgcagg gacctgtgtc  
721 tgttccctgg acgggtgtt cccagttctg gaggcccagg tccacctgc actgggggac  
781 cagaggttga accccacagt cacctatggc aacgactcct tctcgccaa ggcctcagtc  
841 agtgtgaccg cagaggacga gggcacccag cggctgacgt gtgcagtaat actggggaac  
901 cagagccagg agacactgca gacagtgacc atctacagct ttccggcgcc caactgtatt  
961 ctgacgaagc cagaggtctc agaaggagac gagggtgac tgaagtgtga ggcccaccct  
1021 agagccaagg tgacgtgaa tggggttcca gccagccac tgggcccag ggcccagctc  
1081 ctgctgaagg ccaccccaga ggacaacggg cgcagcttct cctgctctgc aacctggag  
1141 gtggccggcc agcttataca caagaaccag accogggagc ttcgtgtcct gtatggcccc  
1201 cgaactggac agagggttg tccgggaaac tggacgtggc cagaaaattc ccagcagact  
1261 ccaatgtgac aggttgggg gaaccattg cccgagctca agtgtctaaa ggtatggact  
1321 tccccactgc ccatcgggga atcagtgaat gtcactcgag atcttgagg cacttacctc  
1381 tgtcgggcca ggagcactca aggggaggtc acccgcgagg tgaccgtgaa tgtgtctctc  
1441 ccccggtatg agattgtcat catcactgtg gtacgagccg cagtcataat gggcactgca  
1501 ggcctcagca cgtacctcta taaccgccag cgaagatca agaaatacag actacaacag  
1561 gccaaaaaag ggacccccat gaaaccgaac acacaagcca cgctcctctg aacctatccc  
1621 gggacagggc ctcttcctcg gccttcccat attggtggca gtgggtgccac actgaacaga  
1681 gtggaagaca tatgcatgc agctacacct accggccctg ggacgcccga ggacagggca  
1741 ttgtcctcag tcagatacaa cagcatttgg ggccatggta cctgcacacc taaaacacta  
1801 ggccacgcat ctgatctgta gtcacatgac taagccaaga ggaagg

## (2) INFORMATION FOR SEQ ID NO:122:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1041 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

1 ctaaagatct cctccaggc agccttggc tggctcctgc gagcccgtg agactgccag  
61 agatgtcctc tttcggttac aggacctga ctgtggccct cttcacctg atctgtgtgc  
121 caggatcgga tgagaaggta ttcgaggtac acgtgaggcc aaagaagctg gcggttgagc  
181 ccaaagggtc cctcgaggtc aactgcagca ccacctgtaa ccagcctgaa gtgggtgggtc  
241 tggagacctc ttaataaag attctgtgg acgaacaggc tcagtggaaa cattacttgg  
301 tctcaaacat ctcccatgac acggtcctcc aatgccactt cactgtctcc gggaagcagg  
361 agtcaatgaa ttccaacgtc agcgtgtacc agcctccaag gcaggtcatc ctgacactgc  
421 aaccactttt ggtggtgtg ggcaagtctc tcaccattga gtgcagggtg cccaccgtgg  
481 agcccttgga cagctcacc ctcttctgt tccgtggcaa tgagactctg cactatgaga  
541 ccttcgggaa ggcagccctt gctccgagg aggccacagc cacattcaac agcacggctg  
601 acagagagga tggccaccgc aacttctcct gcctggctgt gctggacttg atgtctcgcg  
661 gtggcaacat cttcacaaa cactcagccc cgaagatgtt ggagatctat gagcctgtgt  
721 cggacagcca gatgtcatc atagtcacgg tgggtgctgt gttgtgtctc ctgttctgta  
781 catctgtcct gctctgcttc atcttcggcc agcacttgcg ccagcagcgg atgggcacct



841 acgggggt agcggcttgg aggaggctgc cccaggcctt ccg tag caaccatgag  
901 tggcatggcc accaccacgg tggctactgg aactcagtgt gactcag ggttgaggtc  
961 cagccctggc tgaaggactg tgacaggcag cagagacttg ggacattgcc ttttctagcc  
1021 cgaatacaaaa cacctggact t

## (2) INFORMATION FOR SEQ ID NO:123:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2887 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

1 ctcagcctcg ctatggtctc cagcagcccc cgcccgcgc tgcccgcact cctggtcctg  
61 ctccgggctc tgttccagg acctggcaat gccagacat ctgtgtcccc ctcaaaagtc  
121 atcctgcccc ggggaggctc cgtgctggtg acatgcagca cctcctgtga ccagcccaag  
181 ttgttgggca tagagacccc gttgcctaaa aaggagtgtc tcctgcctgg gaacaaccgg  
241 aagggtgatg aactgagcaa tgtgcaagaa gatagccaac caatgtgcta ttcaaactgc  
301 cctgatgggc agtcaacagc taaaaccttc ctcaccgtgt actggactcc agaacgggtg  
361 gaactggcac cctccctc ttggcagcca gtgggcaaga accttacctt acgtgcccag  
421 ttggagggtg gggcaccctc ggccaacctc accgtggtgc tgctccgtgg ggagaaggag  
481 ctgaaacggg agccagctgt gggggagccc gctgaggtca cgaccacggt gctggtgagg  
541 agagatcacc atggagccaa tttctcgtgc cgcactgaac tggacctgcg gcccacaggg  
601 ctggagctgt ttgagaacac ctgcggcccc taccagctcc agacctttgt cctgccagcg  
661 actcccccac aacttgtcag cccccgggtc cttagaggtg acacgcaggg gacctgtgtc  
721 tgttccctgg acgggtgttt cccagctcgc gagggccagg tccacctgag actgggggac  
781 cagaggttga accccacagt cacctatggc aacgactcct tctcggccaa ggcctcagtc  
841 agtgtgaccg cagaggacga gggcaccacg cggctgacgt gtgcagtaat actggggaac  
901 cagagccagg agacactgca gacagtgaac atctacagct ttccggcgcc caacgtgatt  
961 ctgacgaagc cagaggtctc agaaggagac gaggtgacag tgaagtgtga ggcccaccct  
1021 agagccaaag tgacgctgaa tggggttcca gccagccac tgggcccag ggcccagctc  
1081 ctgctgaagg ccaccccaga ggacaacggg cgcagcttct cctgctctgc aacctggag  
1141 gtggccggcc agcttataca caagaaccag acccgggagc ttcgtgtcct gtatggcccc  
1201 cgactggacg agagggattg tccgggaaac tggacgtggc cagaaaattc ccagcagact  
1261 ccaattgtgc aggttgggg gaaccattg cccgagctca agtgtctaaa ggtatggcact  
1321 ttcccactgc ccacgggga atcagtgaat gtcactcgag atcttgaggg cacctacctc  
1381 tgtcgggcca ggagcactca aggggaggtc acccgcgagg tgaccgtgaa tgtgtctcc  
1441 ccccggtatg agattgtcat catcactgtg gtacgagccg cagtcataat gggcactgca  
1501 ggcctcagca cgtacctcta taaccgccag cggagatca agaaatacag actacaacag  
1561 gcccacaaag ggacccccat gaaaccgaac acacaagcca cgcctccctt aacctatccc  
1621 gggacagggc ctcttcctcg gccttcccat attggtggca gtggtgccac actgaacaga  
1681 gtggaagaca tatgccatgc agctacacct accggcctg ggacgcggga ggacagggca  
1741 ttgtcctcag tcagatacaa cagcatttgg ggccatggta cctgcacacc taaaacacta  
1801 ggccacgcat ctgatctgta gtcacatgac taagccaaga ggaagg  
1 ctaaagatct cctccaggc agccttggc tggctcctgc gagcccgagg agactgccag  
61 agatgtcctc tttcggttac aggaacctga ctgtggccct cttcaccctg atctgctgtc  
121 caggatcgga tgagaaggta ttcgaggtag acgtgaggcc aaagaagctg gcggttgagc  
181 ccaaagggtc cctcagggtc aactgcagca ccacctgtaa ccagcctgaa gtgggtggtc  
241 tggagacctc tctaaataag attctgctgg acgaacaggc tcagtggaaa cattacttgg  
301 tctcaaacat ctcccatgac acggtcctcc aatgccactt cacctgctcc ggaagcagg  
361 agtcaatgaa ttccaacgtc agcgtgtacc agcctccaag gcaggtcatc ctgacactgc  
421 aatccacttt ggtggtgtg ggcaagtcct tcaccattga gtgcagggtg cccaccgtgg  
481 agcccttggc cagcctcacc ctcttctgt tccgtggcaa tgagactctg cactatgaga  
541 ccttcgggaa ggcagccctt gctccgcagg aggccacagc cacattcaac agcacggctg  
601 acagagagga tggccaccgc aacttctcct gcctggctgt gctggacttg atgtctcgcg  
661 gtggcaacat ctttcacaaa cactcagccc cgaagatgtt ggagatctat gagcctgtgt  
721 cggacagcca gatggtcatc atagtacagg ttgtgtcggg gttgtgtccc ctgttcgtga  
781 catctgtcct gctctgtctc atcttcggcc agcacttgcg ccagcagcgg atgggacact  
841 acgggggtgc agcggttgg aggaggtgc cccaggcctt ccggccatag caaccatgag  
901 tggcatggcc accaccacgg tggctactgg aactcagtgt gactcctcag ggttgaggtc  
961 cagccctggc tgaaggactg tgacaggcag cagagacttg ggacattgcc ttttctagcc  
1021 cgaatacaaaa cacctggact t

## (2) INFORMATION FOR SEQ ID NO:124:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1739 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

1 aatggccacc atggtaccat ccgtgtgtg gccaggggc tgctggactc tgctggtctg  
61 ctgtctgtctg accccagggtg tccaggggca ggagtctctt ttgcgggttg agccccagaa  
121 ccctgtgtct tctgtgtgag ggtccctgtt tgtgaactgc agtactgatt gtcccagctt  
181 ttgagaaaatc gccttggaga cgtccctatc aaaggagctg gtggccagtg gcatgggctg  
241 ggcagccttc aatctcagca acgtgactgg caacagtcgg atcctctgct cagtgtactg  
301 caatggctcc cagataacag gctcctctaa catcaccgtg tacgggctcc cggagcgtgt

361 ggagcggca cccctgcctc cttggcagcc ggtggggccag aacttcaccc tgcgtgccca  
421 agtggagggg gggctgcctc ggaccagcct cacggtggtg ctgcttcgct gggaggagga  
481 gctgagccgg cagcccgagc tggaggagcc agcggaggtc actgccactg tgcgtgccag  
541 cagagacgac cagcgagccc ctttctcatg ccgcacagaa ctggacatgc agccccaggg  
601 gctgggactg ttcgtgaaca cctcagcccc ccgccagctc cgaacctttg tccctcccgt  
661 gacccccccg cgctcgtgg ccccccggtt cttggagggtg gaaacgtcgt ggcgggtgga  
721 ctgcaacctc gacgggcttt ttccagcctc agaggccag gtctacctgg cgctggggga  
781 ccagatgctg aatgcgacag tcatgaacca cggggacacg ctaacggcca cagccacagc  
841 cacggcgcgc gcggatcagg agggtgcccg ggagatcgtc tgcaacgtga ccctaggggg  
901 cgagagacgg gaggcccggg agaacttgac ggtcttttagc ttcctaggac ccattgtgaa  
961 cctcagcgag cccaccgccc atgaggggtc cacagtgacc gtgagttgca tggctggggc  
1021 tcgagtcagc gtcacgtgg acggagtcc cggcgcgcc ccggggcagc cagctcaact  
1081 tcagctaaat gctaccgaga gtgacgacgg acgcagcttc tctcgactg ccactctcga  
1141 ggtggacggc gagttcttgc acaggaacag tagcgtccag ctgcgagtc tgtatggtcc  
1201 caaaattgac cgagccacat gccccagca cttgaaatgg aaagataaaa cgagacacgt  
1261 gctgcagtcg caagccaggg gcaacccgta ccccgagctg cgggtgttga aggaaggctc  
1321 cagccgggag gtgcccgtgg ggtcccgtt cttcgtcaac gtaacacata atggtactta  
1381 tcagtggcaa gcgtccagct cagaggcaca atacaccctg gtcgtggtga tggacattga  
1441 ggctgggagc tcccactttg tccccgtctt cgtggcggtg ttactgacct tggcggtggt  
1501 gactatcgta ctggccttaa tgtacgtctt caggagacac caacggagcg gcagttacca  
1561 tgtaggggag gagagcacct atctgcccc cactgtctat cagccgacag aagcaatggg  
1621 ggaagaaccg tccagagctg agtgacgtg ggatccggga tcaaagtgg cggggcttg  
1681 gctgtgccc cagattccgc accaataaag ccttcaaacc ctaaaaaaa aaaaaaaa

## (2) INFORMATION FOR SEQ ID NO:125:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 920 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

1 gcacggagg gacagaccc cggagcccca gccccaccat gaccctcggc cgccgactcg  
61 cgtgtctttt cctcgcctgt gtctgcggc ccttgctgct ggggggcacc gcgctggcct  
121 cggagattgt ggggggcccg cgagcgccgc cccacgcgtg gcccttcactg gtgtccctgc  
181 agctgcgcgg aggcacttc tgcggcgcca cctgattgc gcccaacttc gtcattgctg  
241 ccgcgcactg cgtggcgaat gtaaacgtcc gcgcggtgcg ggtggtcctg ggagcccata  
301 acctctcggc gcgggagccc acccggcagg tgttcgctgt gcagcgcatc ttcgaaaacg  
361 gctacgaccc cgtaaacttg ctcaacgaca tcgtgattct ccagctcaac gggctcgcca  
421 ccatcaacgc caacgtgcag gtggcccagc tgccggctca gggacgccc cgtgcaacg  
481 ggggtcagtg cctggccatg ggctggggcc ttctgggcag gaaccgtggg atcgccagcg  
541 tcctgcagga gctcaacgtg acggtggtga cgtccctctg ccgtcgcagc aacgtctgca  
601 ctctcgtgag gggccggcag gccggcgctt gtttcgggga ctccggcagc cccttggtct  
661 gcaacgggct aatccacgga attgcctctc tcgtccgggg aggctgcgac tcagggtctc  
721 accccgatgc ctttgcctcg gtggcacagt ttgtaaactg gatcgactct atcatccaac  
781 gctccgagga caacccctgt cccaccccc gggacccgga cccggccagc aggaccact  
841 gagaagggtt gcccggttca cctcagctgc ccacaccac actctccagc atctggcaca  
901 ataaacattc tctgttttgc

## (2) INFORMATION FOR SEQ ID NO:126:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

1 ttgtcagagc cccagctggt gtccaggagc tgaccgtgag cctgggtgaa agtgagttcc  
61 ccgttgagg caccagacga ggagaggatg gaaggcctgg ccccaagaa tgagccctga  
121 ggttcaggag cggctggagt gagccgcccc cagatctccg tccagctgcg ggtcccagag  
181 gcctgggtta cactcgagc tcctggggga ggcccttgac gtgctcagtt cccaaacagg  
241 aaccctggga aggaccagag aagtgcctat tgcgcagtga gtgcccagca cagctgcagt  
301 tggccggtat cacaggcccc tgggtaaact gaggcaggcg acacagctgc atgtggccgg  
361 tatcacaggg ccctgggtaa actgaggcag gcgacacagc tgcatgtggc cggatcacca  
421 gggccctggg taaactgagg caggcgacac agctgcagtgt ggccggtatc acaggccct  
481 gggtaactg aggcaggcga cacagctgca tgtggccggt atcacggggc cctggataaa  
541 cagaggcagg cgaggccacc cccatcaagt ccctcaggtc taggtttggc caggtttgga  
601 aaaacacagc aacgctcggg aaatctgaat ttccgggtaag tatatcctgg gcctcatttg  
661 gaagagactt agattaaaaa aaaaacgtcg agaccagccc ggccaacacg tgaacccccg  
721 tctctactaa aaatacaaaa aattagccag gcgcagtgct cagcctgtg atcccagcac  
781 tctgggaggt gaggcaggcg gatcacccga ggtcagctgt tcaagaccag cctggccgag  
841 tgggcgaac actgtctcta ctacaaatac aaaaattagc cgggagtggg ggcaggtgac  
901 tgaatctca gctattcagg aggtcgaggc aggaagaatca cttgaacctg ggaggcggag  
961 gttgcccgtg gccgggatca gccaccgcca ctccagcctg ggcgatagag caagactctg  
1021 tctccaaaaa aataaattaa aaaaccaca ttgattatct gacatttgaa tgcgattgtg  
1081 catcctgaat tttgtctgga ggcaccccc gagccaatcc agcgtcttgt cccctctctc  
1141 ccccttttca tcaacgcctg tgccagggga gaggaagtgg agggcgctgg ccggccgtgg

1201 ggcaa ggcgcctccca gcacagggtc ataagaggag cgggc acggaggggc  
1261 agagaccccg gagccccagc cccaccatga ccctcgcccg cgtctcgcg tgtcttttcc  
1321 tcgcctgtgt cctgcccggc ttgctgctgg ggggtgagtt ttgagtcga acctcccgct  
1381 gctcctcttg tcccgggttc tcttccatga gggccccaac agtctgggtc  
1441 cctcatcttc acaggggagg tggcagctgg gacaaggaga ccagaagaga ctgagggtct  
1501 gagcgggtgaa gccaccacca ggagcccaga gttggggttt gaaaaccggg gagggggggg  
1561 gtggcagggtc gccctctggg ttcaagtcca ggtctgtctg tgccttggag gggcaccgtg  
1621 gggaggtccc ttgctctcgc cgtgcctcag ttctctcatc tgaacaacag ggggtgcgaac  
1681 gggcccagtc cctggtgttc ccggtggggg atccagaggc ccggtggccg ggaggggaca  
1741 ggctccttgg caggcactca gcccccgcac ccggtgtgtc cccaggcacc gcgctggcct  
1801 cggagattgt ggggggcccg cgaagcgggc cccacgcgtg gcccttcatg gtgtccctgc  
1861 agctgcgcgg agggcacttc tgcggcgcca cctgattgc gcccaacttc gtcattgtcg  
1921 ccgcgcactg cgtggcgaat gtgtgagtag ccgggagtg ggcgcgcccg ctcggagccc  
1981 cgtcccgggt ctgtgagtg ggtgggggga ggcgggggccc ggggtctgtg cggggggggg  
2041 gtccgtccag ggcccgcggg gccctcgag caccttcgcc ctcaggcccg tcgcccggatg  
2101 gggacgacaa ggcgcggctg agccccgacc cccggggccg cccctgagcc ccgcctctcc  
2161 ctcttttggc agaaacgtcc gcgcggtgcg gttggctctg ggagcccata acctctcgcg  
2221 cgggagccc acccggcagg tgttcgcccg gcagcgcac ttcgaaaacg gctacgaccc  
2281 cgtaaacttg ctcaacgaca cgtgattct ccagggtccc ccgggcgggc gggggcgagg  
2341 ggcgagggcc agaggcctgg ggagggtgga ggctgggga ggggtggaggc tgcgacggag  
2401 gggcgctcg gggccgctcg tggggacctg ggtggcatc gtgggtggg tggctccctc  
2461 tccgcgcctc ggtctgcacc tctgtgaac gggaaaatac ccgcatggg ccgttgaggg  
2521 gttaaatgag atcctgcagg gaggccccga tctgtgtca atcaacaac ttactgagaa  
2581 gggaggcccc gatctgttgc caatcaaca acttactgag aaggggaggc ccgactgtt  
2641 gtcaatcaac aaacttactg agaaggagg ccccgatctg ctgtcaatca acaaacttac  
2701 tgagaaggga ggccecgatg ttgtcaatca acaaacttac tgagaaggga ggccecgatc  
2761 tgcgtgcaat caacaaaact tactgagaag ggagggccc atctgtgtc aatcatcaaa  
2821 cttactgaga agggaggccc cgatctgtc tcaatcaaca aacttactga gaaggaggc  
2881 cccgatctg ttgtcaatca acaaacttac tgagaaggga ggccecgatc tgcgtgcaat  
2941 caacaaactt actgagattc tgtgtgtctc tccattcacc agtctgtgg ccaggggcag  
3001 gggccgcctc tgtctttggg aaaaggggca aaagtcccca cctttccacc cctgtcccg  
3061 gcttgagatt ctggttattt cctgggcgcc gggcccggtg gctcaggcct gtcattcccag  
3121 cactttggga ggctgaggcg ggtggatcac gaggtcaggt gttcgagacc agcctgagca  
3181 acatagtga accccgtctc tactaaaata cacaaaaaaa aaattagccg agtgtggtg  
3241 tgggtgcctg taatgccaac tactcaggag gctgaggaag gagaatcgct tgaaccocgg  
3301 aggcggagat tgcagtgagc tgagatcaca ccactgcact ccagcctggg tctcaaaaaa  
3361 aaaaaaaaag attcctccct gggaagggtt agaggagag tttccttgtc actaagtttt  
3421 ctcatagctc tcacccagtg cagtggcgcg atcgagctc actacacctc catctcctgg  
3481 gctcaagcca cctctcagc ttggaatggg gggtagctg aaccacaggt gccaccagct  
3541 ggtccaccac gtctggctaa tatatatata tacacacaca catacatata tataaataa  
3601 taaatatata ttttatttaa ataaaatata taatatttat aattatttta taattataat  
3661 aatatttata taattataaa tatcatttat aattataata tttattattt tataaataa  
3721 taaatatata atatatataa atatttttat aaataataaa atatatatat acacacatat  
3781 atatatattt tttagacaa gtctcgctct gtcgcccagg ctggagcgca gtgcacatc  
3841 tcactcactg cacctccgct tcccagggtc aagcgattct cctgcctcag cctcccaggt  
3901 agctgggact acaggcgccc gccaccacgc ctggctaatt tttggtattg ttagtagaga  
3961 cggggtttaa ccatgttagc caggatggtc ttgatctct gaccttttga ttggccacc  
4021 tcagcctccc aaaatgctgg gattatagcg gtgagcaccg cacctggcaa tttttttta  
4081 ttatttttgt agacatgggg ctttgccaca ttgcccaggc tggcttgaa tgcctggcct  
4141 ggctaagtgt atoctcctgc ctgcccctcc caaagtgtg ggcttacaag catgagccac  
4201 cgcgcccggc tgtagttttt ttgttaactg agcacctact gcttctgca ctcaagccac  
4261 atccagggac aacctccaac gccctgagcc ttggtgacgg ctcccactct acagatgggg  
4321 aaaccgagge ttgccttggg gagcagagtg tggggtgggt atctgcccct gcaggatccc  
4381 agaaccacag tggaacctga gatggggaaa ctgaggcccg gagaggggag ggtcatcatc  
4441 actgcccgtg gtgacgcgct gacgatctgt ccccacggcc acagctcgca ctggcgcca  
4501 ccatcaacgc caacgtgcag gtggcccagc tggcggtca gggacggcg atcgccagcg  
4561 ggtgagctg cctggccatg ggtggggccc ttctgggcag gaaccgtggg aacgtctgca  
4621 tctgagga gctcaacgtg acggtggtga cgtccctctg ccgtcgagc gtcctctgc  
4681 ctctcgtgag gggccggcag gccggcgtct gtttcgtacg tgcctgggt gtcctctgc  
4741 tccccaccgc ctcccagccc ggtactgcag caacaggcac cgtgggtcag ccttaggatg  
4801 ggacttccca accctgacac gtccggggc aggtgggcag ggcctcgag tccagcttcc  
4861 ccacctgtgc tgcctccaca ggggactcc ggcagccct tggctgcaa cgggctaate  
4921 cacggaattg cctccttctg ccggggaggc tgcgctcag ggcttacc ccatgcctt  
4981 gcccgggtgg cacagtttgt aaactggatc gactctatca tccaacgctc cagggacaac  
5041 cctgtcccc acccccgga cccggaccgc gccagcagga cccactgaga agggtgccc  
5101 ggtcacctc agctgcccac accacactc tccagcatc ggcacaataa acattctctg  
5161 tttgtagaa tgtgtttgat gctccttggc tgtgtgattg ggtgtgaaa atggtcagta  
5221 ggtcggcggt ggtggtcac acctgtaate ccagcactt gggaggttga ggcaggcgga  
5281 tcacttgagc tc

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6212 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TECHNOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

```
1 gcacggagg gacagagacc cggagcccca gcccaccat gaccctggc cgccgactcg
  61 cgtgtctttt cctcgctgt gtctgcccg ccttgctgt ggggggcacc ggcgtggcct
  121 cggagattgt ggggggcccg cgagcgccg cccacgcgt gcccttcac gtgtccctgc
  181 agctgcgcg aggcacttc tggcgccca ccttgattg gcccaactc gtcattgtcg
  241 ccgcgcactg cgtggcgaat gtaaacgtc gcgcggtgc ggtggtcct ggagccata
  301 acctctcgcg gcgggagccc accggcagg tgttcgccc gcagcgcat ttcgaaaacg
  361 gctacgaccc cgtaaacttg ctcaacgaca tcgtgattc ccagctaac gggtcggcca
  421 ccatcaacgc caacgtgcag gtggcccag tgcgggtca gggacgcgc ctgggcaacg
  481 ggggtgcagt cctggccatg ggctggggc ttctgggag gaaccgtgg atcgccagcg
  541 tctgacagga gctcaacgtg acggtgtga cgtccctct cgtgcgaca aacgtctgca
  601 ctctcgtgag gggccggcag gccggcgtc gtttcgggga ctccggcag cccttggtct
  661 gcaacgggct aatccacgga attgctcct tcgtccggg aggctgcgc tcagggtctt
  721 accccgatgc ctttgcccc gtggcacagt ttgtaaact gatcgactc atcatccaa
  781 gctccgagga caaccctgt cccaccccc gggacccga cccggccagc aggacccact
  841 gagaagggtc gcccggtca cctcagctg ccacaccac actctccagc atctggcaca
  901 ataacattc tctgtttgt

1 ttgtcagag cccagctgt gtccaggagc tgaccgtgag cctgggtgaa agtgagtcc
  61 ccgttgagg caccagacga ggagaggat gaaggcctg ccccaagaa tgagccctga
  121 ggttcaggag cggttgagt gagccgccc cagatctcc tccagctgc ggtccagag
  181 gcttgggtta cactcgagc tcttgggga ggccttgac gtgtcagt ttccaaacag
  241 aacctggga aggaccagag aagtgcctg tgcgcagtga gtgccgaca cagctgcatt
  301 tggccggtat cacaggccc tgggtaact gaggcaggc acacagctg atgtggcgg
  361 tatcacagg ccctgggtaa actgaggcag gcgacacag tgcattggc cggatcaca
  421 gggccctggg taaactgagg caggcgacac agctgcatt ggcgggtatc acaggccctt
  481 gggtaactg aggcaggcga cacagctga tgtggccgt atcacgggc cctggataaa
  541 cagaggcagg cgaggccacc cccatcaagt cctcaggtc taggtttggc caggtttgga
  601 aaaacacagc aacgctcgtt aaatctgaat ttcgggtaag tatatcctg gcctcattt
  661 gaagagactt agattaaaaa aaaaacgtc agaccagcc ggccaacac tgaaaccccg
  721 tctctactaa aatacaaaa aattagccag gcgcagtgt cacgcctgt atccacgac
  781 tctgggaggt gaggcaggcg gatcaccca ggtcagctg tcaagaccg cctggccgag
  841 tggcgaaac actgtctcta ctacaaatac aaaaattagc cgggagtga ggcaggtgac
  901 tgtaattctc gctattcagg aggtgaggc aggagaatc cttgaacct ggaggcggag
  961 gttgccgtga gccgggatca cgcaccgca ctccagcct ggcgatagag caagactctg
  1021 tctccaaaaa aataaattaa aaaaccaca ttgattatc gacatttgaa tgcgattgtg
  1081 cactctgaat tttgtctgga ggcccaccc gagccaatc agcgtcttgt ccccttctc
  1141 ccccttttca tcaacgcctg tgcagggga gaggaagtg agggcgctg ccggccgtgg
  1201 ggcaatgcaa cgccctccca gcacagggtc ataagaggag ccgggcgggc acggaagggc
  1261 agagaccccg gagccccagc cccaccatga cctcggccc cgcactcgc tgtcttttc
  1321 tgcctgtgt cctgcccggc ttgtgtctg ggggtgagtt tttagtoca acctccgct
  1381 gctccctctg tcccgggttc tgttccacc tctccataga gggccccacc agtgtgggtc
  1441 cctcactctc acaggggagc tgccagctg gacaaggaga ccagaagaga ctgaggttct
  1501 gagcggtgaa gccaccacga ggagccaga gttggggtt gaaaacccg ggagggggg
  1561 gtggcaggtc gccctctggg ttcaagtcca ggtctgtctg tgccttgag gggcaccgtg
  1621 gggaggtccc tttgcctctc cgtgcctcag ttctctcatc tgaacaacag gggtcgaac
  1681 ggccccgatc ccgtgggttc ccggtggggg atccagaggc cccgtggccc ggaggggaca
  1741 cgtcctttg caggcactca gcaccgcac ccggtgtgt cccaggcac gcgctggcct
  1801 cggagattgt ggggggcccg cgagcgctg cccacgcgt gcccttcac gtgtcctgc
  1861 agctgcgcg aggcacttc tgcggcgcca cctgattgc gcccaactc gtcattgtcg
  1921 ccgcgcactg cgtggcgaat gtgtgagtag ccgggagtgt gcgcgccgg ctccgacccc
  1981 cgtcccgggt ctgtgagggt ggtgggggga ggcggggggc ggggtgctg gcggggggg
  2041 gtcggtccag ggcccgccgg gccctcagc cacttcgcc ctccaggccc tcgcccgatg
  2101 gggacgacaa ggcgcggctg agcccgacc cccggggcg cccctgagc ccgctctcc
  2161 ctcttttggc agaaacgtc gcgcggtgc ggtggtcct ggagccata acctctcgc
  2221 gcgggagccc acccggcagg tgttcgccgt gcagcgcat ttcgaaaac gctacgacc
  2281 cgtaaacttg ctcaacgaca tcgtgattc ccaggtgcc cccggcgggc gggggcgagg
  2341 ggccgaggcc agaggcctg ggagggtga ggcctggga ggggtggagg tgcagcgagg
  2401 gggcgctcg gggcgctcg tggggacct ggggtggcat gttggctgg tggccccctc
  2461 tccgcgcctc ggtctgcacc tctgtgaaac gggaaaaata ccgttgaggc cgttgaggg
  2521 gttaaatgag atcctgcagg gagggcccga tctgtgtca atcaaaaaa ttactgagaa
  2581 gggaggcccc gatctgttgt caatcaacaa acttactgag aaggaggcc ccgatctgtt
  2641 gtcaatcaac aaacttactg agaaggagg cccgatctg ctgtcaatca aaaaacttac
  2701 tgagaaggga ggccccgat ttgtcaatca aaaaacttac tgagaaggga gggcccgatc
  2761 tgtgttcaat caaccaaact tactgagaag ggaggcccc atctgtgtc aatcatcaaa
  2821 ctactgaga agggaggccc cgtctgtctg tcaatcaaca aacttactga gaaggaggc
  2881 cccgatctg ttgtcaatca aaaaacttac tgagaaggga gggcccgatc tgtgtcaat
  2941 caaaaaactt actgagattc tgtgtgtctc tccattcacc agtctgtgg ccaggggcag
  3001 gggccgctc tgtctttggg aaaaggggga aaagtcccca ccttccacc cctgtccgcg
  3061 ccttgcagtt cgtgttattt cctggcgcc gggcccggt gctcaggcc gtcatcccg
  3121 cactttggga ggctgaggc ggtggatcac gaggtcagg gttcgagac agcctgagca
  3181 acatagtga accccgtctc tactaaaaa caaaaaaaaa aaattagcc agtgtggtt
  3241 tgggtgcctg taatgccaac tactcaggag gctgaggag gagaatcgt tgaaccccg
  3301 aggcggagat tgcagtgagc tgagatcaca ccactgcact ccagcctgg tctcaaaaaa
  3361 aaaaaaaaaa attcctccct ggaagggtt agaggagag tttcctgtc actaagttt
```

3421 ctcata tcaccagtg cagtggcgcg atcgagctc a cctc catctcctgg  
3481 gctcaagcca cctctcagc ttggaatggg gggtagctgg a aggt gccaccacgt  
3541 ggtccaccac gtctggctaa tatatatata tacacacaca catacatata ttataaataa  
3601 taaatatata ttttatttaa ataaaatata taatatttat aattatttta taattataat  
3661 aatatttata taattataaa tatcatttat aattataata tttattattt tataaaataa  
3721 taaatataaa atatataaaa atatttttat aaataataaa atatataat acacacatat  
3781 atatatattt tttgagacaa gtctcgctct gtcgccagg ctggagcgca gtgcacaatc  
3841 tcaactcactg cacctccgcc tcccagggtt aagcgattct cctgcctcag cctcccaggt  
3901 agctgggact acaggcgccc gccaccacgc ctggctaatt tttggatttg ttagtagaga  
3961 cgggggtttaa ccatgttagc caggatggtc ttgatctcct gaccttttga ttggcccacc  
4021 tcagcctccc aaaatgctgg gattatagc gtgagcaccg cacctggcaa tttttttta  
4081 ttatttttgt agacatgggg ctttgccaca ttgccaggc tggctctgaa tgcctggcct  
4141 ggcctaagtg atcctcctgc ctgcctctcc caaagtgtg ggctttacaag catgagccac  
4201 cgcgcccgcc tgtagttttt ttgttaactg agcacctact gcttcttgca ctcaagccac  
4261 atccaggagc aacctccaac gccctgagcc ttggtgacgg ctccactct acagatgggg  
4321 aaaccgagc ttgccttggg gagcagagtg tggggtgggt atcctgccct gcaggatccc  
4381 agaaccacag tggaacctga gatggggaaa ctgagggccg gagaggggag ggtcatcatc  
4441 actgccccgt gtgacgcgt gacgatctgt cccacccgcc acagctcaac ggttcggcca  
4501 ccatcaacgc caacgtgcag gtggcccagc tgcggctca gggacgccgc ctgggcaacg  
4561 ggggtgcagtg cctggccatg ggctggggcc ttctgggcag gaaccgtggg atcgccagcg  
4621 tctgcagga gctcaacgtg acggtggtga cgtccctctg ccgtcgcagc aacgtctgca  
4681 ctctcgtgag gggccggcag gccggcgtct gttcgtacg tgcctgggt gtcctctgct  
4741 tccccaccg ctcccagccc ggtactgcag caacaggcac cgtggctgaa cctaggatg  
4801 ggacttccca acctgacac gtgcggcgcc aggtgggcag ggctcgcag tccagcttcc  
4861 ccacctgtc tgcctccaca gggggactcc ggcagcccct tggctgcaa cgggctaate  
4921 cacggaattg cctcctctgt ccgggagggc tgcgcctcag ggctctacc cgatgccttt  
4981 gccccgggtg cacagtttgt aaactggatc gactctatca tccaacgctc cgaggacaac  
5041 cctgttcccc acccccggga cccggaccgc gccagcagga cccactgaga agggctgccc  
5101 gggtcacctc agctgcccac acccacactc tccagcatct ggcacaataa acattctctg  
5161 tttttagaaa tgtgtttgat gtccttggc tgtgtgattg ggtgttgaat atggtcagta  
5221 ggtcggcggt ggtggctcac acctgtaate ccagcacttt gggaggttga ggcaggcgga  
5281 tcaattgagc tc

## (2) INFORMATION FOR SEQ ID NO:128:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1755 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

1 ctattgcagt atcttccagc ttccagtctt atctgaagac cccggcacca aagtgaccag  
61 gaggcagaga agaacttcag aggagtctcg tcttgggctg cccgtgggtg agtgggaggg  
121 tccgggactg cagaccggtg gcgatggcca ctctcccagc agcagaaacc tggatagacg  
181 ggggtggagg cgtgggtgca gacgccgtga acctgaccgc ctgcctagct gccggggcgg  
241 ccacgggggc agttgagact ggggtggctg aactgctgga ccaagctggc aacctctcct  
301 cctccccttc cgcgctggga ctgcctgtgg cttccccgc gccctcccag ccttgggcca  
361 acctcaccaa ccagttcgtg cagccgtcct ggcgcatcgc gctctgggtc ctggcgatg  
421 gtgtgggtgt ggcagtggca gttttgggaa atctcatcgt catctggatc atcctggccc  
481 acaagcgcat gaggactgtc accaactact tcttgtgaa cctggcttct tccagcgcct  
541 ccatggccgc cttcaacacg ttggtcaatt tcatctacgc gcttcatagc gattgggtact  
601 ttggcgccaa ctactgccgc ttccagaact tctttcctat cacagctgtg ttcgccagca  
661 tctactccat gacggccatt gcggtggaca ggtatatggc tattattgat ccttgaac  
721 ccagactgtc tgctacagca accaagattg tcattggaag tatttggatt ctgacatttc  
781 tacttgccct cctcagtggt ctttattcca aaaccaaagt catgccagc cgtactctct  
841 gctttgtgca atggccagaa ggtcccaaac aacatttcac ttaccatatt atcgctatta  
901 tactggtgta ctgtttccca ttgctcatca tgggtattac atacaccatt gttggaatta  
961 ctctctgggg aggagaaatc ccaggagata cctgtgacaa gtatcatgag cagctaaagg  
1021 ccaaaagaaa ggtgttcaaa atgatgatta ttgtgtcat gacatttgat atctgctggc  
1081 tgccctatca tatttacttc attctcactg caatctatca acaactaaat agatggaat  
1141 acatccagca ggtctacctg gctagctttt ggctggcaat gagctcaacc atgtacaatc  
1201 ccatcatcta ctgctgtctg aataaaagat ttcgagctgg cttcaagaga gcatttcgct  
1261 ggtgtccttt catcaaagt tccagctatg atgagctaga gctcaagacc accaggtttc  
1321 atccaaaccg gcaaagcagt atgtacaccg tgaccagaat ggagtccatg acagtcgtgt  
1381 ttgaccccaa cgatgcagac accaccaggt ccagtcggaa gaaaagagca acgccaagag  
1441 acccaagttt caatggctgc tctcgagga attccaaatc tgcctccgcc acttcaagtt  
1501 tcataagctc accctatacc tctgtggatg aatattctta attccatttc ctgaggtaaa  
1561 agattagtgt gagaccatca tgggtgccagt ctaggacccc attctcctat ttatcagtc  
1621 tgcctatat accctctaga aacagaaagc aatttttagg cagctatggt caaattgaga  
1681 aaggtagtgt ataaatgtga caaagacact aataacatgt tagcctccac ccaaaataaa  
1741 atgggcttta aattt

## (2) INFORMATION FOR SEQ ID NO:129:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 600 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```
1 ctgcagaccg gtggcgatgg ccctcctccc agcagcagaa acctggatag acgggggtgg
  61 aggcgtgggt gcagacgccg tgaacctgac cgcctcgcta gctgccgggg cggccacggg
 121 ggcagttgag actgggtggc tgcaactgct ggaccaagct ggcaacctct cctcctcccc
 181 ttccgcgctg ggactgcctg tgcgttcccc cgcgcctccc cagccctggg ccaacctcac
 241 caaccagttc gtgcagccgt cctggcgat cgcgctctgg tccctggcgt atggtgtggt
 301 ggtggcagtg gcagttttgg gaaatctcat cgtcatctgg atcatcctgg cccacaagcg
 361 catgaggact gtcaccaact acttccttgt gaacctggct ttctccgacg cctccatggc
 421 cgccttcaac acgttgggtca atttcattca cgcgcttcat agcgagtggg actttggcgc
 481 caactactgc cgcttcaga acttctttcc tatcacagct gtgttcgcca gcattactc
 541 catgacggcc attgcggtgg acaggtgagg agaggacaga cagagaggaa agaggagaa
```

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

```
1 ggtatatggc tattattgat cccttgaac ccagactgtc tgctacagca accaagattg
  61 tcattggaag tatttggatt ctagcatttc tacttgctt ccctcagtg ctttattcca
 121 aaaccaaagt catgccaggc cgtactctct gctttgtgca atggccagaa ggtcccaaac
 181 aacatttcac gtaagttaat tctctattat ggttttcaat tcagttt
```

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```
1 catgtgtttt tcttatttt catagttacc atattatcgt cattatactg gtgtactgtt
  61 tcccattgct catcatgggt attacatata ccattgttgg aattactctc tggggaggag
 121 aaatcccagg agatacctgt gacaagtatc atgagcagct aaaggccaaa agaaaggtag
 181 tgggccatgt gtttaccta g
```

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```
1 caaatgactt tttctttata gttgtgcaaa atgatgatta ttgtgtcat gacatttgct
  61 atctgtggc tgcctatca tatttacttc attctactg caatctatca acaactaaat
 121 agatggaaat acatccagca ggtctacctg gctagctttt ggctggcaat gagctcaacc
 181 atgtacaatc ccatactcta ctgctgtctg aataaaagggt aaaaacaaaa ctacgaaatg
 241 caagttgctt gtcac
```

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 449 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```
1 aaaataactt ttctttctgt ggcctgcttt tcctcagatt tcgagctggc ttcaagagag
  61 catttcgctg gtgtcctttc atcaaaagtt ccagctatga tgagctagag ctcaagacca
 121 ccaggtttca tccaaccgg caaagcagta tgtacaccgt gaccagaatg gagtccatga
 181 cagtcgtggt tgacccaac gatgcagaca ccaccaggtc cagtcggaag aaaagagcaa
 241 cgccaagaga cccaagtttc aatggctgct ctgcaggaa ttccaaatct gcctccgcca
 301 cttcaagttt cataagctca ccataacct ctgtggatga atattcttaa ttccatttcc
 361 tgaggtaaaa gattagtgtg agaccatcat ggtgccagtc taggaccca ttctcctatt
 421 tatcagtcct gtcctatata ccctctaga
```

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3128 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

```
1 ctgcagaccg gtggcgatgg ccattctccc agcagcagaa acctggatag acgggggtgg
  61 aggcgtgggt gcagacgcgc tgaacctgac cgcctcgcta gctgccgggg cgccacggg
 121 ggcagttgag actgggtggc tgcaactgct ggaccaagct ggcaacctct cctcctccc
 181 ttccgcgctg ggactgctg tgcgttcccc cgcgccctcc cagccctggg ccaacctcac
 241 caaccagttc gtgcagccgt cctggcgat cgcgctctgg tccctggcgt atggtgtggt
 301 ggtggcagtg gcagttttgg gaaatctcat cgtcatctgg atcatcctgg ccacaagcg
 361 catgaggact gtcaccaact atttcttgt gaacctggct ttctccgacg cctccatggc
 421 cgccttcaac acgttgggtca atttcatcra cgcgcttcat agcagtggt actttggcgc
 481 caactactgc cgcttccaga atttctttcc tatcacagct gtgttcgcca gcattactc
 541 catgacggcc attgcggtgg acaggtgagg agaggacaga cagagaggaa agaggggagaa

1 ctattgcagt atttctcagc ttccagtctt attctgaagac cccggcacca aagtggaccg
  61 gaggcagaga agaacttcag aggagtctcg tcttgggctg cccgtgggtg agtgggaggg
 121 tccgggactg cagaccggtg gcgatggcca ctctccagc agcagaaacc tggatagacg
 181 ggggtggagg cgtgggtgca gacgccgtga acctgaccgc ctgctagct gccggggcgg
 241 ccacgggggc agttgagact ggggtggctg aactgctgga ccaagctggc aacctctct
 301 cctccccttc cgcgctggga ctgcctgtgg ctcccccg gccctccag cctggggcca
 361 acctaccaa ccagttcgtg cagccgtcct ggcgcatcgc gctctgttcc ctggcgatg
 421 gtgtgggtgt ggcagtggca gttttgggaa atctcatcgt catctggatc atctggccc
 481 acaagcgcat gaggactgtc accaactact tcttgtgaa cctggcttcc tccgacgcct
 541 ccatggccgc cttcaacacg ttggtcaatt tcatctacgc gttcatagc gagtgtact
 601 ttggcgccaa ctactgccc ttccagaact tcttctctat cacagtgtg ttcccgagca
 661 tctactccat gacggccatt gcggtggaca ggtatatggc tattattgat ccttgaaac
 721 ccagactgtc tgctacagca accaagattg tcattggaag tatttgatt ctagcatttc
 781 tacttgctt cctcagtggt ctttattcca aaaccaaagt catgcccagg cgtactctct
 841 gctttgtgca atggccagaa ggtcccaaac aacatttcac ttaccatatt atcgctatta
 901 tactggtgta ctgtttccca ttgctcatca tgggtattac atacaccatt gttggaatta
 961 ctctctgggg agggagaaat ccaggagata cctgtgacaa gtatcatgag cagctaaagg
1021 ccaaaagaaa ggttgtcaaa atgatgatta ttgttgcac gacatttgc atctgctggc
1081 tgccctatca tatttacttc attctcactg caatctatca acaactaaat agatggaaat
1141 acatccagca ggtctacctg gctagctttt ggctggcaat gagctcaacc atgtacaatc
1201 ccatcatcta ctgctgtctg aataaaagat ttcgagctgg cttcaagaga gcatttcgt
1261 ggtgtccttt catcaaagtt tccagctatg atgagctaga gctcaagacc accaggttcc
1321 attcaaaccg gcaaagcagt atgtacaccg tgaccagaat ggagtcctat acagtcgtgt
1381 ttgaccccaa cgatgcagac accaccaggt ccagtcggaa gaaaagagca acgccaagag
1441 acccaagttt caatggctgc tctcgagga attccaaatc tgcctccgcc acttcaagtt
1501 tcataagctc acctataacc tctgtggatg aatattctta attccatttc ctgaggtaaa
1561 agattatgtg gagaccatca tgggtccagt ctaggacccc attctctat ttatcagtc
1621 tgtcttatat accctctaga aacagaaagc aatttttagg cagctatggt caaattgaga
1681 aaggtagtgt ataatgtga caaagacact aataacatgt tagcctccac caaaaataaa
1741 atgggcttta aattt

1 ggtatatggc tattattgat cccttgaac ccagactgtc tgctacagca accaagattg
  61 tcattggaag tatttgatt ctagcatttc tacttgctt cctcagtggt ctttattcca
 121 aaaccaaagt catgcccagg cgtactctct gcttgtgca atggccagaa ggtcccaaac
 181 aacatttcac gtaagttaat tctctattat ggttttcaat tcagttt

1 catgtgtttt tcttattttt catagttacc atattatcgt cattatactg gtgtactgtt
  61 tcccattgct catcatgggt attacataca ccattgttgg aattactctc tggggaggag
 121 aaatcccagg agatacctgt gacaagtatc atgagcagct aaaggccaaa agaaaggtag
 181 tggccatgt tgtttaccta g

1 caaatgactt ttcttttata gtttgtcaaa atgatgatta ttgttgcac gacatttgc
  61 atctgctggc tgccctatca tatttacttc attctcactg caatctatca acaactaaat
 121 agatggaaat acatccagca ggtctacctg gctagctttt ggctggcaat gagctcaacc
 181 atgtacaatc ccatcatcta ctgctgtctg aataaaaggt aaaaacaaaa ctacgaaatg
 241 caagttgctt gtcac

1 aaaataactt ttctttctgt ggctgcttt tctcagatt tcgagctggc ttcaagagag
  61 catttoctg gtgtcctttc atcaaagttt ccagctatga tgagctagag ctcaagacca
 121 ccagggtttc tccaaaccgg caaagcagta tgtaaccgt gaccagaatg gagtccatga
 181 cagtcgtgtt tgaccccaac gatgcagaca ccaccaggtc cagtcggag aaaagagcaa
 241 cgccaagaga ccaagtttcc aatggctgct ctgcagga ttccaaatct gcctccgcca
 301 cttcaagttt cataagctca ccctatacct ctgtggatga atattcttaa ttccatttcc
 361 tgaggtaaaa gattagtgtg agaccatcat ggtgccagtc taggaccca ttctctatt
 421 tatcagtcct gtccatatata cctctaga
```

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2206 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

```
1 ctagtctttc agccttcagg ctgtttttgg cttgaagctc tcttggcctc ctagtcttcta
  61 cctaatacatg tccctgttgg aggccatcag cctctggaat gaaggggtgc tggcagcgga
```



121 caagaaggac tggaagggag ccctggatgc cttcagtgcc gtccaggacc cccactccc  
181 gatttgcttc aacattggct gcatgtacac tatcctgaag aacatgactg aagcagagaa  
241 ggcttttacc agaagcatta accgagacaa gcacttggca gtggcttact tccaacgagg  
301 gatgctctac taccagacag agaaatatga tttggctatc aaagacctta aagaagcctt  
361 gattcagctt cgagggaaacc agctgataga ctataagatc ctggggctcc agttcaagct  
421 gtttgctgt gaggtgttat ataacattgc tttcatgtat gccaagaagg aggaatggaa  
481 aaaagctgaa gaacagttag cattggccac gagcatgaag tctgagccca gacattccaa  
541 aatcgacaag gcgatggagt gtgtctggaa gcagaagcta tatgagccag tggatgaccc  
601 tgtgggcaag ctgtttcgac caaatgagag acaagtggct cagctggcca agaaggatta  
661 ctaggcaag gcgacggctg tggcatctgt ggtggatcaa gacagtttct ctgggtttgc  
721 ccctctgcaa ccacaggcag ctgagcctcc acccagaccg aaaaccccag agatcttcag  
781 ggctctggaa ggggaggctc accgtgtgct atttgggttt gtgcctgaga caaaagaaga  
841 gctccaggtc atgccaggga acattgtctt tgtcttgaag aagggcaatg ataactgggc  
901 cacggtcatg ttcaacgggc agaaggggct tgttcctgc aactaccttg aaccagtga  
961 gttgcgatc caccctcagc agcagcccca ggaggaaagc tctccgcagt ccgacatccc  
1021 agctcctcct agttccaaag cccctggaaa acccagctg tcaccaggcc agaaacaaaa  
1081 agaagagcct aaggaaagtga agctcagtg tcccatgccc tacacactca aggtgacta  
1141 caagtacacg gtagtcatga agactcagcc cgggctcccc tacagccagg tccgggacat  
1201 ggtgtctaag aaactggagc tccggctgga acacactaag ctgagctatc ggctcggga  
1261 cagcaatgag ctggtgcccc ttccagaaga cagcatgaag gatgcctggg gccaggtgaa  
1321 aaactactgc ctgactctgt ggtgtgagaa cacagtgggt gaccaaggct ttccagatga  
1381 acccaaggaa agtgaaaaag ctgatgctaa taaccagaca acagaacctc agcttaagaa  
1441 aggcagccaa gtggaggcac tcttcagtta tgaggctacc caaccagagg acctggagtt  
1501 tcaggaaggg gatataatcc tgggtttatc aaaggtgaat gaagaatggc tgggaaggga  
1561 gtgcaaaagg aaggtgggca ttttcccaa agttttgtt gaagactgcg caactacaga  
1621 tttgaaaagc actcggagag aagtctagga tgtttcacia actacaaagc tgaagaaaat  
1681 gaagccctat tacttgtttg taagatttag cacccttctg ctgtatactg tactgagaca  
1741 ttacagtttg gaagtgttaa ctattttatc cctgttaaaa ttaacctac tagacaatga  
1801 tgtgagtacc caggatgatt tcctggggca cagtgggtga ggagatggg acagggtgaat  
1861 gatgctctac ggggagagga aaagtggatg gaagtgtctg gaaagggcag gagagatct  
1921 tccaggtact gatcctgtt cttgctctga gtgctagcta gccagctgtg ttcacactgt  
1981 aaacattcat caagctgtac atttgggtgca cttttctgtg tcataaccaca ataaaaaaa  
2041 acctatcatc atcttacaaa aacaagacac ccaagtccag gccaaggag taagtacaaa  
2101 tattcctgtt tctgaacat tactgtaatt ggctcttaag gcttgaagta accttatagg  
2161 ttactcataa ggcataata aataaacttg tttgtttct tttttc

## (2) INFORMATION FOR SEQ ID NO:136:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1739 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

1 ctagtctttc agccttcagg ctgttttttg cttgaagctc tcttggctc ctagtcttcta  
61 cctaatacatg tccctggttg aggccatcag cctctggaat gaaggggtgc tggcagcgga  
121 caagaaggac tggaagggag ccctggatgc cttcagtgcc gtccaggacc cccactccc  
181 gatttgcttc aacattggct gcatgtacac tatcctgaag aacatgactg aagcagagaa  
241 ggcttttacc agaagcatta accgagacaa gcacttggca gtggcttact tccaacgagg  
301 gatgctctac taccagacag agaaatatga tttggctatc aaagacctta aagaagcctt  
361 gattcagctt cgagggaaacc agctgataga ctataagatc ctggggctcc agttcaagct  
421 gtttgctgt gaggtgttat ataacattgc tttcatgtat gccaagaagg aggaatggaa  
481 aaaagctgaa gaacagttag cattggccac gagcatgaag tctgagccca gacattccaa  
541 aatcgacaag gcgatggagt gtgtctggaa gcagaagcta tatgagccag tggatgaccc  
601 tgtgggcaag ctgtttcgac caaatgagag acaagtggct cagctggcca agaaggatta  
661 ctaggcaag gcgacggctg tggcatctgt ggtggatcaa gacagtttct ctgggtttgc  
721 ccctctgcaa ccacaggcag ctgagcctcc acccagaccg aaaaccccag agatcttcag  
781 ggctctggaa ggggaggctc accgtgtgct atttgggttt gtgcctgaga caaaagaaga  
841 gctccaggtc atgccaggga acattgtctt tgtcttgaag aagggcaatg ataactgggc  
901 cacggtcatg ttcaacgggc agaaggggct tgttcctgc aactaccttg aaccagtga  
961 gttgcgatc caccctcagc agcagcccca ggaggaaagc tctccgcagt ccgacatccc  
1021 agctcctcct agttccaaag cccctggaaa acccagctg tcaccaggcc agaaacaaaa  
1081 agaagagcct aaggaaagtga agctcagtg tcccatgccc tacacactca aggtgacta  
1141 caagtacacg gtagtcatga agactcagcc cgggctcccc tacagccagg tccgggacat  
1201 ggtgtctaag aaactggagc tccggctgga acacactaag ctgagctatc ggctcggga  
1261 cagcaatgag ctggtgcccc ttccagaaga cagcatgaag gatgcctggg gccaggtgaa  
1321 aaactactgc ctgactctgt ggtgtgagaa cacagtgggt gaccaaggct ttccagatga  
1381 acccaaggaa agtgaaaaag ctgatgctaa taaccagaca acagaacctc agcttaagaa  
1441 aggcagccaa gtggaggcac tcttcagtta tgaggctacc caaccagagg acctggagtt  
1501 tcaggaaggg gatataatcc tgggtttatc aaaggtgaat gaagaatggc tgggaaggga  
1561 gtgcaaaagg aaggtgggca ttttcccaa agttttgtt gaagactgcg caactacaga  
1621 tttgaaaagc actcggagag aagtctagga tgtttcacia actacaaagc tgaagaaaat  
1681 gaagccctat tacttgtttg taagatttag cacccttctg ctgtatactg tactgagaca



1741 ttacag gaagtgttaa ctattttatt cctgttaaaa tt ctac tagacaatga  
1801 tgtgagtaac caggatgatt tcctggggca cagtgggtga gga tgggg acaggtgaat  
1861 ggaggagtta ggggagagga aaagtggatg gaagtgtctg gaaagggcac gagagagtct  
1921 tccaggtact gatcctgttt cttgctctga gtgctagcta gccagctgtg ttcacactgt  
1981 aaacattcat caagctgtac atttggtgca cttttctgtg tcataccaca ataaaaaaaa  
2041 acctatcatc atcttacaaa aacaagacac ccaagtcacg gcccaaggag taagtacaaa  
2101 tattcctgtt tctgaacat tactgtaatt ggctcttaag gcttgaagta accttatagg  
2161 ttactcataa ggcataata aataaacttg tttgttttct tttttc

## (2) INFORMATION FOR SEQ ID NO:137:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

1 gcagagctgg gcaccacagg gagctaggct ctgtgagccg tggctcatct cacacctcct  
61 cactgccttg catcatggcc atgtctggac ctttctctcc tcaggccttt accagaagca  
121 ttaaccgaga caagcacttg gcagtggctt acttccaacg agggatgctc tactaccaga  
181 cagagaagta agtggttcaa tgttgacca actggaggat ttcagagaga aacccaaggg  
241 gtctcaagtgt tgcgggcttg gtgtttgagc agt

## (2) INFORMATION FOR SEQ ID NO:138:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

1 ggtcagaagg aactgaaagg cttcttgtcc cagtgaagata gctggggaag ggagaagcag  
61 actcacattt tatgttgcatt ttatttctcc atccactaga ctgetgattt tctcctctg  
121 tcttgagat atgatttggc tatcaaagac cttaaagaag cttgattca gcttcgaggg  
181 aaccagctga tagactataa gatcctgggg ctccagtcca agctgtttgc ctgtgaggt  
241 aggagaacag gcctggctg gcaggagggg gatcatggct ggatggatgg ctgacagtca  
301 gatgcacagt gatctgttga cacctccagg agcttgaaa agccatttct cctctgcctt  
361 gagactcaga ttttcttga agaaaagact gagatggatt atttcaggct catcaaggca

## (2) INFORMATION FOR SEQ ID NO:139:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

1 ttccttgcca ccttgatttg gagtagtctc aagttttatg tttgcgtct gtacttttct  
61 aggtgttata taacattgct ttcattgtat ccaagaagga ggaatggaaa aaagctgaag  
121 aacagtttagc attggccacg agcatgaagt ctgagcccag acattccaaa atcgacaagg  
181 cgatggagtg tgtctgggta agcgtatttg tgatgcaggt gttgagagga tgtcactgga  
241 ttctcatttg ttcagagga catgccattg agaagccata aaagtgggtc ttttactttc  
301 tgtgagtctg ggtaacactg atcttagggg atagttccac ttaagatctt gaatctgtgc  
361 tgagaagctg aggcctagag tatgggatgg cagagcctgg catcacacca cccttgaggt  
421 ggggctcctt ggcaatgcag gagaacagga tattggatgc tggagcagtg ctgcacagac  
481 tctaagcact gagagggcag agtccatgtc tgcctgatca ccactgagtc ctcacagcct  
541 ggcacagtgc taggccacat aacagctctc agcaaaaatg ttttgttttg ttttgagatg  
601 gagtctcgtc ctgttgccca gcctggagtg cagtgggtgt atctcagctc actgcagcct  
661 ctgcctcctg ggttcaagca attctgctgc ctcagccgcc caagtagctg ggattacagg  
721 tgcatgccac catgcctggc taatttttgt atttttaata gagacggggg tttgccatgt

## (2) INFORMATION FOR SEQ ID NO:140:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

1 gaattcttgc atctattcac tgagggaggc aggacaagca tcgtcacccc cattttcaca  
61 taaggggaatg ctacgttttc tgtgttacag aagcagaagc tatatgagcc agtgggtgatc  
121 cctgtgggca agctgtttcg accaaatgag agacaagtgg ctgagctggc caagaaggat  
181 tacctaggca aggcagcggg aggtggggatt gctcagcttc ccctgagtct tcctgtggcc  
241 cgggcatgtg gagcaagggt ggagggactc ttgagaag

## (2) INFORMATION FOR SEQ ID NO:141:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

```
1 gcaggagaat cacttgaacc tggaaggcag aggttgagc gagctgagtc actccactgc
61 actccagtct gggtaacaga gcggtgctcg tctcaaaaaa aaaaaaaaaa aaaaagataa
121 tttgatgtta tacaaattgc acctcaatta aaaacatttc tttttaaga gagaagaaag
181 caagcctgtg ttagcagggg tgggtggaat gctcgtttct tcagttgctg aaatcctaata
241 ccagaggctc aggaatctaa tccttagtta ctgtccacgt ctgaaaccag gctcacgtaa
301 gaacaggtct agggcatgag caaagaggga gaccagaag aatggaaaca gtgctggcag
361 agcctcacac cctcctgtcc ttgattttag gtcgtggcat ctgtggtgga tcaagacagt
421 ttctctgggt ttgcccctct gcaaccacag gtaaggcagt cctgaccttc tccatggacc
481 taggtctcga gagctttctg tgaagcattc aattcgagag actatgtgtg ctgagttgcc
541 tgattgtaag ggctccttca agtggccctc agtgcagctg aggattctgc ctgccctctc
601 tcagtcctgg tttccatggc tggtaggaa ataaggcagt gtcaggcttc accccaagtc
661 ctctgaagct aactctcctg cttccccaca aatgccggtc ttcac
```

## (2) INFORMATION FOR SEQ ID NO:142:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

```
1 actgaattgc tgtgctagt aaacctgtac ctgggagctg gtgggaggtg ttatttccca
61 gtgttttagtc agggtgactg tgccctcttc ctagacagtg ttctcatcag tcagaatgc
121 gttatttgat tttctgtctt ggaagaatgc tcaaattacc attagccgtt tgtgtctct
181 cccctgcttt cctcattgc cttttccgtt ttcacttctc ctgaatgttc aataggcagc
241 tgagcctcca cccagaccga aaacccaga gatcttcagg taagttagat tcaaatccat
301 aaatagaata tcaagcgcca agcctgagct gatggcaaga aaggagggga agaagatgaa
361 ggtgggggtca gggcttaaat cttgttgaat tttctggaat gtcaggcttc ttctagaatg
421 tcaggctaga aaggaatgcc tagaagaatg tcttctagaa tgtcaggcta gaaaggaatg
481 atatatgggg atgggagctt tgactgtggt ggggctggcc atcagggttc ggctgcagct
541 acgtggtcca ttggccctct gtccacgtgc acagccacca catgcagggg ttgtgctgag
601 ggcagtgtgt cctgtggaac atagctacct gggaccagat gctgacctca ggttgagat
661 cggtttcgca ctggctgcag tctctgacg gggcaggcca gagctctct
```

## (2) INFORMATION FOR SEQ ID NO:143:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

```
1 tgagcagtg acaccagttt cttgctgaga cctcttgac ccaggcaggc tcagtgtcat
61 ctggcagtt gcagttagat gtggagttag agccaggctg agccaagtcc ctggctccaa
121 gttcagtgta tttgcgccat ggcacatgtg gaggggatgg gggctggatc ttgtgtctat
181 cctctgcagg gctctggaag gggaggctca ccgtgtgcta tttgggttg tgctgagac
241 aaaagaagag ctccaggtca tgccaggga cattgtcttt gtctgaaga agggcaatga
301 taactgggcc acggtcatgt tcaacgggca ggtatgcaga ggtcagggg ctggtgcgat
361 gggcatggga tcctggcagc aaatgcagtc tctgtggagc agtatctgct gccttctttg
421 cagaccagcc aagttctttt gtctgttcgt catcccttcc ccaggactct gggctgttct
481 gtggtgtggg tactgatgag cacatcttta tttttcctt tctgattctg ttgtgctgca
541 ctgcagaagg ggcttgttcc ctgcaactac cttgaaccag ttgagctgcy gatccacct
601 cagcagcagc cccaggtaat gtgatgccaa ggcctgacct atttctctc accctttagg
661 atctctccct ggaggagaaa aagcagtgta aaagaggtgt tgtcaggacc cctggagaaa
721 gattcactag tcttgagccc gccttgagat ggcaccagct acccagagct gaacctggga
781 atgaggggaa aaaagcccag atgtgctaag ttggaggcat ctgtaggtcc cattggccca
841 cccacctct
```

## (2) INFORMATION FOR SEQ ID NO:144:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

```
1 aatgtcacta ccattccaac ttttaggacg ttatctgcat gtggctcctt tacatggggg
61 ctctgtaggg gtgtttcccc acatccacct ctgctgggga actttgaatg aaggttctga
121 ccacgtctcc ctgttgctt caggaggaaa gctctccgca gtccgacatc ccagctctc
```

181 ctagt agccccctgga agaccccagc tgtcaccagg tggtcc tggagccaca  
241 gcctaggttt ggggtgcagca gcatgccagg tggtcctgag ttccttccc tgccttcag  
301 gaaattct

## (2) INFORMATION FOR SEQ ID NO:145:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

1 gactgagttt gttcatgtgt tcatgacctt catgcttccc cagggcgaga tttcccaca  
61 gtttactaag gttaataatt gccccacaaa ttaaagggtg agagggttggg ggccttattt  
121 gaagaggttt catctgtgtg tggcaggggc tggccaagga tgttcattca ccattcttct  
181 ttgttttact ccctactttt tccattcagg ccagaaaaca aaagaagagc ctaaggtaac  
241 atttttccct catactgttt caagtggtag aagatgggat agcttgggct atcaaccaca  
301 gacatgtctg tctggattat aggaagagcc caaaggaggg tcgaaccagt tgctacctta  
361 cagagtccat gagctagggg cttctttaat agcctcctcc actatcatgc acacacttcc  
421 tactacccaa gctagtgggc cagatcttac tcagtaggaa ttc

## (2) INFORMATION FOR SEQ ID NO:146:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 784 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

1 gaattcctgt ccaagcaagg gttgggctaa aggacctctg aaggcctttt aggctactgt  
61 gaaaccagtt acttactggc ctctcccctg ctgtattggg taccctctgt gccaaatcac  
121 gaaactgagg tgatccagga tgttgagaga aagcctcaga cactcaggag ttccctttgt  
181 ttcctcccca ctccaggaagt gaagctcagt gtcccatgc cctacacact caaggtgcac  
241 tacaagtaca cggtagtcac gaagactcag ccggggctcc cctacagcca ggtccgggac  
301 atggtgtcta agaaactgga gctccggctg gaacacacta agctgagggt agctccatgc  
361 aggcagctgt gaggggtaca gtgggaacct tgtgctggcc tggaggaggg aagaggagga  
421 tggtttttgt gatgatgttc tttgactgga ttcttactca ttatcccccac ccagctatcg  
481 gcctcgggac agcaatgagc tggtgcccct ttcagaagac agcatgaagg atgcctgggg  
541 ccaggtgaaa aactactgcc tgactctgtg gtgtgagaac acagtgggtg gtgcaatgag  
601 gggcatctaa agttacattt ccactgagcc acttccctcaa caatttgaaa tttatcaagc  
661 accttctgtg tactaggcac tatatgtggt gttggggata tgggtgtgaa taagtccacag  
721 ctctgcctcc cttttacctg catcctcacc ccatttgag cagggagaga gtttcccaca  
781 agag

## (2) INFORMATION FOR SEQ ID NO:147:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

1 ttcataaaga gcatataagc tctacacaag gcactgatca caaactttat gagtttatat  
61 ccaggtttct actttgacat ttcgctgttt cctttagtga tgttcagtgt tcaactggca  
121 ggaaattggg aaaattaaca ggcctttat tatttcaggg tgaccaaggc tttccagatg  
181 aacccaagga aagtgaaaaa gctgatgcta ataaccagac aacagaactc cagcttaaga  
241 aaggcagcca agtgaggcca ctcttcagtt atgaggctac ccaaccagag gacctggagt  
301 ttcaggaagg ggatataatc ctggtgttat caaagggtaa gtgctactcc aagactatag  
361 aaacaaattt acatgttagc agaaacaagg tcaagggcag agagaagaaa tatcaataat  
421 ctacaaacaa aactttagcc agtgttttca

## (2) INFORMATION FOR SEQ ID NO:148:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1145 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

1 gtcaattctt gaccctcttc tctatctggt aactttttga aaacataat ttatcctctc  
61 ttcattttgc tcattatcat gtttaagaca gatcaataag atgggttaaac cctgtgttca  
121 ctctcaaac accctttgcaat actgtctttt ccctgttgat cacaattagg ggtgggggag  
181 ggtgaccgat aacaaattct gtgtggaata gccagacagg gtaatcttcc tacagtgggt  
241 ttagaaatcc atgtgtactt ttccttttat cagtgaatga agaattggctg gaaggggagt  
301 gcaaagggaa ggtgggcatt tccccaaag ttttgttga agactgcgca actacagatt

361 tggagacac tcggagagaa gtctaggatg tttcacaaac tacaaagctg aagaaaatga  
421 agccctatta cttgtttgta agatttagca cccttctgct gtatactgta ctgagacatt  
481 acagtttggga agtggttaact atttattccc tgttaaaatt taacctacta gacaatgatg  
541 tgagtaccca ggatgatttc ctggggcaca gtgggtgagg agatggggac aggtgaatgg  
601 aggagttagg ggagaggaaa agtggtatgga agtgctgga aagggcacga gagagtcttc  
661 caggtactga tcctgtttct tgctctgagt gctagctagc cagctgtgtt cacactgtaa  
721 acattcatca agctgtacat ttggtgcaact tttctgtgtc ataccacaat aaaaaaaaaac  
781 ctatcatctt acaaaaacaa gacacccaag tccaggccca aggagtaagt acaaatattc  
841 ctgtttctga accattactg taattggctc ttaaggcttg aagtaacctt ataggttact  
901 cataaggcat atacaaataa acttgtttgt tttctttttt cattatgtct tgttgcttaa  
961 acagaaccta gactgagtta ggttctcatg gactacaaca ctcaattcca cagagaatta  
1021 atagaattac ataccttgtt acattctcag agaggaacat gtgttaagaa ctcaatactg  
1081 aatatatc aatcgccaac atttaagtga tgaaaagcag cggtgttcat gaagctagtt  
1141 cgtaa

## (2) INFORMATION FOR SEQ ID NO:149:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

1 gtcacatcgc cctgtctggc tttgagaagc gcttcgtacc cagccagcac tatgtgtaca  
61 tgttcttggt gaaat

## (2) INFORMATION FOR SEQ ID NO:150:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

1 ctagtctttc agccttcagg ctgtttttgg cttgaagctc tcttggcctc ctagtcttcta  
61 cctaatacatg tccctgggtg aggccatcag cctctggaat gaaggggtgc tggcagcgga  
121 caagaaggac tggaaggag ccttgatgc cttcagtgc gtccaggacc cccactcccg  
181 gatttgcttc aacattggct gcatgtacac tatcctgaag aacatgactg aagcagagaa  
241 ggcttttacc agaagcatta accgagacaa gcaactggca gtggcttact tccaacgagg  
301 gatgctctac taccagacag agaaatatga tttggctatc aaagacctta aagaagcctt  
361 gattcagctt cgagggaaac agctgataga ctataagatc ctggggctcc agttcaagct  
421 gtttgctgt gaggtgttat ataaccattgc tttcatgtat gccaagaagg aggaatggaa  
481 aaaaagctgaa gaacagttag cattggccac gagcatgaag tctgagccca gacattccaa  
541 aatcgacaag gcatgaggt gtgtctggaa gcagaagcta tatgagccag tgggtgatccc  
601 tgtgggcaag ctgtttcgac caaatgagag acaagtggct cagctggcca agaaggatta  
661 cctaggcaag gcatcggtcg tggcatctgt ggtggatcaa gacagtttct ctgggtttgc  
721 ccctctgcaa ccacaggcag ctgagcctcc acccagaccg aaaaccccag agatcttcag  
781 ggctctggaa ggggaggctc accgtgtgct atttgggttt gtgcctgaga caaaagaaga  
841 gctccaggte atgccaggga acattgtctt tgtcttgaag aagggcaatg ataactgggc  
901 cacggtcatg ttcaacgggc agaaggggct tgttccctgc aactaccttg aaccagttga  
961 gttgcggtac caccctcagc agcagcccca ggaggaaagc tctccgcagt ccgacatccc  
1021 agctcctcct agttccaaag cccctggaaa accccagctg tcaccaggcc agaaacaaaa  
1081 agaagagcct aaggaagtga agctcagttg tcccatgccc tacacactca aggtgacata  
1141 caagtacacg gtatgcatga agactcagcc cgggctcccc tacagccagg tccgggacat  
1201 ggtgtctaa aaactggagc tccggctgga acacactaag ctgagctatc ggctcggga  
1261 cagcaatgag ctggtgcccc tttcagaaga cagcatgaag gatgcctggg gccaggtgaa  
1321 aaactactgc ctgactctgt ggtgtgagaa cacagtgggt gaccaaggct ttccagatga  
1381 acccaaggaa agtgaaaaag ctgatgctaa taaccagaca acagaacctc agcttaagaa  
1441 aggcagccaa gtggaggcac tcttcagtta tgaggctacc caaccagagg acctggagtt  
1501 tcaggaaggg gatataatcc tgggtgtatc aaaggtgaat gaagaatggc tgggaaggga  
1561 gtgcaaggg aaggtgggca ttttcccaa agttttgtt gaagactgag caactacaga  
1621 tttggaaagc actcggagag aagtctagga tgtttcaca actacaaagc tgaagaaaat  
1681 gaagccctat tacttgtttg taagatttag caccctctg ctgtatactg tactgagaca  
1741 ttacagtttg gaagtgttaa ctatttatt cctgttaaaa ttaacctac tagacaatga  
1801 tgtgagtacc caggatgatt tcctggggca cagtgggtga ggagatggg acaggtgaat  
1861 ggaggagtta ggggagagga aaagtggatg gaagtgtctg gaaagggcac gagagagtct  
1921 tccaggtact gatcctgttt cttgctctga gtgctagcta gccagctgtg ttcacactgt  
1981 aaacattcat caagctgtac atttgggtga cttttctgtg tcataaccaca ataaaaaaaa  
2041 acctatcatc atcttaca aaacaagac ccaagtccag gcccaaggag taagtacaaa  
2101 tattcctgtt tctgaacct tactgttaatt ggctcttaag gcttgaagta accttatagg  
2161 ttactcataa ggcataata aataaacttg tttgttttct tttttc  
1 ctagtctttc agccttcagg ctgtttttgg cttgaagctc tcttggcctc ctagtcttcta  
61 cctaatacatg tccctgggtg aggccatcag cctctggaat gaaggggtgc tggcagcgga  
121 caagaaggac tggaaggag ccttgatgc cttcagtgc gtccaggacc cccactcccg  
181 gatttgcttc aacattggct gcatgtacac tatcctgaag aacatgactg aagcagagaa

241 ggcctt agaagcatta accgagacaa gcacttggca gtttact tccaacgag  
301 gatgctctac taccagacag agaaatatga tttggctatc aaacacctta aagaagcctt  
361 gattcagctt cgagggaacc agctgataga ctataagatc ctggggctcc agttcaagct  
421 gtttgctgt gaggtgttat ataacattgc tttcatgtat gccaaagagg aggaatggaa  
481 aaaagctgaa gaacagttag cattggccac gagcatgaag tctgagccca gacattccaa  
541 aatcgacaag gcgatggaat gtgtctggaa gcagaagcta tatgagccag tgggtgatccc  
601 tgtgggcaag ctgtttcgac caaatgagag acaagtggct cagctggcca agaaggatta  
661 cctaggcaag gcgacggtcg tggcatctgt ggtggatcaa gacagtttct ctgggtttgc  
721 ccctctgcaa ccacaggcag ctgagcctcc acccagaccg aaaaccccag agatcttcag  
781 ggctctggaa ggggaggctc accgtgtgct atttgggttt gtgcttgaga caaaagaaga  
841 gctccaggtc atgccaggga acattgtctt tgtcttgaag aagggcaatg ataactggg  
901 caggttcagt ttcaacgggc agaaggggct tgttccctgc aactaccttg aaccagttga  
961 gttgcgatc caccctcagc agcagcccca ggaggaaagc tctccgcagt ccgacatccc  
1021 agctcctcct agttccaaag cccctggaaa acccagctg tcaccaggcc agaaacaaaa  
1081 agaagagcct aaggaagtga agctcagtg tcccatgccc tacacactca aggtgacta  
1141 caagtacacg gtagtcatga agactcagcc cgggctcccc tacagccagg tccgggacat  
1201 ggtgtctaag aaactggagc tccggctgga acacactaag ctgagctatc ggcctcggga  
1261 cagcaatgag ctggtgcccc ttccagaaga cagcatgaag gatgctggg gccagggtga  
1321 aaactactgc ctgactctgt ggtgtgagaa caagtggtg gaccaaggct ttccagatga  
1381 acccaaggaa agtgaaaaag ctgatgctaa taaccagaca acagaacctc agcttaagaa  
1441 aggcagccaa gtggaggcac tcttcagtta tgaggctacc caaccagagg acctggagtt  
1501 tcaggaaggg gatataatcc tgggtgtatc aaaggtgaat gaagaatggc tgggaaggga  
1561 gtgcaaaggg aaggtgggca tttccccaa agtttttgtt gaagactgag caactacaga  
1621 tttggaaaagc actcggagag aagtctagga tgtttcaca actacaaagc tgaagaaaat  
1681 gaagccctat tacttgtttg taagatttag cacccttctg ctgtatactg tactgagaca  
1741 ttacagtttg gaagtgttaa ctatttattc cctgttaaaa tttaacctac tagacaatga  
1801 tgtgagtacc caggatgatt tcctggggca cagtgggtga ggagatggg acaggtgaat  
1861 ggaggagttt ggggagagga aaagtggatg gaagtgtctg gaaagggcac gagagagtct  
1921 tccaggtact gatcctgttt ctgtctctga gtgctagcta gccagctgtg ttcacactgt  
1981 aaacattcat caagctgtac atttggtgca cttttctgtg tcataccaca ataaaaaaa  
2041 acctatcatc atcttcaaaa aacaagacac ccaagtccag gccaaggag taagtacaaa  
2101 tattcctgtt tctgaaccat tactgtaatt ggctcttaag gcttgaagta accttatag  
2161 ttactcataa ggcataata aataaacttg tttgttttct tttttc  
1 gcagagctgg gcaccacagg gagctaggct ctgtgagccg tggctcatct cacacctcct  
61 cactgccttg catcatggcc atgtctggac ccttctctcc tcaggccttt accagaagca  
121 ttaaccgaga caagcacttg gcagtggctt acttccaacg agggatgctc tactaccaga  
181 cagagaagta agtggttcaa tgttgacca actggaggat ttcagagaga aaccaaggg  
241 gtctcagtg tgcgggcttg gtgtttgagc agt  
1 ggtcagaagg aactgaaaag cttctgttc cagtgaata gctggggaag ggagaagcag  
61 actcacattt tatgtgcat ttatttctcc atccactaga ctgctgattt tctccctctg  
121 tcttgagat atgatttggc tatcaaagac cttaaagaag ccttgattca gcttcgaggg  
181 aaccagctga tagactataa gatcctgggg ctccagttca agctgtttgc ctgtgaggta  
241 aggagaacag ggcctggctg ggcaggaggg gatcatggct ggatggatgg ctgacagtca  
301 gatgcacagt gatctgttga cactccag agcttgaaa agccatttct cctctgcctt  
361 gagactcaga ttttccctga agaaaagact gagatggatt atttcaggct catcaaggca  
1 ttccttgcca ccttgatttg gagtagctc aagttttatg tttgcggtct gtacttttct  
61 aggtgttata taacattgct ttcatgtatg ccaagaagga ggaatggaaa aaagctgaag  
121 aacagttagc attggccacg agcatgaagt ctgagcccag acattccaaa atcgacaagg  
181 cgatggagtg tgtctgggta agcgtatttg tgatgcagg gttgagagta tgtcactgga  
241 ttctcatttg tctcagagga catgccattg agaagccata aaagtgggag ttttactttc  
301 tgtgagtctg ggtaacactg atcttagggg atagttccac ttaagatctt gaatctgtgc  
361 tgagaagctg aggcctagag tatgggatgg cagagcctgg catcacacca cccttgaggt  
421 ggggctcctt ggcaatgcag gagaacagga tattggatgc tggagcagtg ctgcacagac  
481 tctaagcact gagagggcag agtccatgct tgcttgatca ccactgagtc ctacagcct  
541 ggcacagtgc taggccacat aacagctctc agcaaaaatg ttttgttttg ttttgagatg  
601 gagtctcgct ctgttgccca gcctggagtg cagtgggtgt atctcagctc actgcagcct  
661 ctgctcctg ggttcaagca attctgctgc ctgagccgcc caagtagctg ggattacagg  
721 tgcagtcac catgcctggc taatttttgt atttttaata gagacggggg tttgccatgt  
1 gaattcttg atctattcac tgagggagc aggacaagca tcgtcaccct cattttcaca  
61 taagggaatg ctacgtttt tgtgttacag aagcagaagc tatatgagcc agtgggtgac  
121 cctgtgggca agctgtttcg accaaatgag agacaagtgg ctgagctggc caagaaggat  
181 tacctaggca aggcgacggt aggtgggatt gctcagcttc ccctgagctc tctgtggcc  
241 cgggcatgtg gagcaagggt ggagggactc ttgagaag  
1 gcaggagaat cacttgaacc tggaggcag aggttgagc gagctgagtc actccactgc  
61 actccagctt gggtaacaga gcgtgctccg tctcaaaaaa aaaaaaaa aaaaagataa  
121 tttgatgtta taaaaattgc acctcaatta aaaacatttc ttttttaaga gagaagaaag  
181 caagcctgtg ttagcagggg tgggtgaaat gctcgtttct tcagttgctg aaatccta  
241 ccagaggctc aggaatctaa tcttagtta ctgtccacgt ctgaaaccag gctcacgtaa  
301 gaacaggtct agggcatgag caaagaggga gaccagaag aatggaaaca gtgctggcag  
361 agcctcacac cctcctgtcc ttgattttag gtcgtggcat ctgtgggtgga tcaagacagt  
421 ttctctgggt ttgccccttc gcaaccacag gtaaggcagt cctgaccttc tccatggacc  
481 taggtctcga gagctttctg tgaagcattc aattcgagag actatgtgtg ctgagttgcc  
541 tgattgtaa ggtccttca agtggccctc agtgcagctg aggattctgc ctgcccctc  
601 tcagtcctgg tttccatggc tggtaggaa ataaggcagt gtcaggcttc accccaagtc  
661 ctctgaagct aactctcctg cttccccaca aatgccggtc ttcac

1 actgaattgc ttagtg aaacctgtac ctgggagctg gtgggaggtg ttatttccca  
61 gtgttttagtc agggtagctg tgcctctctc ctgacacagt ttctcatcag tcagaaatgc  
121 gttatttgat tttctggctc ggaagaatgc tcaaattacc attagccgtt tgtgtctct  
181 ccctgcttt ccctcattgc cttttccgtt ttcacttctc ctgaatgttc aataggcagc  
241 tgagcctcca cccagaccga aaaccccaaga gatcttcagg taagttagat tcaaattccat  
301 aaatagaata tcaagcgcca agcctgagct gatggcaaga aagggagga agaagatgaa  
361 ggtgggttca ggggtctaaat cttgttgaat tttctggaat gtcaggcttc tctagaatg  
421 tcaggctaga aaggaatgcc tagaagaatg tcttctagaa tgtcaggcta gaaaggaatg  
481 atatatggg atgggagctt tgactgtggt ggggctggcc atcagggtt ggctgcagct  
541 acgtgggtcca ttggcctctc gtccacgtgc acagccacca catgcagggt ttgtgctgag  
601 ggcatgtgt cctgtggaac atagctacct gggaccagat gctgacctca ggttgagat  
661 cggtttcgca ctggctgcag tctctgacg gggcaggcca gagctctc  
1 tgagcagtg acaccagtt cttgctgaga cctcttgac ccaggcaggc tcagtgtcat  
61 ctggcagtt gcagtttagat gtggagttag agccaggctg agccaagtc ctggtccaa  
121 gttcagtgta tttgcgccat ggcacatagt gaggggatgg gggctggatc ttgtgtctat  
181 cctctgcagg gctctggaag gggaggctca cctgtgcta tttgggttg tgcctgagac  
241 aaagaagag ctccaggtca tgccaggga cattgtctt gtctgaaga agggcaatga  
301 taactgggccc acggtcatgt tcaacgggca ggtatgcaga ggatcagggt ctggtgcgat  
361 gggcatggga tctgtgcagc aaatgcagtc tctgtggagc agtatctgct gcctctttg  
421 cagaccagcc aagttctttt gtctgtctgt catccttcc ccaggactct gggctgttct  
481 gtggtgtggg tactgatgag cacatcttta tttttcctt tctgattctg tgggtctgca  
541 ctgcagaagg ggcttgttcc ctgcaactac cttgaaccag ttgagctcg gatccacct  
601 cagcagcagc cccaggtaat gtgatgccaa ggcctgaccc atttctctc acccttagg  
661 atctctccct ggaggagaa aagcagtgta aaagaggtg tgtcaggacc cctggagaaa  
721 gattcactag tcttgagccc gccttgagat ggcaccagct acccagagct gaacctggga  
781 atgaggggaa aaaagcccag atgtgctaa ttggaggcat ctgtaggctc cattggccca  
841 ccacctct  
1 aatgtcacta ccattccaac ttttaggacg ttatctgcat gtggctcctt tacatgggt  
61 ctctgtagg gtgtttccc acatccacc ctgcctggga actttgaatg aaggttctga  
121 ccacgtctcc ctgttgctt caggaggaaa gctctccga gtcagacatc ccagctcctc  
181 ctagtccaa agcccttga agacccagc tgtcaccagg tgagtgttc tggagccaca  
241 gctaggttt ggggtgcagc gcagtcagg tgttctgag ttcctctccc tgcttccag  
301 gaaattct  
1 gactgagttt gttcatgtg tcatgacct catgcttccc cagggcgaga tttcccaca  
61 gttactaag gtttaataatt gccccacaaa ttaaagggtg agaggttggg ggcctattt  
121 gaagaggtt catctgtgtg tggcaggggc tggccaagga tgttcattca ccactcttct  
181 ttgtttact cctactttt tccattcagg ccagaaacaa aaagaagagc caaggtaac  
241 atttttccct catactgtt caagtgttag aagatgggat agcttgggt atcaaccaca  
301 gacatgtctg tctggattat aggaagagcc caaaggagg tgaaccagt tgcactta  
361 cagagtccat gagctaggga ccttcttaat agcctcctc actatcatgc acacacttcc  
421 tactaccaa gctagtggc cagatcttac tcagtaggaa ttc  
1 gaattcctg ccaagcaagg gttgggctaa aggcctctg aaggccttt aggtactgt  
61 gaaaccagtt acttactggc ctctccctg ctgtattggg taccctgt gccaatcac  
121 gaaactgagg tgatccagga tgttgagaga aagcctcaga cactcaggag ttcctttgt  
181 ttctcccca ctccaggaagt gaagctcagt gttcccatgc cctacacact caaggtgcac  
241 tacaagtaca cggtagtcat gaagactcag cccgggctcc cctacagcca ggtccgggac  
301 atggtgtcta agaaactgga gctccggctg gaacacacta agctgaggtg agtccatgc  
361 aggcagctgt gagggtgaca tgggaaacct tgtgtggcc tggaggagg aagagaggga  
421 tggttttgt gatgatgtt tttgactgga ttcttactca ttatccccc ccagctatcg  
481 gcctcgggac agcaatgagc tgggtcccct ttcagaagac agcatgaagg atgctgggg  
541 ccaggtgaaa aactactgcc tgactctgtg gtgtgagaac acagtgtgta gtgcaatgag  
601 gggcatctaa agttacattt ccaactgagc acttctcaa caatttgaa tttatcaagc  
661 accctctgtg tactaggcac tatatgtgtt gttggggata tgggtgttaa taagtacag  
721 ctctgcctcc cttttacctg catcctcacc ccatttgag caggagaga gtttccaca  
781 agag  
1 ttcatataaga gcatataagc tctacacaag gcactgatca caaactttat gagtttatat  
61 ccaggttct actttgacat ttcgtgttt ctttagtga tgttcagtg tcacttgga  
121 gaaattggg aaaattaca ggcctttat ttttcagg tgaccaagg tttccagatg  
181 aaccaagga agtgaaaaa gctgatgcta ataaccagac aacagaacct cagcttaaga  
241 aaggcagcca agtgaggga ctcttcagt atgaggctac ccaaccagag gacgtggagt  
301 ttcaggaagg ggatataatc ctggtgttat caaagggtaa gtgctactcc aagactatag  
361 aaacaaattt acatgttagc agaaacaagg tcaagggcag agagaagaaa tatcaataat  
421 ctacaaaca aactttagc agtgtttca  
1 gtcaattctt gaccctctc tctatctgt aacttttga aaaacataat ttatctctc  
61 ttcattttg tcattatcat gtttaagaca gatcaataag atggttaaac cctgtgttca  
121 ctctcaaac actttgcaat actgtcttt cctgttgat cacaattagg ggtggggaag  
181 ggtgaccgat aacaaattct gtgtggaata gccagacagg gtaatcttc tacagtgggt  
241 ttgaaatcc atgtgtactt ttcttttat cagtgaatga agaaggtcg gaaggggagt  
301 tcagaaaggaa ggtgggcatt tccccaaag tttttgtga agactgcga actacagatt  
361 tggaaagcac tgggagagaa gtctaggatg tttcacaac tacaagctg aagaaaatga  
421 agccctatta cttgtttgta agatttagca ccttctgct gtatactgta ctgagacatt  
481 acagtgttga agtgtaact atttattccc tgttaaaatt taacctacta gacaatgatg  
541 tgagtaccca ggatgatttc ctggggcaca gtgggtgagg agatggggac aggtgaatgg  
601 aggagttagg ggagaggaaa agtgatgga agtgtctgga aagggcagga gagagtctc  
661 caggtactga tctgtttct tgcctgagt gctagctagc cagctgtgtt cacactgtaa

721 acattt a agctgtacat ttggtgcact tttctgtgtc a acaat aaaaaaaaaac  
781 ctatcatctt acaaaaaacaa gacaccaag tccaggccca agtaagt acaaatattc  
841 ctgtttctga accattactg taattggctc ttaaggcttg aagtaacctt ataggttact  
901 cataaggcat atacaaataa acttgtttgt tttctttttt cattatgtct tgttgcttaa  
961 acagaacctt gactgagtta ggttctcatg gactacaaca ctcaattcca cagagaatta  
1021 atagaattac atacctttgt acattctcag agaggaacat gtgtaagaa ctcaatactg  
1081 aatatatac aatcgccaac atttaagtga tgaaaagcag cggtgttcat gaagctagtt  
1141 cgtaa

1 gtcacatcgc cctgtctggc tttgagaagc gcttcgtacc cagccagcac tatgtgtaca  
61 tgttctgtgt gaaat

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1064 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

1 ccagctgata ttccagccca cagcaatgga gccacatgac tctcccaca tggactctga  
61 gtccgatac actctcttcc cgattgttta cagcatcatc tttgtgtctg gggctattgc  
121 taatggctac gtgctgtggg tctttgccg cctgtaccct tgcaagaaat tcaatgagat  
181 aaagatcttc atggtgaacc tcaccatggc ggacatgctc ttcttgatca ccttgccact  
241 ttggattgtc tactacaaaa accagggcaa ctggatactc cccaaattcc tgtgcaacgt  
301 ggctggctgc cttttcttca tcaacacctt ctgctctgtg gccttcctgg gcgtcatcac  
361 ttataaccgc ttccaggcag taactcgccc catcaagact gtcaggcca acaccgcaa  
421 gcgtggcatc tctttgtcct tggctcatctg ggtggccatt gtgggagctg catcctactt  
481 cctcatcctg gactctacca acacagtgcg cgacagtgtt ggctcaggca acgtcactcg  
541 ctgctttgag cattacgaga agggcagcgt gccagtctc atcatccaca tcttcatcgt  
601 gtccagcttc ttctgtgtct tctcatcat cctcttctgc aacctgggta tcatccgtac  
661 ctgtctcatg cagccggtgc agcagcagcg caacgctgaa gtcaagcgcc gggcgctgtg  
721 gatggtgtgc acggtcttgg cgggtgtcat catctgtctc gtgcccacc acgtggtgca  
781 gctgccctgg acccttgctg agctgggctt ccaggacagc aaattccacc aggccattaa  
841 tgatgcacat caggtcaccc tctgcctcct tagcaccaac tgtgtcttag accctgttat  
901 ctactgtttc ctcaccaaga agttccgcaa gcacctcacc gaaaagttct acagcatgcg  
961 cagtagccgg aaatgtctcc gggccaccac ggatacggtc actgaagtgg ttgtgccatt  
1021 caaccagatc cctggcaatt ccctcaaaaa ttagtccttg cttc

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

1 ttcacgaggg ctggggccag gacccagaca gagacacacg gtcactgcag ctgaagccgc  
61 tgcccctgct acaggcacca ccaggaccag ctgacattc cagcccacag caatggagcc  
121 acatgactcc tcccacatgg actctgagtt ccgatacact ctcttcccga ttgtttacag  
181 catcatcttt gtgctcgggg tcatgtctaa tggctacgtg ctgtgggtct ttgccgcct  
241 gtacccttgc aagaaattca atgagataaa gatcttcatg gtgaacctca ccatggcgga  
301 catgctcttc ttgatcacc tgccactttg gattgtctac taccaaaacc agggcaactg  
361 gatactcccc aaattcctgt gcaacgtggc tggctgcctt ttcttcatca acacctactg  
421 ctctgtggcc ttctgtggcg tcatcactta taaccgcttc caggcagtaa ctcggccat  
481 caagactgct caggccaaca cccgcaagcg tggcatctct ttgtccttgg tcatctgggt  
541 ggccattgtg ggagctgcat cctacttctt catcctggac tccaccaaca cagtgccga  
601 cagtgtggc tcaggcaacg tcaactcgtg ctttgagcat tacgagaagg gcagcgtgcc  
661 agtctctatc atccacatct tcatcgtgtt cagcttcttc ctggtcttcc tcatcatctt  
721 cttctgaac ctggtcatca tccgtacctt gctcatgcag ccggtgcagc agcagcgcaa  
781 cgctgaagtc aagcgccggg cgctgtggat ggtgtgcacg gtcttggcgg ttcttcatc  
841 ctgcttctgt cccaccacg tgggtgcagct gccctggacc cttgtgtgag tgggcttcca  
901 ggacagcaaa ttccaccagg ccattaatga tgcacatcag gtcacctct gcctccttag  
961 caccaactgt gtcttagacc ctgttatcta ctgtttcctc accaagaagt tccgcaagca  
1021 cctcaccgaa aagttctaca gcatgcgcag tagccgaaa tgctcccgg ccaccacgga  
1081 tacggtcact gaagtgttg ttgccattcaa ccagatccct ggcaattccc tcaaaaatta  
1141 gtcccgtgct ccaggcctga agtcttcttc tccatgaaac atcatgactg agctggggga  
1201 agaagggata tctactgtgg gtctgggac cactctgtg gactgggtgg gccattagat  
1261 ttggaggcta cctcacctgg gcagggatga tgcagagcca ggctgttgg aaatccagaa  
1321 ctcaaatgag ccccttcatc cgctgtggg cgcatactac agtaactgtg actgatgact  
1381 ttatcctgag tcccttaatc ttatggggcc ggaaggatg tcagggccag gtgcagacct  
1441 tgggggaaga ctttaaacca cctagttctc ccactggggc atcggtctaa agcttgggg  
1501 gagtggcccc agtggctcac acctgtaac ccagcacttt gggaggccga ggtgggcaga  
1561 tcatgggtca agagatcgag acatcctggc caacattgta aaacccatc tctactaaaa  
1621 catacaaaaa ttagccgggc atggtgcaca cgctgtagt cccagctact caggaggctg  
1681 aggcaggaga atcgcttgaa cctgggaggg agaggttgca gtgaacctag attgcaccat

1741 tgcaatag cctggcaaca gaggcagatt cctcctgccc

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

```
1 cgggagcgg aggttgccgt gagctgagat cagccactg cactccagcc tgggcagcaa
61 gaggtaaact ccatctgaaa aaaaaaaaaa gattcaacat gaacttctga ggggacatca
121 tcattctaac catggcaagg agtcttgaaa ctgatgaaat ggaacagtc cttcttgctc
181 ctttattaac cagaattttt gtgtggtctt ccaggcacca ccaggaccag ctgatcattc
241 cagccacag caatggagcc acatgactcc tcccacatgg actctgagtt ccgatacact
301 ctcttcccga ttgtttacag catcatcttt gtgctcgggg tcattgctaa tggctacgtg
361 ctgtgggtct ttgcccgcct gtacccttgc aagaaattca atgagataaa gatcttcatg
421 gtgaacctca ccattggcga catgctcttc ttgatcacc tgccactttg gattgtctac
481 taccaaaacc agggcaactg gatactcccc aaattcctgt gcaacgtggc tggctgcctt
541 ttcttcatca acacctactg ctctgtggcc ttctggggcg tcatcactta taaccgcttc
601 caggcagtaa ctcgcccat caagactgct caggccaaca ccgcaagcg tggcatctct
661 ttgtccttgg tcatctgggt ggccattgtg ggagctgcat cctacttctc catcctggac
721 tccaccaaca cagtgccga cagtgtggc tcaggcaacg tcaactcgctg ctttgagcat
781 tacgagaagg gcagcgtgcc agtctcatc atccacatct tcatcgtgtt cagcttcttc
841 ctggtcttcc tcatcctctt ctctgcaac ctggtcatca tccgtacctt gctcatgcag
901 ccggtgcagc agcagcgcaa cgctgaagtc acaggccggg cgctgtggat ggtgtgcagc
961 gtcttgccgg ttgtcatcat ctgcttcgtg cccaccacag tgggtgcagct gccctggacc
1021 cttgctgagc tgggcttcca ggacagcaa ttccaccagg ccattaatga tgcacatcag
1081 gtacacctct gctccttag caccaactgt gtcttagacc ctgttatcta ctgtttctc
1141 accaagaagt tccgcaagca cctcaccgaa aagtctaca gcatgcgcag tagccggaaa
1201 tgctccggg ccaccacgga tacggtcact gaagtgggtg tgccattcaa ccagatccct
1261 ggcaattccc tcaaaaatta gtccctgctt ccaggcctga agtcttctcc tccatgaaca
1321 tcatggactg agctggggga agaaggata tctactgtgg tctgggcacc acctctgtgg
1381 gcaactgggt gccattagat ttggaggcta cctcacctgg gcagggatga tggcagacga
1441 ggctgttga aaatccagaa ctcaaat
```

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

```
1 ccagtgata ttccagccca cagcaatgga gccacatgac tctcccaca tggactctga
61 gtccgatac actctcttcc cgattgttta cagcatcatc tttgtgctcg gggctattgc
121 taatggctac gtgtgtggg tctttgccg cctgtaccct tgcaagaaat tcaatgagat
181 aaagatcttc atggtgaacc tcaccatggc ggacatgctc ttcttgatca ccttgccact
241 ttggattgtc tactaccaa accagggcaa ctggatactc cccaaattcc tgtgcaacgt
301 ggctggctgc cttttcttca tcaacaccta ctgctctgtg gccttcttgg gcgtcatcac
361 ttataaccgc ttccaggcag taactcggcc catcaagact gctcaggcca acaccgcaa
421 gcgtggcatc tctttgtcct tggtcactg ggtggccatt gtgggagctg catcctactt
481 cctcatcctg gactctacca acacagtgcc cgacagtgtc ggctcaggca acgtcactcg
541 ctgctttgag cattacgaga agggcagcgt gccagtcctc atcatccaca tcttcatcgt
601 gttcagcttc ttctggtct tctcatcat cctcttctgc aaactgggtc tcatccgtac
661 cttgctcatg cagccgtgc agcagcagcg caacgctgaa gtcaagcgcc gggcgctgtg
721 gatggtgtgc acggtcttgg cggtgttcat catctgcttc gtgccccacc acgtggtgca
781 gctgccctgg acccttctg agctgggctt ccaggacagc aaattccacc aggccattaa
841 tgatgcacat caggtcacc tctgctcct tagaccaac tgtgtcttag acctgttat
901 ctactgtttc tccaccaaga agttccgcaa gcacctcacc gaaaagttct acagcatgcg
961 cagtagccgg aaatgctccc gggccaccac ggatacggtc actgaagtgg ttgtgccatt
1021 caaccagatc cctggcaatt cctcaaaaa ttagtccttg cttc
1 ttcacgagg ctggggccag gaccagaca gagacacag gtcactgcag ctgaagccgc
61 tgcccctgct acaggcacca ccaggaccag ctgatcattc cagccacag caatggagcc
121 acatgactcc tcccacatgg actctgagtt ccgatacact ctcttcccga ttgtttacag
181 catcatcttt gtgctcgggg tcattgctaa tggctacgtg ctgtgggtct ttgcccgcct
241 gtacccttgc aagaaattca atgagataaa gatcttcatg gtgaacctca ccattggcga
301 catgctcttc ttgatcacc tgccactttg gattgtctac taccaaaacc agggcaactg
361 gatactcccc aaattcctgt gcaacgtggc tggctgcctt ttcttcatca acacctactg
421 ctctgtggcc ttctggggcg tcatcactta taaccgcttc caggcagtaa ctcgcccat
481 caagactgct caggccaaca ccgcaagcg tggcatctct ttgtccttgg tcatctgggt
541 ggccattgtg ggagctgcat cctacttctc catcctggac tccaccaaca cagtgccga
601 cagtgtgtgc tcaggcaacg tcaactcgctg ctttgagcat tacgagaagg gcagcgtgcc
661 agtctcatc atccacatct tcatcgtgtt cagcttcttc ctggtcttcc tcatcatctc
721 ctctgcaac ctggtcatca tccgtacctt gctcatgcag ccggtgcagc agcagcgcaa
```



781 cgctgaa aagcgccggg cgtgtggat ggtgtgcacg gtc cgg tgttcacat  
841 ctgcttcgtg cccaccacg tgggtgcagct gccctggacc cttg gacg tgggtttcca  
901 ggacagcaaa ttccaccagg ccattaatga tgcacatcag gtcaccctct gcctccttag  
961 caccaactgt gtcttagacc ctgttatcta ctgtttcctc accaagaagt tccgcaagca  
1021 cctcaccgaa aagttctaca gcatgcgcag tagccggaaa tgctcccggg ccaccacgga  
1081 tacggctact gaagtgggtg tgccattcaa ccagatccct ggcaattccc tcaaaaatta  
1141 gtccctgctt ccaggcctga agtcttctcc tccatgaaac atcatgactg agctggggga  
1201 agaagggata tctactgtgg gtctgggac caccctgtgt gcactgggtg gccattagat  
1261 ttggaggcta cctcacctgg gcagggatga tgcagagcca ggctgttgga aaatccagaa  
1321 ctcaaatgag ccccttcac cgctgtggg cgatactac agtaactgtg actgatgact  
1381 ttatcctgag tcccttaatc ttatggggcc ggaaggaatg tcagggccag gtgcagacct  
1441 tgggggaaga ctttaaacca cctagtcttc ccactggggc atcgggtctaa agctttgggg  
1501 gagtggcccc agtggctcac acctgtaatc ccagcacttt gggaggccga ggtgggcaga  
1561 tcatgggtca agagatcgag acatcctggc caacattgta aaaccccatc tctactaaaa  
1621 catacaaaaa ttagccgggc atggtgcaca cgctgtagt ccagctact caggaggctg  
1681 aggcaggaga atcgcttgaa cctgggaggc agagggtgca gtgaacctag attgcacat  
1741 tgcactctag cctggcaaca gaggcagatt cctcctgccc  
1 cgggaggcgg aggttgcgt gagctgagat cagccactg cactccagcc tgggcagcaa  
61 gagtgaact ccatctgaaa aaaaaaaa gattcaacat gaacttctga ggggacatca  
121 tcattctaac catggcaagg agtcttgaa ctgatgaaat ggaacagtcc cttctgtgcc  
181 ctttattaac cagaattttt gtgtgtctt ccaggcacca ccaggaccag ctgatcattc  
241 cagcccacag caatggagcc acatgactcc tcccacatgg actctgagtt ccgatacact  
301 ctcttccga ttgtttacag catcatcttt gtgctcgggg tcattgctaa tggctacgtg  
361 ctgtgggtct ttgccgcct gtacccttgc aagaaattca atgagataaa gatcttcag  
421 gtgaacctca ccatggcgga catgctcttc ttgatcacc tgccactttg gattgtctac  
481 taccaaaacc agggcaactg gatactcccc aaattcctgt gcaacgtggc tggctgcctt  
541 ttcttcatca acacactact ctctgtggcc ttcttggggc tcatcactta taaccgcttc  
601 caggcagtaa ctcgcccat caagactgct caggccaaca cccgcaagcg tggcatctct  
661 ttgtccttgg tcatctgggt ggccattgtg ggagctgcat cctacttct catcctggac  
721 tccaccaaca cagtgcgga cagtgtggc tcaggcaacg tcatcgctg ctttgagcat  
781 tacgagaagg gcagcgtgcc agtctcctc atccacatct tcatcggtt cagcttcttc  
841 ctggtcttcc tcatcatcct cttctgcaac ctggtcatca tccgtacct gctcatgcag  
901 ccggtgcagc agcagcgcaa cgctgaagtc acaggccggg cgctgtggat ggtgtgcag  
961 gtcttggcgg tgttcacat ctgcttcgtg cccaccacg tgggtgcagct gcctggacc  
1021 cttgctgagc tgggcttcca ggacagcaaa ttccaccagg ccattaatga tgcacatcag  
1081 gtcaccctct gcctccttag caccaactgt gtcttagacc ctgttatcta ctgtttcctc  
1141 accaagaagt tccgcaagca cctcaccgaa aagttctaca gcatgcgcag tagccggaaa  
1201 tgctcccggg ccaccacgga tacggctact gaagtgggtg tgccattcaa ccagatccct  
1261 ggcaattccc tcaaaaatta gtccctgctt ccaggcctga agtcttctcc tccatgaaca  
1321 tcatggactg agctggggga agaaggata tctactgtgg tctgggcacc acctctgtgg  
1381 gcactggtg gccattagat ttggaggcta cctcacctgg gcagggatga tggcagacga  
1441 ggctgttga aaatccagaa ctcaaat

## (2) INFORMATION FOR SEQ ID NO:155:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

1 ctctctctgc acacttccg cacactccc tcgtctccc acaccactgg caccaggccc  
61 cgcacacctg ctcggtgca ggagaatggc tactcatcac acgtgtgga tgggactggt  
121 cctgctgggg ctgctggggc gcctacaggc agcaccgag gccagggtct ccgtgcagcc  
181 caacttccag ccggacaagt tctgggggc ctggttcagc ggggctctg cctccaactc  
241 gagctggctc caggagaaga aggcagcgt gtccatgtgc aagtcggtg tggccctgc  
301 ggcgatggt ggcttcaacc tgacctccac cttctcagg aaaaaccagt gtgagaccg  
361 aaccatgctg ctgcagcccg gggactcct cggctctac agtaccgga gtcccactg  
421 gggcagcacc tactctgtgt cagtgttggg gactgactac gaccactacg cctgtctga  
481 cagccagggc agcaaggggc ccggcgaggc cttccgcatg gccacctct acagccgaac  
541 ccagaccccc agggctgagt taaaggagaa atttaccgcc ttctgcaagg cccagggctt  
601 cacagaggat tccattgtct tctgccccca aaccgataag tgcatgacg aacaatagga  
661 ctccccagag ctgaagctgg gaccgcagcc agccagggtga cccctgcgat ctggatgttt  
721 ccgtctgtt ctttcccga gccctgccc cggctccccg ccaaagcacc cctgccccct  
781 cgggcttct cctggtctg cgaataaac tccggaagca agtctgt

## (2) INFORMATION FOR SEQ ID NO:156:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

1 ggagcaagag gtggttggg ggggacctg gctgacgtt tcccgggcaa cgactccag  
61 gcgtctcagg acgtggccaa ccgttcgcc cgaaagggg cgctgaggca gaagaacgtg

121 cacgaagga aggaccacaa attcatcgcg cgcttcttca agcagccac cttctgcage  
181 cactgcaccg acttcatctg ggggtttggg aaacaaggct tccagtgcc a gtttgcgtg  
241 tttgtggtcc acaagaggtg ccatgaattt gttactttt cttgtccggg tgcggataag  
301 ggacccgaca ctgatgacc caggagcaag cacaagttca aaatccacac ttacggaagc  
361 cccaccttct gcgatcactg tgggtcactg ctctatggac ttatccatca agggatgaaa  
421 tgtgacacct gcgatatgaa cggtcacaa caatgcgtca tcaatgtccc cagcctctgc  
481 ggaatggatc acactgagaa gagggggcgg atttacctaa aggctgagg tgcgatgaa  
541 aagctccatg tcacagtacg agatgcaaaa aatctaattc ctatggatcc aaacgggctt  
601 tcagatcctt atgtgaagct gaaacttatt cctgatccca agaatgaaag caagcaaaaa  
661 accaaaacca tccgctccac actaaatccg cagtggaaat agtccctttac attcaaattg  
721 aaaccttcag acaaagaccg acgactgtct gtagaaatct gggactggga tcgaacaaca  
781 aggaatgact tcatggatc cctttccttt ggagtctcg agctgatgaa gatgccggcc  
841 agtggatggt acaagttgct taaccaagaa gaaggtagt actacaagct acccattccg  
901 gaaggggacg aggaaggaaa catggaactc aggcagaaat tcgagaaagc caaacttggc  
961 cctgctggca acaaagtcac cagtccctct gaagacagga aacaaccttc caacaacctt  
1021 gaccgagtga aactcacgga cttcaatttc ctcatggtgt tgggaaaggg gatttttga  
1081 aaggtgatgc ttgcccagag gaagggcaca gaagaactgt atgcaatcaa aatcctgaag  
1141 aaggatgtgg tgattcagga tgatgcactg gagtgcacca tggtagaaaa gcgagctttg  
1201 gccctgcttg aaaaaccccc gttcttgacg cagctgcact cctgcttcca gacagtggat  
1261 cggctgtact tgcgtcatga atatgtcaac ggtggggacc tcatgtacca cattcagcaa  
1321 gtaggaaaat ttaaggaacc acaagcagta ttctatgagg cagagatttc catcggattg  
1381 ttctttcttc ataaaagagg aatcatttat agggatctga agttagataa cgtcatgtt  
1441 gattcagaag gacatatcaa aattgctgac tttgggatgt gcaaggaaaca catgatggat  
1501 ggagtcacga ccaggacctt ctgtgggact ccagattata tcgccccaga gataatcgct  
1561 tatcagccgt atggaaaatc tgtggactgg tgggcctatg gcgtcctgtt gtatgaaatg  
1621 cttgccgggc agcctccatt tgatggtgaa gatgaagacg agctatttca gtctatcatg  
1681 gagcacaacg ttctctatcc aaaatccttg tccaaggagg ctgtttctat ctgcaaagga  
1741 ctgatgacca aacacccagc caagcggctg ggctgtgggc ctgaggggga gagggacgtg  
1801 agagagcatg ccttcttcgg gaggatcgac tgggaaaaac tggagaacag ggagatccag  
1861 ccaccattca agcccaaagt gtgtggcaca ggagcagaga actttgacaa gttcttcaca  
1921 cgaggacagc cgtcttaaac accacctgat cagctggtta ttgctaacat agaccagtct  
1981 gattttgaag ggttctcgta tgtcaacccc cagtttgtgc accccatctt acagagtga  
2041 ctgtgaaact caccagcgag aacaaaaccc tcccagccc ccagccctcc ccgagtgga  
2101 agtgaatcct taaccctaaa attttaaggc cacggcttgt gtctgattcc atatggaggc  
2161 ctgaaaattg tagggttatt agtccaaatg tgatcaactg ttcagggtct ctctcttaca  
2221 accaagaaca ttatcttagt ggaag

## (2) INFORMATION FOR SEQ ID NO:157:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 636 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

1 cttatcacag ttcaagtgat ttccagaagt tccagggtt ctgagagacc atcaaggga  
61 ctttaacaac ttgacaaatg tcttgaagt aagatgcctc atctttaggg aaaaaatggg  
121 tttggatttc tgcttaggca aagtctcctg cagttcatcc ttctctgtcc tcttctgtc  
181 tcaggcttgg ggaccgtccc tgctgtcccc actgtgtgg caatcaggac ctaagggtga  
241 gcaaacttga agttctatct gacaagtta ggcagtaaga gaaggaggga aatcggagca  
301 aagctccctc actttattgt tgagaaactg gcactctgaa agaagaagga atttgcccaa  
361 agtcagtcag ctgggataaa aacctgggtg tctgtccag aaagtgcagg gtgctttctg  
421 ctctgtagca aggcagcaga catctctgag ccaggccac caacaggccc ttatctgggtg  
481 gttggatcat gatccattt tgcttgaca tgctctcagg aagataaaaa ccatggagaa  
541 acactaggcc attgacaaat gatctgagac aactttagaa aacaatgtag gatgaatgga  
601 aagagaaaga aaggaaagaa aaaaaaaaaa aaaagg

## (2) INFORMATION FOR SEQ ID NO:158:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2574 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

1 cagagccggc gcaggggaag cgcccgggc cccgggtgca gcagcgccc cgccctccc  
61 ggtctcccc gcccgcagcc cggggtccc ggcccgggg ccggcacctc tcgggctccc  
121 gctccccgcg cgcaagatgg ctgaccgcgc tgccggggcc cgccgagcg agggcgagga  
181 gagcaccgtg cgcttcgccc gcaaaggcgc cctccggcag aagaacgtgc atgaggtcaa  
241 gaaccacaaa ttcaccgccc gcttcttcaa gcagcccacc ttctgcagcc actgcaccga  
301 cttcatctgg ggcttcggga agcagggatt ccagtgcaca gtttgcgtct ttgtggtgca  
361 caagcgggac catgaatttgc tcacattctc ctgccctggc gctgacaagg gtcacgctc  
421 cgatgacccc cgcagcaaac acaagtttaa gatccacacg tactccagcc ccacgttttg  
481 tgaccactgt gggtcactgc tgtatggact catccaccag gggatgaaat gtgacacctg  
541 catgatgaat gtgcacaagc gctgcgtgat gaatgttccc agcctgtgtg gcacggacca  
601 cacggagcgc cgccggccga tctacatcca ggccacatc gacagggacg tcctcattgt

661 cctcgt gatgctaaaa accttgatcc tatggacccc aaatgtgt cagatcccta  
721 cgtaaaactg aaactgattc ccgatcccaa aagtgaagc aaaaaga ccaaaaccat  
781 caaatgctcc ctcaaccctg agtggaaatga gacatttaga tttcagctga aagaatcgga  
841 caaagacaga agactgtcag tagagatttg ggattgggat ttgaccagca ggaatgactt  
901 catgggatct ttgtcctttg ggatttctga acttcagaag gccagtgttg atggctggtt  
961 taagttactg agccaggagg aaggcgagta cttcaatgtg cctgtgccac cagaaggaaag  
1021 tgaggccaat gaagaactgc ggcagaaatt tgagagggcc aagatcagtc agggaaaccaa  
1081 ggtcccggaa gaaaagacga ccaacactgt ctccaaattt gacaacaatg gcaacagaga  
1141 ccggatgaaa ctgaccgatt ttaacttcct aatggtgctg gggaaaggca gctttggcaa  
1201 ggtcatgctt tcagaacgaa aaggcacaga tgagctctat gctgtgaaga tcctgaagaa  
1261 ggacgttggtg atccaagatg atgacgtgga gtgcactatg gtggagaagc ggggtgtggc  
1321 cctgcctggg aagccgccct tctgaccca gctccactcc tgcttcaga ccatggaccg  
1381 cctgtacttt gtgatggagt acgtgaatgg gggcgacctc atgtatcaca tccagcaagt  
1441 cggccgggtc aaggagcccc atgctgtatt ttacgctgca gaaattgcc a tcggtctgtt  
1501 cttcttacag agtaagggca tcatttaccg tgacctaaaa cttgacaacg tgatgctcga  
1561 ttctgaggga cacatcaaga ttgccgattt tggcatgtgt aaggaaaaca tctgggatgg  
1621 ggtgacaacc aagacattct gtggcactcc agactacatc gcccccgaga taattgctta  
1681 tcagccctat gggaaagtccg tggattgggtg ggcatttgga gtccgtgtgt atgaaatgtt  
1741 ggctgggagc gcaccctttg aaggggagga tgaagatgaa ctcttccaat ccatcatgga  
1801 acacaacgta gcctatccca agtctatgtc caaggaagct gtggccatct gcaaagggct  
1861 gatgaccaa caccagga aacgtctggg ttgtggacct gaaggcgaac gtgatataa  
1921 agagcatgca tttttccggt atattgattg ggagaaactt gaacgcaaag agatccagcc  
1981 cccttataag ccaaaagcta gagacaagag agacacctcc aacttcgaca aagagttcac  
2041 cagacagcct gtggaactga ccccactga taaactcttc atcatgaaat tggaccaaaa  
2101 tgaatttgct ggttctctt atactaacc agagtttgct attaatgtgt aggtgaatgc  
2161 aaactccatc gttgagcctg ggggtgaaga cttcaagcca agcgtatgta tcaattctag  
2221 tcttccagga ttcacgtgac acatgctggc attcaacatg tggaaagctt gtcttagagg  
2281 cctttcttgt atgtgtagct tgctagtttg ttttctacat ttgaaaatgt ttagttaga  
2341 ataagcgc atccaatta tagaggtaca attttccaaa cttccagaaa ctcataaat  
2401 gaacagacaa tgtcaaaact actgtgtctg ataccaaaat gcttcagtat ttgtaatttt  
2461 tcaagtcaga agctgatgtt cctggtaaaa gtttttacag ttattctata atattctctt  
2521 tgaatgctaa gcatgagcga tatttttaaa aattgtgagt aagcttcgga attc

## (2) INFORMATION FOR SEQ ID NO:159:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3321 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

1 cagagccggc gcagggaag cgccggggc ccgggtgca gcagcgccg ccgctcccg  
61 ggccctcccc gcccgcagcc cggggtcccg ggccccggg ccggcacctc tcgggctccg  
121 gctccccg cgcaagatgg ctgaccggc tgccgggccc ccgcccagc agggcgagga  
181 gagcaccgtg cgcttcgccc gcaaaggcgc cctccggcag aagaacgtgc atgaggtcaa  
241 gaaccacaaa ttcaccgccc gcttcttcaa gcagcccacc ttctgcagcc actgcaccga  
301 cttcatctgg ggttcggga agcagggatt ccagtgccaa gtttgcgtct ttgtgggtga  
361 caagcgggtg catgaatttg tcacattctc ctgccctggc gctgacagg gtccagctc  
421 cgatgacccc cgcagcaaac acaagtttaa gatccacacg tactccagcc ccaggtttg  
481 tgaccactgt ggttactgc tgtatggact catccaccag gggatgaaat gtgacacctg  
541 catgatgaat gtgcacaagc gctgcgtgat gaattgtccc agcctgtgtg gcacggacca  
601 cacggagcgc cggggccgca tctacatcca ggcccacatc gacagggagc tcctcattgt  
661 cctcgtaaga gatgctaaaa accttgatcc tatggacccc aatggcctgt cagatcccta  
721 cgtaaaactg aaactgattc ccgatcccaa aagtgaagc aaacagaaga ccaaaaccat  
781 caaatgctcc ctcaaccctg agtggaaatga gacatttaga tttcagctga aagaatcgga  
841 caaagacaga agactgtcag tagagatttg ggattgggat ttgaccagca ggaatgactt  
901 catgggatct ttgtcctttg ggatttctga acttcagaag gccagtgttg atggctggtt  
961 taagttactg agccaggagg aaggcgagta cttcaatgtg cctgtgccac cagaaggaaag  
1021 tgaggccaat gaagaactgc ggcagaaatt tgagagggcc aagatcagtc agggaaaccaa  
1081 ggtcccggaa gaaaagacga ccaacactgt ctccaaattt gacaacaatg gcaacagaga  
1141 ccggatgaaa ctgaccgatt ttaacttcct aatggtgctg gggaaaggca gctttggcaa  
1201 ggtcatgctt tcagaacgaa aaggcacaga tgagctctat gctgtgaaga tcctgaagaa  
1261 ggacgttggtg atccaagatg atgacgtgga gtgcactatg gtggagaagc ggggtgtggc  
1321 cctgcctggg aagccgccct tctgaccca gctccactcc tgcttcaga ccatggaccg  
1381 cctgtacttt gtgatggagt acgtgaatgg gggcgacctc atgtatcaca tccagcaagt  
1441 cggccgggtc aaggagcccc atgctgtatt ttacgctgca gaaattgcc a tcggtctgtt  
1501 cttcttacag agtaagggca tcatttaccg tgacctaaaa cttgacaacg tgatgctcga  
1561 ttctgaggga cacatcaaga ttgccgattt tggcatgtgt aaggaaaaca tctgggatgg  
1621 ttcagcaacc aagacattct gtggcactcc agactacatc gcccccgaga taattgctta  
1681 tcagccctat gggaaagtccg tggattgggtg ggcatttgga gtccgtgtgt atgaaatgtt  
1741 ggctgggagc gcaccctttg aaggggagga tgaagatgaa ctcttccaat ccatcatgga  
1801 acacaacgta gcctatccca agtctatgtc caaggaagct gtggccatct gcaaagggct  
1861 gatgaccaa caccagga aacgtctggg ttgtggacct gaaggcgaac gtgatataa

1921 agagcagca tttttccggt atattgattg ggagaaactt gaacgcaaag agatccagcc  
1981 cccttataag ccaaaagctt gtgggcgaaa tgctgaaaac ttcgaccgat ttttcacccg  
2041 ccattccacca gtccaaacac ctcccgacca ggaagtcac aggaatattg accaatcaga  
2101 attcgaagga ttttcctttg ttaactctga atttttaaaa cccgaagtca agagctaagt  
2161 agatgtgtag atctccgtcc ttcattttctg tcattcaagc tcaacggcta ttgtggtgac  
2221 atttttatgt ttttcattgc caagttgcat ccatgtttga ttttctgatg agactagagt  
2281 gacagtgttt cagaacccaa atgtcctcag gtatgtttgga gcattctctat gagatgggat  
2341 tatgcagatg gcctatggaa aatgcagctg cataattaac acattatcaa agtcctctta  
2401 caatttattt tccgcagcat gtcagctaag tagacccaat ggggagagaa aatgcctgct  
2461 ttctttccct ctttttctgc actgccatat tcaccccaa ccatccaatc tgtggataat  
2521 tggatgttag cgttactctt ccacttccgg tcttgagct tggcttgat ccaagtgtat  
2581 ggttgctttg cctaagagga atccctctat ttcacctgtt ctggaggcac cagaccttga  
2641 aaagaacatg ctcaaaataa aatgttatct gttatttttg taaactcaaa gttaaagtga  
2701 tcaaagttct aaaattccaa gaatgtgctt ttagacggtc tcaatctaaa agcacttcaa  
2761 ggggtcaaag ggcaaccagc ttggtgctac ctgagtggtg tagtttctga tactttatgt  
2821 ctttgcctac cctcatcccc aaactacttg aaaagggcat ttggcaccac tctctgaaac  
2881 aacacagtca ctctagcaag gccccaaaag ggccctggtt ttacattaca tttcaaaact  
2941 tatttgcttt ggggttttgt ttctgttgtt gttcaaatgc aaaaaaaga aaaaaaaag  
3001 aaaaaaaaag gtgactcaca ttgttacaca tgctttaaaa tatgtgttca aatgttatta  
3061 accacaatga cgactgttt tgatttaacc aagaagacgg ctgaggagcc tgcagactc  
3121 aggcctgttg gaatgggatt tgttacaaat ctaggttgt tactggcttc agaaagctaa  
3181 ttaagtgtc tgaaaaagac accgtttctt gaaacaaaga tgggtgtatt cctcactttg  
3241 atgtgtttt gcaagatgtt tgtggaaatg ttcatttgta tctggatctc tgttatgtgc  
3301 catttttctt ctgcatcga g

## (2) INFORMATION FOR SEQ ID NO:160:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

1 gtccttcatt cttccacaa ctatttatcc agcaccgttt ctgggcacag ggctccagcg  
61 atggccccaa caggtacaat gacctctggg gaccaagttc agttcttggg gagttctcca  
121 gtgcctctcg atgtaggatg aaccgttggc atgtccact gacgtggct cttctgttg  
181 tttctcttgg ctccaggacc ccgcagcaa acacaagttt aagatccaca cgtactccag  
241 cccacgttt tgtgaccact gtgggtcact gctgtatgga ctcatccacc aggggatgaa  
301 atgtgacagt aagtactttc tctcttggg ggcattctgt gatggcagaa gcaatgggaa  
361 gggctgcttc cacttggtt ggggtccagg tctgccatac attccccct gtcctcggtg  
421 gggctggtgt accagttatc tgtgtgtgca taatgatcct cccaccccaa aacactgtga  
481 ctgaagacaa taaacatttt ttagctcat gactctgcaa ggcagtcctt tgaatctggg  
541 ctggcctcag ctgatgtcac gcatgttcat aaagcatgaa ctcatggttc atggtggatt  
601 agcagatgga ggtgggctgg g

## (2) INFORMATION FOR SEQ ID NO:161:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1559 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

1 acatcaagga gacgagtcct gttggatag taatgtcttt aacaccctc tagcatttat  
61 taatttcctc tcttaacaaa taaaagatgc cttcagtcga gatgcttagg acagatgacg  
121 cacctagaga tattttaata atgtagatac tcttctgtt caaactcaga ccaaatgac  
181 gataggcttt ttggccccc agagggtgca caaatacgac cagaatttgt gaagacgagt  
241 cagaaatgaa tgaaatttgg aaaaatattg atctactgaa atccttctc cccacactat  
301 tagccctatg ttacagttgg gaaacggag tctgtttgca gaggggatgg acagaaggta  
361 gggagtcttc ttccaaacgt gcaggaggca agcaaagcca agaattctt ctgtgtgtgag  
421 ttagagacat ataaaaataa gatcgctcct cccctacctc tgcagaacgt gtgtgtgtat  
481 gtgtgtgtaa gtgtgtgcgg ccacaagcct ttccgaatga gtgacagcgg gagcccattc  
541 ctccaggaga cgcgtgcaga atgaccaatg ggatggatgg ggggtggatgg gtaccagtct  
601 ccgcagaggc cgggtgggga attcgctgcg cccacccct tccaccgct ccccttcgcc  
661 ccgtaggtct ttccactctc gtcctcccc tgggcacatc tctgaacgc agccccggg  
721 gccgaggacg ggggtgggtg gggggcgagg ctccgggtccg acgaccccg gctgcggtcc  
781 cggcgtgca gagctgcggc tgtgcacgt tagccgcgag gccgcggtg gccggggcgc  
841 cgatatgtaa agcagctggc agcgtgggc ggggcctggg cgcgactgca aatgaggagg  
901 gcgcgggctg gcccgggg cccgctccc tccccgcag ctggggccag cggctgcca  
961 gcgcactggt cgagcggcag cagctgggag aggtgacagc cccggctccg cgcgcggcc  
1021 gccagagccg gcgcagggga agcgcggcg gccccgggtg cagcagcggc cgcgcctcc  
1081 cgcgcctccc cggcccgag cccgcggctc cgcgcggcg ggcgggacc tctcgggctc  
1141 cggctccccg cgcgcaagat ggctgacctg gctgcggggc cgcggcgag cgaggcgag

1201 gagagc tgcgcttcgc ccgcaaagcc gccctcagcc agcgcgt gcatgaggtc  
1261 aagaaccaca aattcaccgc ccgcttcttc aagcagccca cctcgcag ccactgcacc  
1321 gacttcattc ggtgaccccc caggcactcc ggccccagcc cagcccgcc caggaccccc  
1381 tctccgccc cctctgcgcc tccgcacct ggaccccgcc tccccggact ccccgctccg  
1441 gaccctgctg cccgggactc ccggatggac agtcctagcc gttgcctgt cccaccctg  
1501 gtcccgagcc ggccgcccgc ggccgctct gccctctct gctctcagcc gcctctaga

## (2) INFORMATION FOR SEQ ID NO:162:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2510 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

1 gtgcactgca ggtcaacgga cacatcaagg agagagtcct ggttgatag taatgtcttt  
61 aacacccctc tagcatttat taatttcttc tcttaacaaa taaaagatga cttcagttga  
121 agatcccttag gacagatgac ggcacctgga gatattttta taatgtagat accctcttgc  
181 tgttcaaact cagacaaaaa gagatggctt ttttccccc agaggggtgca caaatagcag  
241 agaattttgtg aagacgagtc agaaatgaat gaaatttggg aaaatattga tctactgaaa  
301 tccttcctcc ccacactatt agccctatgt tacagtggg gaaacggagt cgttttgcag  
361 aggggagtag cagaagtag ggagttctct tccaacgtgc agaggcaag caaagccaag  
421 catcttctct gtgttgaggt tagagacata taaaataaga tcgctcctcc cctacctctg  
481 cagaacgtgt gtgtgtatgt gtgtgtaacg tgtgtgcggc cacaagcctt tccgaatgag  
541 tgacagcggg agcccatccc tccaggagac gcgtgcagaa tgaccaatgg gatggatggg  
601 ggtggatggg tacgctctcc gcgagccgg ggtggaattc gctgcgccc accccttcca  
661 cccgctcccc ttgcgccgt aggtctttcc actctcgctc ctccctggg cacatctcct  
721 gaacgcagcc ccgggggccc aggcgggggt ggggtgggg gcgaggtctg ggtccgacga  
781 ccccgggctg cggctccggc gctgcagagc tgcgctgtg cacgcttagc cgcgaggccc  
841 gcggtagccc gggcgccgat atgtaaagca gctggcagcg ctggcgggg cctggcgcg  
901 atgcaaatga ggagggcggg gctggccgg ggctccgct cctcccccg cagctggggc  
961 cagcggtgcc aagcgcagct ggacgagcgg cagcagctgg gcgagtga cccccggctc  
1021 cgcgcgccgc ggccgcaga gccggcgag ggaagcgcc cgcgccccg ggtgcagcag  
1081 cgcccgccgc ctcccgccgc tcccggccc gcagcccgcg gtcccgccc cccggggccg  
1141 gcacctctcg ggctccggct ccccgcgcgc aagatggctg acccggtgc gggcgcccg  
1201 ccgagcgagg gcgaggagag caccgtgcgc ttcgcccga aaggcgccct caggcagaag  
1261 aacgtgcatg aggtcaagaa ccacaaattc accgcccgt tctcaagca gccaccttc  
1321 tgcagccact gcaccgactt catctgttgg agcgcgcgcg caaggcacct tccggggccc  
1381 ccgagcgagc gccgcgcca gggacccctc ctccgccctc tgcgccctc gcaccctgga  
1441 ccccgcgctc ccggactccc cgctccggac cctgtgcgg ggactcccg atggacagtc  
1501 ctgccgttgc cctgtcccca cctgtgtccc aggcggggg cgccctctgc cctctcttgc  
1561 tctcaggcgc ctctagagcg cccaggggca gcgtcgcggg cgctttgtt ccacctgact  
1621 aggagcgcg gcgggtctgt cctgccctgg agggcagcgc ctcggtgtt ctccgacccg  
1681 gggttcccta tctctcgcc tgettccgg cgcgaggagc cctcgcccc cacccttgt  
1741 ttccgggggg gggggggcgc gccctgggtg tcttctctta tctctcggg catgggacat  
1801 cctttctcac tctctgtgc ctggcagcg cctgtgttta tctccattg cctccccga  
1861 gggcctggtt cccctttcca ctctcggtc acatcactgc gggcccttt ctccccagt  
1921 ccctccagta gtggggcacc ctttctctt tccagtcgc cctccagag gaccacccg  
1981 ccgcggggtc actctcgccc tccctctgaa tgcgtcttta tctctctct tttccgagg  
2041 tgcctggggc atctatgggt acatctgtcg cctgccttca gcccctacc cgacggaaac  
2101 gctcccaact atcccgccac ctgggtgtcg cagcctctc tcttctgcag gagtgaaggc  
2161 agatcggggt tacagccgag ctcccaccta cccccaaaa ggcggaagac tcttgggac  
2221 ccgctgttgg ctgggagttt gcacctgggg tacagaggca gggaggaag cgggtgactc  
2281 tgtgggtaac tagctggagg ctggggcccc gggtgcctg acatacacct ccttctgctt  
2341 ttgcaggggc ttccgggaagc agggattcca gtgccaaggt aggtcttggg gctttgggga  
2401 tgctatttgt gggaagagag ggtgaaaaat actttataga agaagttact gagttaggca  
2461 gagaagtgaat gaatcacgtt ggtcggagtg acctcccagg ctaggaaattc

## (2) INFORMATION FOR SEQ ID NO:163:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2163 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

1 aaagcgacca tgtatctga gtggaagtcg acgttcgatg cccacatcta tgagggggcg  
61 gtcaccaga ttgtgcta atgcggcagca gaggagccag tgtctgaggt gaccgtgggt  
121 gtgtcggtgc tggccgagcg ctgcaagaag acaatggca aggtgagtt ctggctggac  
181 ctgcagcctc aggccaaggt gttgatgtct gttcagtatt tctggaagga cgtggattgc  
241 aaacagtcta tgcgcagtga ggacgaggcc aagttcccaa cgatgaaccg ccgaggagcc  
301 atcaaacagg ccaaaatcca ctacatcaag aacctagat ttatcgccac cttctttggg  
361 caaccacact tctgttctgt gtgcaaagac tttgtctggg gcctcaaca gcaaggctac  
421 aaatgcaggc aatgtaacgc tgccatccac aagaaatgca tcgacaagat catcggcaga  
481 tgactggca ccgcgcccaa cagccgggac actatatcc agaagaacg cttcaacac

541 gacatgc accgcttcaa ggttcacaac tacatgagcc ccaccttctg tgaccactgc  
601 ggcagcctgc tctggggact ggtgaagcag ggattaaagt gtgaagactg cgcatgaat  
661 gtgcaccata aatgccggga gaaggtggcc aacctctgcg gcatcaacca gaagcttttg  
721 gctgaggcct tgaaccaagt caccagaga gcctcccgga gatcagactc agcctcctca  
781 gagcctgttg ggatatatca gggtttcgag aagaagaccg gaggttgctgg ggaggacatg  
841 caagacaaca gtgggaccta cggcaagatc tgggagggca gcagcaagtg caacatcaac  
901 aacttcatct tccacaaggt cctgggcaaa ggagcttctg ggaaggtgct gcttgagag  
961 ctgaagggca gaggagagta ctttgccatc aaggccctca agaaggatgt ggtcctgate  
1021 gacgacgacg tggagtgcac catggttgag aagcgggtgc tgacacttgc cgcagagaat  
1081 ccctttctca ccacctcat ctgcacctc cagaccaagg accacctgtt ctttgtgatg  
1141 gacttctca acggggggga cctgatgtac cacatccagg acaaaggcgg ctttgaactc  
1201 taccgtgcca cgttttatgc cgctgagata atgtgtggac tgcagtttct acacagcaag  
1261 ggcacatttt acagggacct caaactggac aatgtgctgt tggaccggga tggccacatc  
1321 aagattgccg actttgggat gtgcaaagag aacatattcg gggagagccg gggcagcacc  
1381 ttctgcgcca ccctgacta tatcgccct gagatcctac agggcctgaa gtacacattc  
1441 tctgtggact ggtggtcttt cggggtcctt ctgtacgaga tgctcattgg ccagtcccc  
1501 ttccatggtg atgatgagga tgaactcttc gagtccatcc gtgtggacac gccacattat  
1561 ccccgctgga tcaccaagga gtccaaggac atcctggaga agctctttga aagggaacca  
1621 tccaagagc tgggagtgc gggaaacatc aaaatccacc ctttcttcaa gaccataaac  
1681 tggactctgc tggaaaagcg gaggttggag ccaccttca ggcccaaagt gaagtcaccc  
1741 agagactaca gtaactttga ccaggagttc ctgaacgaga aggcgcgcct ctctacagc  
1801 gacaagaacc tcatcgactc catggaccag tctgcattcg ctggcttctc ctttgtgaac  
1861 cccaaattcg agcacctcct ggaagattga ggttcctgga cagatcaggc tagccctgcc  
1921 ctccaccac acctgcccgc tccccacgat aagcaccagt gggactgtgg tgacttctgc  
1981 tgctggcccc gccctgccc ccagagcgtc cttggctgcc gtctggccgg gctctcatgg  
2041 tacttctct gtgaactgtg tgtgaatctg ctttctctt gccttcggag ggaattgta  
2101 aatcctgtgt ttcattactt gaatgtagtt atctattgaa aatatacttt agagcacaat  
2161 gga

## (2) INFORMATION FOR SEQ ID NO:164:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2104 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

1 tgccgcgcgcg acccttggcg cctgcccctg caacgggagc cccactgcag gccccaccat  
61 ggccgcgttc ctgcgcacgc ccttcaactc ctatgagctg ggctccctgc aggccgagga  
121 cgaggcgaa cagcccttct gtgcgtgaa gatgaaggag gcgctcagca cagagcgtgg  
181 gaaaacactg gtgcagaaga agccgacct gtatcctgag tggaaagtcga cgttcgatgc  
241 ccacatctat gaggggcgcg tcattccagat tgtgctaag cgggcagcag aggagccagt  
301 gtctgaggtg accgtgggtg tgtcgtgct ggccgagcgc tgcaagaaga acaatggcaa  
361 ggctgagttc tggctggacc tgcagcctca ggccaaggtg ttgatgtctg ttcagtattt  
421 cctggaggac gtggattgca aacaatctat gcgcagtgc gacgaggcca agttcccaac  
481 gtagaacgc cgccgagcca tcaaacaggc caaaatccac tacatcaaga accatgagtt  
541 tatcgccacc ttctttgggc aaccacctt ctgttctgtg tgcaaagact ttgtctgggg  
601 cctcaacaag caaggctaca aatgcaggca atgtaacgct gccatccaca agaaatgcat  
661 cgacaagatc atcggcagat gcaactggc cgcggccaac agccgggaca ctatattcca  
721 gaaagaacgc ttcaacatcg acatgccga ccgcttcaag gttcacaact acatgagccc  
781 cacttctgt gaccactgc gacgctgct ctggggactg tggaagcagg gattaaagt  
841 tgaagactgc ggcatgaatg tgcaccataa atgcggggag aaggtggcca acctctgcg  
901 catcaaccag aagcttttgg ctgaggcctt gaaccaagtc acccagagag cctcccgag  
961 atcagactca gcctcctcag agcctgttgg gatatatcag ggttctgaga agaagaccgg  
1021 agttgctggg gaggacatgc aagacaacag tgggacctac ggcaagatct gggagggcag  
1081 gaagaagtgc aacatcaaca acttcatctt ccacaaggtc ctgggcaag cgcagcttgcg  
1141 gaaggtgctg cttggagagc tgaaggcgag aggagagtag tctgccatca agccctcaa  
1201 gaaggtatgt gtctgatcg acgacgacgt ggagtgcacc atggttgaga agcgggtgct  
1261 gacacttgcc gcagagaatc ctttctcac ccacctcatc tgaccttcc agaccaagga  
1321 ccacctgttc tttgtgatgg agttcctcaa cgggggggac ctgatgtacc acatccagga  
1381 caaaggccgc tttgaactct accgtgccac gttttatgcc gctgagataa tgtgtggact  
1441 gcagtttcta cacagcaagg gcatcattta cagggacctc aaactggaca atgtgtgtt  
1501 ggaccgggat ggccacatca agattgccga ctttgggatg tgcaaaagaga acatattcgg  
1561 ggagagccgg gccagcacct tctgcggcac ccctgactat atcggccctg agatcctaca  
1621 gggcctgaag tacacattct ctgtggactg gtggtcttcc ggggtccttc tgtacgagat  
1681 gctcattggc cagtccccct tccatggtga tgatgaggat gaactcttgc agtccatccg  
1741 tctggacacg ccacattatc cccgtggat caccaaggag tccaaggaca tcttgagaa  
1801 ggtctttgaa agggaaccaa ccaagggct ggaatgacg ggaacatca aaatccacc  
1861 cttcttcaag accataaact ggactctgct ggaagagcgg aggttgagc cacccttcag  
1921 gcccgaagtg aagtcaccca gagactacag taactttgac caggagttcc tgaacgagaa  
1981 ggccgcgcctc tctacagcg acaagaacct catcgactcc atggaccagt ctgattcgc  
2041 tggcttctcc tttgtgaacc ccaaattcga gcacctcctg gaagattgag gttcctggac  
2101 agat

## (2) INFORMATION FOR SEQ ID NO:165:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2146 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

```
1 cccaagatgg aagggagcgg cgccgcgctc cgcctcaagg cgcattacgg gggggacatc
61 ttcacaccca gcgtggacgc cgccacgacc ttcgaggagc tctgtgagga agtgagagac
121 atgtgtcgtc tgcaccagca gcaccgcgtc accctcaagt ggggtgacag cgaaggtgac
181 ccttgacagg tgctctccca gatggagctg gaagaggctt tccgcctggc ccgtcagtgc
241 agggatgaag gctcatcatc tcatgttttc ccgagcacc ctagcagacc tggcctgcc
301 tgtccgggag aagacaaatc tatctaccgc cggggagcca gaagatggag gaagctgtac
361 cgtgccaaac gccacctctt ccaagccaag cgctttaaca ggagagcgta ctgcggtcag
421 tgcagcgaga ggatatgggg cctcgcgagg caaggctaca ggtgcatcaa ctgcaaactg
481 ctggtccata agcgtgcga cgccctcgtc ccgctgacct gcaggaagca tatggattct
541 gtcattgcctt cccaagagcc tccagttagc gacaagaacg aggacgccga ccttccttcc
601 gaggagacag atggaattgc ttacatttcc tcatcccgga agcatgacag cattaaagac
661 gactcggagg accttaagcc agttatcgat gggatggatg gaatcaaaat ctctcagggg
721 cttgggctgc aggactttga cctaatacaga gtcacgggc gcgggagcta cgccaaggtt
781 ctctcgtgct ggttgaagaa gaatgaccaa atttacgcca tgaaagtggg gaagaaagag
841 ctggtgcatg atgacgagga tattgactgg gtacagacag agaagcacgt gtttgagcag
901 gcatccagca accccttcct ggteggatta cactcctgct tccagacgac aagtcgggtg
961 ttcttggtca ttgagtacgt caacggcggg gacctgatgt tccacatgca gaggcagagg
1021 aagctccctg aggagcacgc caggttctac gcggcggaga tctgcatcgc cctcaacttc
1081 ctgcacgaga gggggatcat ctacagggac ctgaagctgg acaacgtcct cctggatgcg
1141 gacgggcaca tcaagctcac agactacggc atgtgcaagg aaggcctggg ccctgggtgac
1201 acaacgagca ctttctgcgg aaccccgaaat tacatcgccc ccgaaatcct gcggggagag
1261 gactacgggt tcagcgtgga ctggtgggag ctgggagctc tcatgtttga gatgatggcc
1321 gggcgctccc cgctcgacat catcaccgac aacccggaca tgaacacaga ggactacctt
1381 ttccaagtga tcctggagaa gcccatccgg atcccccggt tcctgtccgt caaagcctcc
1441 catgttttaa aaggattttt aaataaggac ccaaagaga ggctcggctg ccggccacag
1501 actggatttt ctgacatcaa gtcccacgag ttcttccgca gcatagactg ggacttgctg
1561 gagaagaagc aggcgtctcc tccattccag ccacagatca cagacgacta cggctctggc
1621 aactttgaca cacagttcac cagcgagccc gtgcagctga ccccagacga tgaggatgcc
1681 ataaagagga tcgaccagtc agagtctgaa ggctttgagt atatcaacc attattgctg
1741 tccaccgagg agtcggtgtg aggcgcgtg cgtctctgtc gtggacacgc gtgattgacc
1801 ctttaactgt atccttaacc accgcatatg catgccaggc tgggcacggc tccgagggcg
1861 gccagggaca gacgcttgcg ccgagaccgc agagggaagc gtcagcgggc gctgctggga
1921 gcagaacagt cctcacacc tggcccggca ggcagcttcg tgctggagga acttgctgct
1981 gtgctgctg cgcgggcgat ccgcggggac cctgccgagg gggctgtcat gcggtttcca
2041 aggtgcacat tttccacgga aacagaactc gatgactga cctgtccgcg caggaaagtg
2101 agcgtgtagc gtcttgagga ataaaatggt ccgatgaaaa aaaaaa
```

## (2) INFORMATION FOR SEQ ID NO:166:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1423 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

```
1 gggccggcgg cgccggcgac tctggacgag agccggggccc ttcccgtaga tcgccccagc
61 tgccgagggc gtcgaggcgc ccccggggtg gcacttccgt gtgcccgggc gccggagccc
121 gagcgggctg tagccacat ctcccgagcg accccggcg cccgcccgc gcgaggagcc
181 ccgggcccaca cctcactggc cgcttgccc atccagtcga gcgcccgcgc gaaccccgctc
241 cgcgcgcgcc ggggagcggc gcccgcgcgc ctgcccgcgc gaccttggc gcctgcccct
301 gcaacgggag cccactgca ggcccacca tggcgccgtt cctgcgcac gccttcaact
361 cctatgagct gggctccctg caggccgagg acgaggcgaa ccagcccttc tgtgccgtga
421 agatgaagga ggcgctcagc acagagcgtg ggaaaacact ggtgcagaag aagccgacca
481 tgtatcctga gtggaagtcg acgttcgatg cccacatcta tgaggggcgc gtcattccaga
541 ttgtgctaata gcgggcagca gaggagccag tgtctgaggt gaccgtgggt gtgtcggtgc
601 tggccgagcg ctgcaagaag aacaatggca aggctgagtt ctggctggac ctgcagcctc
661 aggcgaaggt gttgatgtct gttcagtatt tcctggagga cgtggattgc aaacagtcta
721 tgcgacgtga ggacgaggcc aagttcccaa cgatgaaccg ccgcgaggcc atcaaacagg
781 ccaaaaatcca ctacatcaag aacctagagt ttatcgccac cttctttggg caaccacact
841 tctgttctgt gtgcaaaagc tttgtctggg gcctcaacaa gcaaggctac aaatgcaggc
901 aatgtaacgc tgccatccac aagaaatgca tcgacaagat catcggcaga tgcaatggca
961 ccgcccgaac cagccgggac actatatccc agaaagaacg cttcaacatc gacatgccgc
1021 accgcttcaa ggttcacaac tacatgagcc ccacttctg tgaccactgc ggcagcctgc
1081 tctggggact ggtgaagcag ggattaaagt gtgaagactg cggcatgaat gtcaccata
```

1141 aatgga gaaggtggcc aacctctgcg gcatcaacca gaagcttttg gctgaggcct  
1201 tgaaccaagt caccagaga gcctcccgga gatcagactc agcctcctca gagcctgttg  
1261 ggatataatca gggtttcgag aagaagaccg gagttgctgg ggaggacatg caagacaaca  
1321 gtgggacctt cggcaagatc tgggagggca gcagcaagtg caacatcaac aacttcattc  
1381 tccacaaggt cctgggcaaa ggcagcttcg ggaaggtgct gct

## (2) INFORMATION FOR SEQ ID NO:167:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2244 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

1 ctccccgccc cgaccatggt agtgttcaat ggccttctta agatcaaaat ctgagggcc  
61 gtgagcttga agccacagc ctggtcgcgt cgccatgcgg tgggaccccg gccgcagact  
121 ttccttctcg accctacat tgccctcaat gtggacgact cgcgcacatcgg ccaaaccggcc  
181 accaagcaga agaccaacag cccggcctgg cagcagagt tcgtcaccga tgtgtgcaac  
241 ggacgcaaga tcgagctggc tgtctttcac gatgccccca taggctacga cgacttcgtg  
301 gccaaactgca ccatccagtt tgaggagctg ctgcagaacg ggagccggca cttcaggagc  
361 tggattgatc tggagccaga aggaagagt tatgtgatca tcgatctctc aggtcgtcg  
421 ggtgaagccc ctaaagacaa tgaagagcgt gtgttcaggg aacgcacatcg gccgaggaag  
481 cggcaggggg ccgtcaggcg cagggtccat cagggtcaacg gccacaagtt catggccacc  
541 tatcttcggc agccaccta ctgctcccat tgcagagact tcactctggg tgtcatagga  
601 aagcagggat accagtgtca agtctgcacc tgcgtggtcc acaagcggtg ccacgagctc  
661 ataatacaaa agtgtgctgg gttaaagaag caggagaccc ccgaccaggt gggctccag  
721 cggttcagcg tcaacatgcc ccacaagttc ggtatccaca actacaaggt ccctaccttc  
781 tgcgatcact gtgggtccct gctctgggga ctcttcgagg agggtttgca gtgtaaaagtc  
841 tgcaaaatga atgttcaccg tcgatgtgag accaactggt ctcccaactg tggagtggat  
901 gccagaggaa tcgcaaaagt actggccgac ctgggcgtta cccagacaaa aatcacaac  
961 agcggccaga gaaggaaaaa gctcattgct ggtgcagagt ccccgacgac tgcctctgga  
1021 agctcaccat ctgaggaaga tcgatccaag tcagcaccga cctccccttg tgaccaggaa  
1081 ataaaagaac ttgagaacaa cattcggaag gccttgatc ttgacaaccg aggagaggag  
1141 caccgggcag catcgtctcc tgatggccag ctgatgagcc ccggtgagaa tggcgaagtc  
1201 cggcaaggcc aggcgaagcg cctgggcctg gatgagttca acttcataaa ggtgttgggc  
1261 aaaggcagct ttggcaaggt catgttggca gaactcaagg gcaaagatga agtatatgct  
1321 gtgaaggtct taaagaagga cgtcatcctt caggatgatg acgtggactg cacaatgaca  
1381 gagaagagga ttttggtctt ggcacggaaa caccctgacc ttaccctact ctactgctgc  
1441 tctcagacca aggaccgcct cttttctgct atggaatatg taaatggtgg agacctcatg  
1501 tttcagattc agcgctcccg aaaattcgac gagcctcgtt caggttcta tgcgcagag  
1561 gtcacatcgg ccctcatggt cctccatcag catggagtca tctacaggga tttgaaactg  
1621 gacaacatcc ttctggatgc agaaggtcac tgcaagctgg ctgacttcgg gatgtgcaag  
1681 gaagggattc tgaatggtgt gacgaccacc acgttctgtg ggactcctga ctacatagct  
1741 cctgagatcc tgcaggagtt ggagtatggc cctccgtgg actggtgggc cctgggggtg  
1801 ctgatgtacg agatgatggc tggacagcct ccctttgagg ccgacaatga ggacgacctc  
1861 tttgagtcca tctccatga cgacgtgctg taccagctc ggctcagcaa ggagctgtc  
1921 agcatcttga aagctttcat gacgaagaat cccacaagc gcctgggctg tgtggcatcg  
1981 cagaatggcg aggacgcat caagcagcac ccattcttca aagagattga ctgggtgctc  
2041 ctggagcaga agaagatcaa gccacccttc aaaccacgca ttaaaaccaa aagagacgct  
2101 aataattttg accaagactt taccgggaa gagccgtac tcaccctgtt ggacgaagca  
2161 attgtaaagc agatcaacca ggaggaattc aaaggtttct cctacttttg tgaagacctg  
2221 atgccctgag agccactgc agtt

## (2) INFORMATION FOR SEQ ID NO:168:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

1 agccggcttc tggaaactcc ctgtgtgagt gtgaggaat gagtatgaac aaggcacatt  
61 atgtcttact tattgtatta gtttcctgtt gctgctgtag caagttacca ccaatttatg  
121 gcttaaagca attcaaattt tttctcttga attcttaaga tcagaagttc taaatgagtc  
181 taatggggct aaaatcaagg tgtaggcaa aggcagct

## (2) INFORMATION FOR SEQ ID NO:169:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1830 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

1 tgcagctgga gatccgggt cccacagcag atgagatcca cgtaactgtt ggagaggccc  
61 gtaacctaat tcctatggac cccaatggtc tctctgatcc ctatgtgaaa ctgaagctca  
121 tcccagaccc tcggaacctg acgaaacaga agaccggaac ggtgaaagcc acgctaaacc



181 ctgtg tgagacctt gtgttcaacc tgaagccagg g tggag cgccggctca  
241 gcgtggaggt gtgggactgg gaccggacct cccgcaacga ctccatgggg gccatgtcct  
301 ttggcgtctc ggagctgctc aaggcgcccg tggatggctg gtacaagtta ctgaaccagg  
361 aggaggcgga gtattacaat gtgccgggtg cccgatgctga caactgcagc ctctccaga  
421 agtttgaggc ttgtaactac cccctggaat tgtatgagcg ggtgcggtg ggccctctt  
481 cctctcccat cccctccct tccctagtc ccaccgacct caagcgctgc ttcttcggg  
541 cgagtccagg acgctgcac atctccgact tcagcttctt catggttcta ggaaaaggca  
601 gttttgggaa ggtgatgctg gccgagcgca ggggctctga tgagctctac gccatcaaga  
661 tcttgaaaaa ggacgtgatc gtccaggacg acgatgtgga ctgcacgctg gtggagaaac  
721 gtgtgctggc gctggggggc cggggtcctg gcggccggcc cacttctc accagctcc  
781 actccacctt ccagaccccg gaccgctgt atttctgtat ggagtacgtc accgggggag  
841 acttgatgta ccacattcaa cagctgggca agtttaagga gcccctatgca gcgttctacg  
901 cggcagaaat cgctatcggc ctcttcttcc ttcacaatca gggcatcatc tacagggacc  
961 tgaagctgga caatgtgatg ctggatgctg agggacacat caagatcact gactttggca  
1021 tgtgtaagga gaacgtcttc cccgggacga caaccgcac ctctgcggg acccggact  
1081 acatagcccc ggagatcatt gcctaccagc cctatgggaa gtctgtcgat tgggtgtcct  
1141 ttggagttct gctgtatgag atgttggcag gacagcctcc ctctgatggg gaggacgagg  
1201 aggagctgtt tcaggccatc atggaacaaa ctgtcaccta cccaagtcg ctttcccg  
1261 aagccgtggc catctgcaag ggttctctga ccaagcacc agggaagcgc ctgggctcag  
1321 ggctgatgg ggaacctacc atccgtgcac atggctttt ccgctggatt gactgggagc  
1381 ggctggaacg attggagatc ccgctcctt tcagaccccg cccgtgtggc cgcagcggcg  
1441 agaactttga caagtcttc acgcgggcg cgccagcgt gacccctcca gaccgctag  
1501 tcttgccag catcgaccag gccgatttcc agggcttcac ctacgtgaa cccgactcg  
1561 tgcacccgga tgcccgcagc cccaccagcc cagtgcctgt gccgtcatg taatctacc  
1621 cgcgcgcaat aggtgtcccc aacgtccct ccgctgtgc gccgcagcc cacttacc  
1681 cccaacttca ccacccctg tccattcta gatctgcac cccagcttc cagctctgc  
1741 cccgcggtt ctagacgcc ctccaagc ttctggcct tctgaactcc atacagcctc  
1801 tacagccgtc ccgcttcaa gacttgagcg

## (2) INFORMATION FOR SEQ ID NO:170:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2196 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

1 cggggtgtct tgggcccggg cgctgtaga ggcggcgcg cctacgggca gtgggaggag  
61 ccgcgcggtt ccggtgctc cggcgaggcg acccttgggt cggcgctgcg ggcagggtggc  
121 aggtaggtgg cggacggcg cggttctccg gcaagcgag gcggcgaggt cccccacggc  
181 gcccgaagcg ccccccgca ccccgccct ccagcgttga ggcgggggag tgaggagatg  
241 ccgaccaga gggacagcag caccatgtcc cacacggctc caggcgggcg cagcggggac  
301 cattcccacc aggtccgggt gaaagcctac taccgcgggg atatcatgat aacacatttt  
361 gaaccttcca tctcctttga gggcctttgc aatgaggttc gagacatgtg ttcttttgac  
421 aacgaacagc tttcaccat gaaatggata gatgaggaag gagaccgtg tacagtatca  
481 tctcagttgg agttagaaga agcctttaga ctttatgagc taaacaagga ttctgaactc  
541 ttgattcatg tgttcccttg tgtaccagaa cgtcctggga tgccttgtcc aggagaagat  
601 aaatccatct accgtagagg tgcacggcg tggagaaagc tttattgtgc caatggccac  
661 actttccaag ccaagcgtt caacaggcgt gctcactgtg ccactctcac agaccgaata  
721 tggggacttg gacgccaagg atataagtgc atcaactgca aactcttggc tcataagaag  
781 tgccataaac tcgtcacat tgaatgtggg cggcattctt tgccacagga accagtgatg  
841 cccatggatc agtcatccat gcattctgac catgcacaga cagtaattcc atataatctc  
901 tcaagtcag agagtgtgga tcaagttggt gaagaaaaag aggcgaatgaa caccaggaa  
961 agtggcaag cttcatccag tctaggtctt caggattttg atttgctccg ggtaattgga  
1021 agagggaagt atgccaaagt actgttgggt cgattaaaaa aaacagatcg tatttatgca  
1081 atgaaagtgg tgaaaaaaga gcttgtaaat gatgatgagg atattgattg ggtacagaca  
1141 gagaagcatg tgtttgagca ggcattccaat catcctttcc ttgttgggtg gcattcttgc  
1201 tttcagacag aaagcagatt gttctttgtt atagagtatg taaatggagg agacctaatg  
1261 tttcatatgc agcgacaaa gaaaacttct gaagaaacat ccagatttta ctctgcagaa  
1321 atcagtctag cattaaatta tcttcatgag cgagggataa tttatagaga tttgaaactg  
1381 gacaatgtat tactggactc tgaaggccac attaaactca ctgactacg catgtgtaag  
1441 gaaggattac ggccaggaga tacaaccagc actttctgtg gtactcctaa ttacattgct  
1501 cctgaaattt taagaggaga agattatggt ttcagtgttg actggtggg tcttggagtg  
1561 ctcagtgttg agatgatggc aggaaggtct ccatttgata ttgttggag ctcggataac  
1621 cctgaccaga acacagagga ttatctcttc caagttattt tggaaaaaca aattcgcata  
1681 ccacgttctc tgtctgtaaa agctgcaagt gttctgaaga gtttcttaa taaggaccct  
1741 aaggaacgat tgggttgta tcttcaaaac ggatttgctg atattcaggg acaccggttc  
1801 ttccgaaatg ttgattggga tatgatggag caaaaacagg tggtaacctc ctttaaacca  
1861 aatatttctg gggaatttgg tttggacaac tttgattctc agtttactaa tgaacctgtc  
1921 cagctcactc cagatgacga tgacattgtg aggaagattg atcagtctga atttgaaggt  
1981 tttgagtata tcaatcctct tttgatgtct gcagaagaat gtgtctgatc ctcatTTTTT  
2041 aaccatgtat tctactcatg ttgccattta atgcatggat aaacttgcgt caagcctgga  
2101 tacaattaac cattttatat ttgccaccta caaaaaaaca cccaatatct tctcttgtag

2161 actat gaa tcaattatta catctcgacc cggaat

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2389 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

```
1 gaattcggac ggaggaggca gaatggccag tcgaggggcg cttaggcggtg gcctttcccc
61 agggctgcct cgactcctgc acctgtcccc agggctggcc tgagacggga ctccccggttc
121 tcccgtctcg aagcaggccc cccggggccc gggcagcgcc gccggcatgt cgtctggcac
181 catgaagtctc aatggctatt tgagggtccc catcggtgag gcagtggggc tgcagcccac
241 ccgctgggtcc ctgcgccact cgctcttcaa gaaggggccac cagctgctgg acccctatct
301 gacggtgagc gtggaccagg tgcgcgtggg ccagaccagc accaagcaga agaccaacaa
361 acccacgtac aacgaggagt tttgcgtaa cgtcaccgac ggcgggccacc tcgagttggc
421 cgtcttccac gagaccccc tgggtacga cttcgtggcc aactgcacc tcgagttcca
481 ggagctcgtc ggcacgaccg gcgcctcgga cacttcgag ggttgggtgg atctcgagcc
541 agaggggaaa gtatttgtgg taataaccct taccgggagt ttactgaag ctactctcca
601 gagagaccgg atcttcaaac attttaccag gaagcgccaa agggctatgc gaaggcgagt
661 ccaccagatc aatggacaca agttcatggc cactatctcg aggcagccca cctactgctc
721 tcactgcagg gagtttatct ggggagtgtt tgggaaacag ggttatcagt gccaaagtgt
781 cactgtgtc gtccataaac gctgccatca tctaattgtt acagcctgta cttgccaaaa
841 caatattaac aaagtggatt caaagattgc agaacagagg ttcgggatca acatcccaca
901 caagttcagc atccacaact acaaagtgcc aacattctgc gatcactgtg gctcactgct
961 ctggggaata atgcgacaag gacttcagtg taaaatatgt aaaatgaatg tgcataatcg
1021 atgtcaagcg aacgtggccc ctaactgtgg ggtaaatgag gtggaacttg ccaagaccct
1081 ggcagggatg ggtctccaac ccggaatat tctccaacc tcgaaactcg ttccagatc
1141 gaccctaaga cgacagggaa aggagagcag caaagaagga aatgggattg ggtttaattc
1201 ttccaaccga cttggtatcg acaactttga gttcatccga gtgttgggga aggggagttt
1261 tgggaaggtg atgcttgcaa gagtaaaaga aacaggagac ctctatgctg tgaaggtgct
1321 gaagaaggac gtgattctgc tggatgatga tgtggaatgc accatgaccg agaaaaggat
1381 cctgtctctg gcccgcaatc accccttctt cactcagttg ttctgtgctt ttcagacccc
1441 cgatcgtctg ttttttgtga tggagtttgt gaatgggggt gacttgatgt tccacattca
1501 gaagtctcgt cgttttgatg aagcacgagc tcgcttctat gctgcagaaa tcatctcgcc
1561 tctcatgttc ctccatgata aaggaatcat ctatagagat ctgaaactgg acaatgtcct
1621 gttggaccac gagggtcact gtaactggc agacttcgga atgtgcaagg aggggatttg
1681 caatggtgtc accacggcca cattctgtgg cagccagac tatatcgctc cagagatcct
1741 ccaggaaaatg ctgtacgggc ctgcagtaga ctggtgggca atgggcgtgt tgctctatga
1801 gatgctctgt ggtcacgcgc cttttgaggc agagaatgaa gatgacctct ttgaggccat
1861 actgaatgat gaggtggtct accctacctg gctccatgaa gatgccacag ggatcctaaa
1921 atctttcatg accaagaacc ccaccatgag cttgggcagc ctgactcagg gaggcgagca
1981 cgccatcttg agacatcctt ttttaagga aatcgactgg gccagctga accatcgcca
2041 aatagaaccg cttttcagac ccagaatcaa atcccagaa gatgtcagta attttgacc
2101 tgacttcata aaggaagagc cagttttaac tccaattgat gagggacatc ttccaattgat
2161 taaccaggat gagtttagaa acttttcta tgtgtctcca gaattgcaac catagcctta
2221 tggggagtgag gagagagggc acgagaaccc aaaggaatag agattctcca ggaatttct
2281 ctatcggaac ttcccagcat cagccttaga acaagaacct taccttcaag gagcaagtga
2341 agaactctgt cgaaggatgg aactttcaga tatcaactat ttagagtc
```

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3742 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

```
1 gaattccttc tctcctctc ctcgcccttc tctcgccct cctcctctc ctcgccctcc
61 cctcccgate ctcatccctt tgccctcccc cagcccaggg actttttcgg aaagttttta
121 ttttccgtct gggctctcgg agaaaagaag tcctggctca gcggctgcaa aactttcctg
181 ctgcgcgcgc gccagcccc gccctccgct gcccgccct gcgccccgc gagcgatgag
241 cgcctctcgc gtcctgcggc cgccagtcct gctgctgccc gtggcgggcg cagctgcccgc
301 agcggccgccc gactggtccc cagggtccgg gcccgggccc gcgcggttct tggctcctgt
361 cgcgcccccg gtcgggggca tctcgttcca tctgcagatc ggcctgagcc gtgagccggt
421 gctgtgctg caggactcgt ccggggacta cagcctggcg cacgtccgcg agatggcttg
481 ctccattgtc gaccagaagt tccctgaatg tggtttctac ggaatgtatg ataagatcct
541 gctttttcgc catgacccta cctctgaaaa catccttcag ctggtgaaag cggccagtga
601 tatccaggaa ggcgatctta ttgaagtggc cttgtcacgt tccgccacct ttgaagactt
661 tcagattcgt ccccacgctc tctttgttca ttcatacaga gctccagctt tctgtgatca
721 ctgtggagaa atgctgtggg ggctggtagc tcaaggtctt aaatgtgaag ggtgtggtct
781 gaattaccat aagagatgtg catttaaat acccaacaat tgcagcggtg tgaggcgag
841 aaggctctca aacgtttccc tcactggggt cagcaccatc cgcacatcat ctgctgaact
901 ctctacaagt gccctgatg agcccttct gcaaaaaatc ccatcagagt cgtttattgg
961 tcgagagaag aggtcaaat ctcaatcata cattggacga ccaattcacc ttgacaagat
1021 tttgatgtct aaagttaaa tgccgcacac atttgcacac cactcctaca cccggccac
```

1081 agtgtg tactgcaaga agcttctgaa ggggcttttc agtggct tgcagtgc aa  
1141 agattgcaga ttcaactgcc ataaacgttg tgcaccgaaa gtaaaaca actgccttgg  
1201 cgaagtgcacc attaatggag atttgcttag cccctggggca gactctgatg tggctcatgg  
1261 agaagggagt gatgacaatg atagtgaag gaacagtggg ctcatggatg atatggaaga  
1321 agcaatggtc caagatgcag agatggcaat ggcagagtgc cagaacgaca gtggcgagat  
1381 gcaagatcca gacccagacc acgaggacgc caacagaacc atcagtccat caacaagcaa  
1441 caatatccca ctcatgaggg tagtgacgtc tgtcaaacac acgaagagga aaagcagcac  
1501 agtcatgaaa gaaggatgga tgggtccacta caccagcaag gacacgtgc ggaacggca  
1561 ctattggaga ttggatagca aatgtattac cctctttcag aatgacacag gaagcaggta  
1621 ctacaaggaa attcctttat ctgaaatttt gtctctggaa ccagtaaaaa cttcagcttt  
1681 aattcctaatt ggggccaatc ctcatgtttt cgaatcact acggcaaatg tagtgtatta  
1741 tgtgggagaa aatgtggtca atccttccag cccatcacca aataacagtg ttctcaccag  
1801 tggcgttggg gcagatgtgg ccaggatgtg ggagatagcc atccagcatg ccttatggc  
1861 cgtcattccc aagggtcct cctgtgggtac aggaaccaac ttgcacagag atatctctgt  
1921 gagtatttca gtatcaaatt gccagattca agaaaatgtg gacatcagca cagtatatca  
1981 gatttttctt gatgaagtac tgggttctgg acagtttgga attgtttatg gaggaaaaaca  
2041 tcgtaaaaaca ggaagagatg tagctattaa aatcattgac aaattacgat ttccaacaaa  
2101 acaagaaagc cagcttcgta atgaggttg aattctacag aaccttcac accctgtgtg  
2161 tgtaaatttg gagtgtatgt ttgagacgcc tgaaagagtg tttgtgtta tggaaaaact  
2221 ccatggagac atgctggaaa tgatctgtgc aagtgaagag ggcaggttgc cagagcacat  
2281 aacgaagttt ttaattactc agatactcgt ggctttgcgg caccttcatt ttaaaaatat  
2341 cgttcaactgt gacctcaaac cagaaaaatg gttgctagcc tcagctgatc cttttcctca  
2401 ggtgaaactt tgtgattttg gttttgccc gatcattgga gagaagtctt tccggaggtc  
2461 agtgggtggg acccccgtt accctggctcc tgaggtccta aggaacaagg gctcaatcg  
2521 ctctctagac atgtggtctg ttgggtcat catctatgta agcctaagcg gcacattccc  
2581 atttaatgaa gatgaagaca tacacgacca aattcagaat gcagctttca tgtatccacc  
2641 aaatccctgg aaggaaatat ctcatgaagc cattgatctt atcaacaatt tgtgcaagt  
2701 aaaaatgaga aagcgctaca gtgtggataa gaccttgagc caccttggc tacaggacta  
2761 tcagacctgg ttgattttgc gagagctgga atgcaaaatc ggggagcgct acatcaccca  
2821 tgaaagtgat gacctgaggt gggagaagta tgcaggcgag cagcggtgc agtaccacac  
2881 acacctgatc aatccaagt ctagccacag tgacactcct gagactgaag aaacagaat  
2941 gaaagccctc ggtgagcgtg tcagcatcct ctgagttcca tctcctataa tctgtcaaaa  
3001 cactgtggaa ctaataaata catacgtca ggtttaacat ttgcttgca gaactgccat  
3061 tattttctgt cagatgagaa caaagctgtt aaactgttag cactgttgat gtatctgagt  
3121 tgccaagaca aatcaacaga agcattttgta tttgtgtga ccaactgtgt tgtattaaca  
3181 aaagtccctt gaaacacgaa acttgttatt gtgaatgatt catgttatat ttaatgcatt  
3241 aaacctgtct cactgtgcc tttgcaaatc agtgttttct ttaactggagc ttcattttgg  
3301 taagagacag aatgtatctg tgaagtagtt ctggttgggtg tgtccattg gtgtgtcat  
3361 tgttaacaaa ctcttgaaga gtogattatt tccagtgtt tatgaacaac tccaaaaccc  
3421 atgtgggaaa aaaaatgaatg agggggtag ggaataaaat cctaagacac aaatgcatga  
3481 acaagtttta atgtatagtt ttgaatcctt tgcctgcctg gtgtgcctca gtatatataa  
3541 actcaagaca atgcacctag ctgtgcaaga cctagtgtc ttaagcctaa atgccttaga  
3601 aatgtaaaat gccatatata acagatacat ttccctctt cttataatac tctgtgtac  
3661 tatggaaaat cagctgtcga gcaaccttt acccttgtgt atttttcaat aataaaaaat  
3721 attcttgtca aaaaaaaaaa aa

## (2) INFORMATION FOR SEQ ID NO:173:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2705 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

1 tgcctgcctc agggcgcaac catgtcgcca ttcttctgga ttggcttgc caactttgac  
61 tgcgggtcct gccagtcttg tcagggcgag gctgttaacc cttactgtgc tgtgctcgct  
121 aaagagtatg tcgaatcaga gaacggcgag atgtatatcc agaaaaagcc ttacatgtac  
181 ccacctggg acagcacttt tgatgcccc atcaacaagg gaagagtcac gcagatcatt  
241 gtgaaaggca aaaacgtgga cctcatctct gaaaccaccg tggagctcta ctgctggct  
301 gagagggtgca ggaagaacaa cgggaagaca gaaatatggt tagagctgaa acctcaaggc  
361 cgaatgctaa tgaatgcaag atactttctg gaaatgagt acacaaaagg catgaatgaa  
421 tttgagacgg aaggcttctt tgccttgcac cagcgccggg gtgccatcaa gcaggcaaaag  
481 gtccaccacg tcaagtgcga cgagttcact gccaccttct tcccacagcc cacattttgc  
541 tctgtctgcc acgagtttgt ctggggcctg aacaaacagg gctaccagt cgcacaatgc  
601 aatgcagcaa ttcacaagaa gtgtattgat aaagtatatg caaagtgcac aggatcagct  
661 atcaatagcc gagaaccat gttccacaag gagagattca aaattgacat gccacacaga  
721 tttaaagtct acaattacaa gagcccgacc ttctgtgaac actgtgggac cctgtgtgg  
781 ggaactggcag gcgaaggact caagtgtgat gcatgtggca tgaatgtgca tcatagatgc  
841 cagacaaagg tggccaacct ttgtggcata aaccagaagc taatggctga agcgtgtggc  
901 atgattgaga gactcaaca ggctcgctgc ttaagagata ctgaacagat cttcagagaa  
961 ggtccggttg aaattgggtct ccatgtctcc atcaaaaatg aagcaaggcc gccatgttta  
1021 ccgacaccgg gaaaaagaga gcctcagggc atttctctgg agtctccgtt ggtgaggtg  
1081 gataaaaatg gccatcttcc agaaccgtga ctgaacaaag aaagaccatc tctgcagatt  
1141 aaactaaaaa ttgaggattt tatcttgac aaaatgttgg ggaaaggaag ttttggcaag  
1201 gtcttctctg cagaattcaa gaaaaccaat caatttttct caataaaggc cttaaagaaa  
1261 gatgtggtct tgatggacga tgatgttgag tgcacgatgg tagagaagag agttcttctc

1321 ttggggggg agcatccggt tctgacgcac atgtttttgta cattccagac caaggaaaac  
1381 ctcttttttg tgatggagta cctcaacgga ggggacttaa tgtaccacat ccaaagctgc  
1441 cacaagtctg acctttccag agcgacgttt tatgtctgtg aaatcattct tggctctgag  
1501 ttccttcatt ccaaaggaat agtctacagg gacctgaagc tagataacat cctgttagac  
1561 aaagatggac atatacaagat cgcggatttt ggaatgtgca aggagaacat gttaggagat  
1621 gccaaagacga atacctctgt tgggacacct gactacatcg cccagagat cttgtgggt  
1681 cagaaatata accactctgt ggaactgttg tcttcgggg ttctccttta tgaaatgtg  
1741 attggtcagt cgcctttcca cgggcaggat gaggaggagc tcttccactc catccgcatg  
1801 gacaatccct tttaccacg gtggtggag aaggaagcaa aggaccttct ggtgaagctc  
1861 ttcgtgcgag aacctgagaa gaggctgggc gtgaggggag acatccgcca gcaccctttg  
1921 tttcgggaga tcaactggga ggaacttgaa cggaaggaga ttgaccacc gttccggccg  
1981 aaagtgaat caccatttga ctgcagcaat ttcgacaaag aattctttaa cgagaagccc  
2041 cggctgtcat ttgccgacag agcactgata aacagcatgg accagaatat gttcaggaac  
2101 ttttcttca tgaaccccg gatggagcgg ctgatctct gaatcttgcc cctccagaga  
2161 caggaaagaa tttgccttct cctgggaac tggttcaaga gacctgctt gggttcctt  
2221 ttcaacttgg aaaaagaaag aaacactcaa caataaagac tgagaccgtt tcgccccat  
2281 gtgactttat ctgtagcaga aaccaagtct acttacttaa tgacgtatc gtgtgtctg  
2341 tctcctgaca tgtctcacag acgtctctga agttaggta ttactaacca tagttattta  
2401 cttgaaagat gggctctccg acttggaag gtttcaagac ttgatactgc aataaattat  
2461 ggctcttcac ctgggcgcca actgctgata aacgaaatgc ttgttgaatc aggggcaaac  
2521 ggagtacaga cgtctcaaga ctgaaacggc cccattgcct ggtctagtag cggatctcac  
2581 tcagccgag acaagtaatc actaaccgt tttattctat cctatctgtg gatgtataaa  
2641 tgcgtggggc cagccctgga taggttttta tgggaattct ttacaataaa catagcttgt  
2701 acttg

## (2) INFORMATION FOR SEQ ID NO:174:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1779 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

1 atgccagca ggaccgacc caagatggaa gggagcggcg gccgcgtccg cctcaaggcg  
61 cattacgggg gggacatctt catcaccagc gtggagcccg ccacgacctt cgaggagctc  
121 tgtgaggaag tgagagacat gtgtcgtctg caccagcagc acccgctcac cctcaagtgg  
181 gtggacagcg aaggtgaccc ttgcacggtg tctctccaga tggagctgga agaggctttc  
241 cgcctggccc gtcagtgcag ggatgaaggc ctcatcattc atgttttccc gagcaccctt  
301 gagcagcctg gcctgccatg tccgggagaa gacaaatcta tctaccgccc gggagccaga  
361 agatggagga agctgtaccg tgccaacggc cactcttccc aagccaagcg ctttaacagg  
421 agagcgtact gcggtcagtg cagcgagagg atatggggcc tcgcgaggca aggtacagg  
481 tgcatacaact gcaaaactgt ggtccataag cgctgccacg gcctcgtccc gctgacctgc  
541 aggaagcata tggattctgt catgccttcc caagagcctc cagtagacga caagaacgag  
601 gacgccgacc ttccttccga ggagacagat ggaattgctt acatttcttc atcccggaa  
661 catgacagca ttaaagacga ctcgaggagc cttaaagccag ttatcgatgg gatggatgga  
721 atcaaaatct ctcaggggct tgggtgcgag gactttgacc taatcagagt catcgggcgc  
781 gggacgtacg ccaaggttct cctggtgcgg ttgaagaaga atgaccaa attacgccatg  
841 aaagtgttga agaaagagct ggtgcatgat gacgaggata ttgactgggt acagacagag  
901 aagcacgtgt ttgagcaggc atccagcaac cccttctctg tcggattaca ctctgcttc  
961 cagacgacaa gtcggttgtt cctggtcatt gactacgtca acggcgggga cctgatgttc  
1021 cacatgcaga ggcagaggaa gctccctgag gagcagccca ggttctacgc gcccagatc  
1081 tgcacgccc tcaacttctt gcacgagagg gggatcatct acagggacct gaagctggac  
1141 aacgtcctcc tggatcgga cggacacatc aagctcacag actacggcat gtgcaaggaa  
1201 ggctggggcc ctggtgacac aacgagcact ttctgcggaa ccccgaaata catcgcccc  
1261 gaaatcctgc ggggagagga gtacgggttc agcgtggact ggtgggcgtc gggagtcttc  
1321 atgttttga tgatggccgg gcgtctccc ttcgacatca tcaccgacaa cccgagatg  
1381 aacacagagg actacctttt ccaagtgtat ctggagaagc ccatccggat ccccggttc  
1441 ctgtccgtca aagcctcca tgttttaaaa ggatttttaa ataaggacct caaagagagg  
1501 ctgggtgcc ggccacagac tggattttct gacatcaagt cccacgcgtt cttccgcagc  
1561 atagactggg acttgctgga gaagaagcag gcgtccctc cattccagcc acagatcaca  
1621 gacgactacg gtctggacaa cttgacaca cagttcacca gcgagccgt gcagctgacc  
1681 ccagacgatg aggatgcat aaagaggatc gaccagtcag agttcgaagg ctttgagtat  
1741 atcaaccat tattgtgtc caccgaggag tcggtgtga

## (2) INFORMATION FOR SEQ ID NO:175:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

1 tgtcatgcct tccaagagc ctccaggatg gctgtcctcc gacctcctcc acctccaggc  
61 tctagatggc aaagcccact tagcaaaagc cacctgctct gtgatgatgg gactggctcc  
121 tgcctgtggg ttcggaaagc ccatccacc ctctacagcc tcttgcctct ctgcaatgac

181 tgtgccc cctgggggtt cccagagac tagtgagagt cgcgt ggaagctat

## (2) INFORMATION FOR SEQ ID NO:176:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38634 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

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121 cagcaggtga aggaccacaa attcatcgcg cgcttcttca agcagccac cttctgcagc  
181 cactgcaccg acttcatctg ggggtttggg aaacaaggct tccagtgcc agtttgctgt  
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## (2) INFORMATION FOR SEQ ID NO:177:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1649 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

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901 ttactcaciaa gggcattccc atggcagcca gcaatttgct cgtcaactac ccagtggggg  
961 ccccagacca catctctgtg aagcagtgcc tgctggccat cctaactctg gcgtgggtgg  
1021 ccactatctt ctctgtgtgc actgtgggtg tggcggtccg cctctcccg caggggccaca  
1081 tgtaacccgt gcgtaattac tccccaccg agatgggtct catctcatcc ctgttgctg  
1141 atgggggtga ggggccctct gccacagcca atgggggcct gtccaaggcc aagagcccg  
1201 gcctgacgcc agagcccagg gaggaccgtg agggggatga cctcaccctg cacagcttcc  
1261 tcccttagct cactctgcca tctgttttgg caagacccca cctccacggg ctctcctggg  
1321 ccacccctga gtgccagac cccaatccac agctctgggc ttcctcggag acccctgggg  
1381 atggggatct tcagggaagg aactctggcc acccaaacag gacaagagca gcctggggcc  
1441 aagcagacgg gcaagtggag ccacctcttt cctccctccg cggatgaagc ccagccacat  
1501 ttcagccgag gtccaaggca ggaggccatt tacttgagac agattctctc ctttttctg  
1561 tcccccatct tctctgggtc cctctaacat ctcccatggc tctccccgt tctcctggtc  
1621 actggagtct cctcccatg tacccaagg

## (2) INFORMATION FOR SEQ ID NO:178:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 703 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

1 ccaccaatct tgggcaagaa gcgagaccat tctctttttt ctctggtcac tctgtcctt  
61 cagggggctc cctctggccc cgactgtcca ttgtgtctga agtaatgtg tggcctttct  
121 cagtttgggc cccacccaaa accgaagaac ttctcccag aagcttctac ttgtttctca  
181 gtgttttcac agttatggga acccaagaac agtgtcagac ctaggagggtg cccactacc  
241 accctgtctt tatcaatgtt gtcaccaaag ctgtcacaaa caatgggggtg tgggctgtca  
301 catggccctg cctaagtaac cacattctcg cttcctctt ccacacacag ccattggggg  
361 ttgtctggat ccgggactgc cgcagggggt gccacagcag tgcctggcag cgtgggctgg  
421 gaccttgtca ctaaagcaga gaagccactt cttctgggcc cagcaggcag ctgtcccatg  
481 cttgtctgag cacggtggta agtgcctggc tgcaaaaacca cagggagtgg ctggagggtc  
541 ccatggggcca agggcctgccc ttatagctgc tggcagggccc gggtaggacc gccaggccct  
601 tcttgagctg cagcacctgg ggagggcaaa ctgaggctcc tccgactcaa gactaaagtc  
661 ttcttgaggt ctgtggcctt attctgtgac tcttctgaat cct

## (2) INFORMATION FOR SEQ ID NO:179:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3409 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

1 tagaagaagt taaaggggccc tcttggtggt ctttattcat gttgatgagt aataataata  
61 actgctactg gctgaggatc ttctccatcc caggcatgtc agggatgcct aagtccccag  
121 tcctgtctcc agaccagaca tcttcagct gtggcagtag aggggtgggtg tctagggtgc  
181 ttgctaagcc caagggtgaa actgtcttga catccctccg cccattgtct cctcctaggt  
241 gccatgcctc tgcaactcct cctgtgtctg atcctactgg gccctggcaa cagcttgacg  
301 ctgtgggaca cctgggcaga tgaagccgag aaagccttgg gtccctgtg tgcccgggac  
361 cggagacagg ccaccgaata tgagtaccta gattatgatt tcttgccaga aacggagcct  
421 ccagaaatgc tgaggaacag cactgacacc actcctctga ctgggcctgg aacccttag  
481 tctaccactg tggagcctgc tgcaaggcgt tctactggcc tggatgcagg aggggcagtc  
541 acagagctga ccacggagct ggccaacatg gggaacctgt ccacggattc agcagctatg  
601 gagatacaga ccaactcaacc agcagccacg gaggcacaga ccaactcaacc agtgcacag  
661 gaggcacaga ccaactccact ggcagccaca gaggcacaga caactcgact gacggccacg  
721 gaggcacaga ccaactccact ggcagccaca gaggcacaga ccaactccacc agcagccacg  
781 gaagcacaga ccaactcaacc cacaggcctg gaggcacaga ccaactgcacc agcagccatg  
841 gaggcacaga ccaactgcacc agcagccatg gaagcacaga ccaactccacc agcagccatg  
901 gaggcacaga ccaactcaaac cacagccatg gaggcacaga ccaactgcacc agaagccacg  
961 gaggcacaga ccaactcaacc cacagccacg gaggcacaga ccaactccact ggcagccatg  
1021 gaggccctgt ccacagaacc cagtggcaca gaggccctgt ccatggaaacc tactaccaaa  
1081 agaggctctg tcataccctt ttctgtgtcc tctgttactc acaagggcat tcccatggca  
1141 gccagcaatt tgcctgtcaa ctaccagtg ggggccccag accacatctc tgtgaagcag  
1201 tgctgtctgg ccatcctaatt cttggcgctg gtggccacta tcttctctgt gtgactgtg  
1261 gtgctggcgg tccgcctctc ccgcaagggc cacatgtacc ccgtgcgtaa ttactcccc  
1321 accgagatgg tctgtctctc atccctgttg cctgatgggg gtgagggggc ctctgccaca  
1381 gccaatgggg gctgttccaa ggccaagagc cggggcctga cggcagagcc cagggaggac  
1441 cgtgaggggg atgacctcac cctgcacagc ttctcctctt agctcactct gccatctgtt  
1501 ttggcaagac cccacctcca cgggtctctc tgggcccacc ctgagtggcc agaccaccaat  
1561 ccacagctct gggcttctct ggagaccctt ggggatgggg atcttcaggg aaggaaactct  
1621 ggccacccaa acaggacaag agcagcctgg ggccaagcag acgggcaagt ggagccacct  
1681 ctttctctcc tccgcgatg aagcccagcc acatttcagc cgagggtcaa ggcaggaggc



1741 catctttg agacagattc tctcttttt cctgtcccc accttctctg ggtccctcta  
1801 acatctccca tggctctccc cgcttctcct ggtcactgga gtctcctccc catgtaccca  
1861 aggaagatgg agctccccc tcccacacgc actgcactgc cattgtcttt tggttgccat  
1921 ggtcaccaaa caggaagtgg acattctaag ggaggagtac tgaagagtga cggacttctg  
1981 aggctgtttc ctgctgctcc tctgacttgg ggcagcttgg gtcttcttgg gcacctctct  
2041 gggaaaaccc aggggtgaggt tcagcctgtg agggctggga tgggtttcgt gggcccaaac  
2101 ggcagacctt tctttgggac tgtgtggacc aaggagcttc catctagtga caagtgaacc  
2161 ccagctatcg cctcttgcc tccctgtgg ccactttcca ggggtggactc tgtcttgttc  
2221 actgcagtat cccaactgca ggtccagtgc aggcataaaa tatgtgatgg acaaacgat  
2281 agcggaaatcc ttcaaggttt caaggctgtc tccctcaggc agccttcccc gaattctcca  
2341 tccctcagtg caggatgggg gctggctcct agctgtctgc cctcagcccc tggcccccca  
2401 ggaagcctct ttcattgggt gttaggttga cttcagtttt gcctcttggg caacaggggg  
2461 tcttgtacat ccttgggtga ccaggaaaag ttcaggctat ggggggcca agggagggt  
2521 gcccttccc caccagtgc cactttattc cacttctcc attaccagt tttggccac  
2581 agagtttggg cccccccaaa cctcggacca atatcctct aaacatcaat ctatcctcct  
2641 gttaaagaaa aaaaaaatg ggactgggag cagtggctca tgcctgtaat cccagcactt  
2701 tgggagggcg aggcaggtac atcacctgag gtcaggagtt caagactagc ctggccaaca  
2761 tagtgaaacc ctgtctctac taaaaataca aagattagtc aggtgtgggtg gcacatgcct  
2821 gtagtccag ctactgggga ggctgaggca ggagaattgc ttgaaccgg gaagcggagg  
2881 gaggttgag tgagctgaga tcacgctact gactccagc ctgggtgaca gtagaagact  
2941 ccgtctcaaa aaaaaaaaaa aagattcaat gacccttgtt aaagcatggt aaggaagact  
3001 ttgttcaagg ggagtgggac tcttcaatc actgcaggga ctgcagctat gggatttgc  
3061 agtgggggca tttgggctca actatgagta cagcaggggc aagtgggagc tgatagccag  
3121 ggaacagggt tggatatctg cagctggaaa attaccaaga ggaacatca ggggaagggg  
3181 aattctggct aaactgactg ctggggatgg gttctcggtc attttctaca ctgacctaac  
3241 aggattcata ctggaggcag gccagggtgc tcagacatca ccggggggat ggtggcagat  
3301 gaggaacgtg atcagatata ggaggtgatc agatatggga ggtgatcaga tatggagtgg  
3361 tggggggagg gttgttgcta agctgactta gcagagttct tgttagaac

## (2) INFORMATION FOR SEQ ID NO:180:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3409 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

1 tagaagaagt taaaggggccc tcttgatgg ctttattcat gttgatgagt aataataata  
61 actgtactg gctgaggatc ttctccatcc caggcatgtc agggatgcct aagtccccag  
121 tccctgtccc agaccagaca tcttccagct gtggcagtag aggggtgggtg tctaggggtg  
181 ttgctaagcc caagggtgaa actgtcttga catccctccg cccattgtct cctctaggt  
241 gccatgcctc tgcaactcct cctgttctg atcctactgg gccctggcaa cagcttgag  
301 ctgtgggaca cctgggcaga tgaagccgag aaagccttgg gtccccgtct tggccgggac  
361 cggagacagg ccaccgaata tgagtaccta gattatgatt tcttgccaga aacggagcct  
421 ccagaaatgc tgaggaacag cactgacacc actcctctga ctgggcctgg aaccctgag  
481 tctaccactg tggagcctgc tgcaaggcgt tctactggcc tggatgcagg aggggcagtc  
541 acagagctga ccacggagct ggccaacatg gggaacctgt ccacggattc agcagctatg  
601 gagatacaga ccaactcaacc agcagccacg gaggcacaga ccaactcaacc agtggccacg  
661 gaggcacaga ccaactccact ggcagccaca gaggcacaga caactcgact gacggccacg  
721 gaggcacaga ccaactccact ggcagccaca gaggcacaga ccaactccacc agcagccacg  
781 gaagcacaga ccaactcaacc cacaggcctg gaggcacaga ccaactgcacc agcagccatg  
841 gaggcacaga ccaactgcacc agcagccatg gaagcacaga ccaactccacc agcagccatg  
901 gaggcacaga ccaactcaaac cacagccatg gaggcacaga ccaactgcacc agaagccacg  
961 gaggcacaga ccaactcaacc cacagccacg gaggcacaga ccaactccact ggcagccatg  
1021 gaggccctgt ccacagaacc cagtgccaca gaggccctgt ccatggaacc tactacaaa  
1081 agaggctctg tcataccctt ttctgtgtcc tctgttactc acaagggtcat tcccatggca  
1141 gccagcaatt tgtccgtcaa ctaccagtg ggggccccag accacatctc tgtgaagcag  
1201 tgcctgttgg ccattccta ctgtggcgtg gtggccacta tcttctctgt gtgactgtg  
1261 gtgctggcgg tccgcctctc ccgcaagggc cacatgtacc ccgtgcgtaa ttactcccc  
1321 accgagatgg tctgcatctc atccctgttg cctgatgggg gtgagggggc ctctgccaca  
1381 gccaatgggg gcctgtccaa ggccaagagc ccgggcctga cgccagagcc caggaggagc  
1441 cgtgaggggg atgacctcac cctgcacagc ttctccctt agctcactct gccatctgtt  
1501 ttggcaagac cccacctcca cgggctctcc tgggcccacc ctgagtggcc agaccccaat  
1561 ccacagctct gggcttcttc ggagaccctt ggggatgggg atcttcaggg aaggaactct  
1621 ggccacccaa acaggacaag agcagcctgg ggccaagcag acgggcaagt ggagccacct  
1681 ctttctctcc tccgcgatg aagcccagcc acatttcagc cgaggtccaa ggcaggaggc  
1741 catttacttg agacagattc tctcttttt cctgtcccc atcttctctg ggtccctcta  
1801 acatctccca tggctctccc cgcttctcct ggtcactgga gtctcctccc catgtaccca  
1861 aggaagatgg agctccccc tcccacacgc actgcactgc cattgtcttt tggttgccat  
1921 ggtcaccaaa caggaagtgg acattctaag ggaggagtac tgaagagtga cggacttctg  
1981 aggctgtttc ctgctgctcc tctgacttgg ggcagcttgg gtcttcttgg gcacctctct  
2041 gggaaaaccc aggggtgaggt tcagcctgtg agggctggga tgggtttcgt gggcccaaac



2101 ggcagc tctttgggac tgtgtggacc aaggagcttc cagtga caagtgaccc  
2161 ccagctatcg cctcttgccct tcccctgtgg ccactttcca ggcagctc tgtcttgctc  
2221 actgcagtat cccaactgca ggtccagtg aggcataaaa tatgtgatgg acaaaacgat  
2281 agcggaaatcc ttcaaggttt caaggctgtc tccctcaggc agccttcccg gaattctcca  
2341 tccctcagtg caggatgggg gctggctctc agctgtctgc cctcagcccc tggcccccca  
2401 ggaagcctct ttcattgggt gtttaggttga cttcagtttt gcctcttga caacaggggg  
2461 tcttgtacat ccttgggtga ccaggaaaag ttcaggctat ggggggcaa agggagggt  
2521 gcccctccc caccagtgc cactttattc cacttcctcc attaccagtt tttggccac  
2581 agagtttggt ccccccaaaa cctcggacca atatccctct aaacatcaat ctatcctct  
2641 gttaaagaaa aaaaaaatg ggactgggag cagtggctca tgctgtaat cccagcactt  
2701 tgggagggcg aggcaggtac atcacctgag gtcaggagtt caagactagc ctggccaaca  
2761 tagtgaacc ctgtctctac taaaaataga aagattagtc aggtgtgtg gcacatgcct  
2821 gtatgccag ctactggga ggctgaggca ggagaattgc ttgaacccg gaagcggagg  
2881 gaggttgag tgagctgaga tcacgtact gcactccagc ctgggtgaca gagtaagact  
2941 cctgtcaca aaaaaaaaaa aagattcaat gacccttgtt aaagcatggt aaggaagact  
3001 ttgttcaagg ggagtgggac tctctcaatc actgcaggga ctgcagctat gggattttgc  
3061 agtgggggca tttgggtcga actatgagta cagcaggggc aagtgggagc tgatagccag  
3121 ggaacagggt tggatatctg cagctggaaa attaccaaga ggaaacatca ggggaagggg  
3181 aattctggct aaactgactg ctggggatgg gttctcgtc attttctaca ctgacctaac  
3241 aggattcata ctggaggcag gccagggtgc tcagacatca ccgggggat ggtggcagat  
3301 gaggaacgtg atcagatata ggaggtgatc agatatggga ggtgatcaga tatggagtgg  
3361 tggggggagg gttgttgcta agctgactta gcagagttct tgttagaac

## (2) INFORMATION FOR SEQ ID NO:181:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9170 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

1 gccactctct ctggggccac gaggcagctg tcccatgctc tgctgagcac ggtggtgcca  
61 tgccctctgca actcctcctg ttgtgatcc tactgggccc tggcaacagc ttgcagctgt  
121 gggacacctg ggcagatgaa gccagaaaag ccttgggtcc cctgttgcc cgggaccgga  
181 gacagggcac cgaatatgag tacctagatt atgatttcct gccagaaacg gacccctcag  
241 aaatgctgag gaacagcact gacaccactc ctctgactgg gcctggaacc cctgagtcta  
301 ccactgtgga gcctgctgca aggcgttcta ctggcctgga tgcaggaggg gcagtcacag  
361 agctgaccac ggagctggcc aacatgggga acctgtccac ggattcagca gctatggaga  
421 tacagaccac tcaaccagca gccacggagg cacagaccac tccactggca gccacagagg  
481 cacagaccac tgcactgacg gccacggagg cacagaccac tccactggca gccacagagg  
541 cacagaccac tccaccagca gccacggaag cacagaccac tcaaccaca ggccctggagg  
601 cacagaccac tgcaccagca gccatggagg cacagaccac tgcaccagca gccatggaag  
661 cacagaccac tccaccagca gccatggagg cacagaccac tcaaccaca gccatggagg  
721 cacagaccac tgcaccagaa gccacggagg cacagaccac tcaaccaca gccacggagg  
781 cacagaccac tccactggca gccatggagg cctgtgccac agaaccaggt gccacagagg  
841 cctgttccat ggaacctact accaaaagag gtctgttcat acccttttct gtgtcctctg  
901 ttactcaca gggcattccc atggcagcca gcaatttgc ctgcaactac ccagtggggg  
961 cccagacca catctctgtg aagcagtgc tgctggccat cctaattctg gcgctggtg  
1021 ccactatctt ctctgtgtgc actgtgtgtg tggcggtccg cctctcccg aagggccaca  
1081 tgtaccccg gcgttaattac tccccaccg agatggtctg catctcatcc ctgtgctg  
1141 atgggggtga ggggccctct gccacagcca atgggggct gtccaaggcc aagagcccg  
1201 gcctgacgcc agagcccagg gaggaccgtg agggggatga cctcaccctg cacagcttcc  
1261 tcccttagct cactctgcca tctgttttgg caagacccca cctccacggg ctctcctggg  
1321 cccccctga gtgcccagac cccaatccac agctctgggc ttcctcggag acccctgggg  
1381 atggggatct tcagggaagg aactctggcc acccaaacag gacaagagca gcctggggcc  
1441 aagcagacgg gcaagtggag ccacctcttt cctccctccg cggatggaag ccagccacat  
1501 ttcagccgag gtccaaggca ggaggccatt tacttgagac agattctctc ctttttctg  
1561 tccccatct tctctgggtc cctctaact ctcccatggc tctccccgt tctcctggtc  
1621 actggagtct cctccccatg tacccaagg  
1 ccaccaatct tgggcaagaa gcgagaccat tctccttttt ctctggtcac tctgtcctt  
61 cagggggctc cctctggccc cgactgtcca ttgctgtga agtaatgctg tggcctttct  
121 cagtttgggc cccacccaaa accgaagaac ttctccccag aagcttctac ttggttctca  
181 gtgttttcac agttatggga acccaagaac agtgcagac ctaggagggtg cccactacc  
241 accctgtctt tatcaatgtt gtcaccaaag ctgtcacaac caatgggggtg tgggctgtca  
301 catggccctg cctaagtaac cacattctcg cttcctcctt ccacacacag ccattggggg  
361 ttgctcggat cgggactgc cgcagggggt gccacagcag tgctggcag cgtgggtgg  
421 gaccttgtca ctaaaagcaga gaagccactt cttctgggccc cagcaggcag ctgtcccatg  
481 ctctgctgag caggtgtgta agtgcgtggt tgcaaaacca cagggagtg ctggaggtcc  
541 ccatgggcca agggcctgcc ttatagctgc tggcaggccc gggtaggacc gccaggccct  
601 tcttgagctg cagcacctgg ggagggcaaa ctgaggctcc tccgactcaa gactaaagtc  
661 ttctggagt ctgtggcctt attctgtgac tcttctgaat cct  
1 tagaagaagt taaagggccc tcttgatgg ctttattcat gttgatgagt aataataata  
61 actgctactg gctgaggatc ttctccatcc caggcatgtc agggatgctt aagtcctccag  
121 tccctgctcc agaccagaca tcttcagct gtggcagtag aggtggtgg tctagggtgc

181 ttgcggcc caaggggtgaa actgtcttga catccctccg cttattgtct cctcctaggt  
241 gccatgcctc tgcaactcct cctgttgctg atcctactgg gccctggcaa cagcttgacg  
301 ctgtgggaca cctgggcaga tgaagccgag aaagccttgg gtccctgtct tgcccgggac  
361 cggagacagg ccaccgaata tgagtacctt gattatgatt tcctgccaga aacggagcct  
421 ccagaaatgc tgaggaacag cactgacacc actcctctga ctgggccttg aacccttgag  
481 tctaccactg tggagcctgc tgcaaggcgt tctactggcc tggatgcagg aggggcagtc  
541 acagagctga ccacggagct ggccaacatg gggaaacctgt ccacggattc agcagctatg  
601 gagatacaga ccactcaacc agcagccacg gaggcacaga ccactcaacc agtgcccacg  
661 gaggcacaga ccactccact ggcagccaca gaggcacaga caactcgact gacggccacg  
721 gaggcacaga ccactccact ggcagccaca gaggcacaga ccactccacc agcagccacg  
781 gaagcacaga ccactcaacc cacaggcctg gaggcacaga ccactgcacc agcagccatg  
841 gaggcacaga ccactgcacc agcagccatg gaagcacaga ccactccacc agcagccatg  
901 gaggcacaga ccactcaaac cacagccatg gaggcacaga ccactgcacc agaagccacg  
961 gaggcacaga ccactcaacc cacagccacg gaggcacaga ccactccact ggcagccatg  
1021 gaggccctgt ccacagaacc cagtgccaca gaggccctgt ccatggaacc tactacaaa  
1081 agaggtctgt tcataccctt ttctgtgtcc tctgttactc acaaggcat tcccatggca  
1141 gccagcaatt tgtccgtcaa ctaccagtg ggggccccag accacatctc tgtgaagcag  
1201 tgectgtctg ccactcctaat cttggcgctg gtggccacta tcttcttctg gtgactgtg  
1261 gtgctggcgg tccgcctctc ccgcaagggc cacatgtacc ccgtgcgtaa ttactcccc  
1321 accgagatgg tctgcacttc atccctgttg cctgatgggg gtgagggggc ctctgccaca  
1381 gccaatgggg gctgtccaa ggccaagagc ccgggcctga cgccagagcc caggaggagc  
1441 cgtgaggggg atgacctcac cctgcacag ttctccctt agctcactct gccatctgtt  
1501 ttggcaagac ccacctcca cgggctctcc tgggccacc ctgagtgcct agacccaat  
1561 ccacagctct gggcttctc ggagaccctt ggggatgggg atcttcaggg aaggaactct  
1621 ggccacccaa acaggacaag agcagcctgg ggccaagcag acgggcaagt ggagccacct  
1681 ctttctctcc tccgcggatg aagccagcc acatttcagc cgaggtccaa ggcaggaggc  
1741 catttacttg agacagattc tctcttttt cctgtccccc atcttctctg ggtccctcta  
1801 acatctccca tggctctccc cgttctctct ggtcactgga gtctctctcc catgtacca  
1861 aggaagatgg agctcccca tcccacacgc actgcactgc cattgtcttt tgggtgccat  
1921 ggtcaccaaa caggaagtgg acattctaag ggaggagtac tgaagagtga cggacttctg  
1981 aggtctgttc ctgctgtctc tctgacttgg ggcagcttgg gtcttcttctg gcacctctct  
2041 gggaaaaccc aggtgtgagt tcagcctgtg agggctggga tgggtttctg gggcccaag  
2101 ggcagacctt tctttgggac tgtgtggacc aaggagcttc catctagtga caagtgacct  
2161 ccagctatcg cctcttgctt tcccctgtgg ccactttcca ggggtggact tgtctgttct  
2221 actgcagtat cccaactgca ggtccagtgc aggaataaaa tatgtgatgg aaaaacgat  
2281 agcggaaatc ttcaaggttt caaggtgtgc tecttcaggc agccttcccc gaattctcca  
2341 tectcagtg caggatgggg gctgttctc agctgtctgc cctcagcccc tggcccccca  
2401 ggaagcctct ttcatgggct gttaggttga cttcagtttt gcctcttggg caacaggggg  
2461 tcttgtacat ccttgggtga ccaggaagaa ttcaggctat ggggggcca agggagggt  
2521 gccccttccc caccagtgc cactttatt cacttctctc attaccaggt tttggccac  
2581 agagtttggg ccccccaaaa cctcggacca atatccctct aaacatcaat ctatctctct  
2641 gttaaagaaa aaaaaaaatg ggaactggag cagtggctca tgcctgtaat cccagcactt  
2701 tgggaggccg aggcaggtac atcacctgag gtcaggagtt caagactagc ctggccaaca  
2761 tagtgaaacc ctgtctctac taaaaataca aagattagtc aggtgtgggt gcacatgcct  
2821 gtatgccag ctactgggga ggtgaggca ggagaattgc ttgaacccgg gaagcggagg  
2881 gaggttgacg tgagctgaga tcacgtact gcactccagc ctgggtgaca gtagaagact  
2941 ccgtctcaaa aaaaaaaatg aagattcaat gacccttgtt aaagcatggt aaggaagact  
3001 ttgttcaagg ggagtgggac tctctcaatc actgcaggga ctgcagctat gggattttgc  
3061 agtgggggca tttgggctca actatgagta cagcaggggc aagtgggagc tgatagccag  
3121 ggaacagggt tggatatctg cagctggaaa attaccaaga ggaacatca ggggaagggt  
3181 aattctggct aaactgactg ctggggatgg gttctcgttc attttctaca ctgacctaac  
3241 aggatcata ctggaggcag gccagggtgc tcagacatca ccggggggt ggtggcagat  
3301 gaggaacgtg atcagatata ggaggtgac agatagggga ggtgatcaga tatggagtgg  
3361 tggggggagg gttgttgcta agctgactta gcagagttct tgttagaac  
1 tagaagaagt taaaggccc tctggatgg ctttattcat gttgatgagt aataataata  
61 actgctactg gctgaggatc ttctccatcc caggcatgtc agggatgect aagtccccag  
121 tccctgtctc agaccagaca tcttccagct gtggcagtag aggggtgggt tctagggtgc  
181 ttgctaagcc caaggggtgaa actgtcttga catccctccg cccattgtct cctcctaggt  
241 gccatgcctc tgcaactcct cctgttgctg atcctactgg gccctggcaa cagcttgacg  
301 ctgtgggaca cctgggcaga tgaagccgag aaagccttgg gtccctgtct tgcccgggac  
361 cggagacagg ccaccgaata tgagtacctt gattatgatt tcctgccaga aacggagcct  
421 ccagaaatgc tgaggaacag cactgacacc actcctctga ctgggccttg aacccttgag  
481 tctaccactg tggagcctgc tgcaaggcgt tctactggcc tggatgcagg aggggcagtc  
541 acagagctga ccacggagct ggccaacatg gggaaacctgt ccacggattc agcagctatg  
601 gagatacaga ccactcaacc agcagccacg gaggcacaga ccactcaacc agtgcccacg  
661 gaggcacaga ccactccact ggcagccaca gaggcacaga caactcgact gacggccacg  
721 gaggcacaga ccactccact ggcagccaca gaggcacaga ccactccacc agcagccacg  
781 gaagcacaga ccactcaacc cacaggcctg gaggcacaga ccactgcacc agcagccatg  
841 gaggcacaga ccactgcacc agcagccatg gaagcacaga ccactccacc agcagccatg  
901 gaggcacaga ccactcaaac cacagccatg gaggcacaga ccactgcacc agaagccacg  
961 gaggcacaga ccactcaacc cacagccacg gaggcacaga ccactccact ggcagccatg  
1021 gaggccctgt ccacagaacc cagtgccaca gaggccctgt ccatggaacc tactacaaa  
1081 agaggtctgt tcataccctt ttctgtgtcc tctgttactc acaaggcat tcccatggca  
1141 gccagcaatt tgtccgtcaa ctaccagtg ggggccccag accacatctc tgtgaagcag  
1201 tgectgtctg ccactcctaat cttggcgctg gtggccacta tcttcttctg gtgactgtg

1261 gtgctg tccgcctctc ccgcaagggc cacatgtacc cc gtaa ttactcccc  
1321 accgagatgg tctgcatctc atccctgttg cctgatgggg gt gggc ccttgccaca  
1381 gccaatgggg gcctgtccaa ggccaagagc ccgggctga cgccagagcc cagggaggac  
1441 cgtgaggggg atgacctcac cctgcacagc ttcctccctt agctactct gccatctgtt  
1501 ttggcaagac cccacctcca cgggctctcc tggggcacc ctagtgccc agacccaat  
1561 ccacagctct gggcttctc ggagaccct ggggatgggg atcttcaggg aaggaactct  
1621 gggcacccaa acaggacaag agcagcctgg ggccaagcag acgggcaagt ggagccact  
1681 ctttctccc tccgcggatg aagcccagcc acatttcagc cgaggccaa ggaggaggc  
1741 catttacttg agacagattc tctcttttt cctgtcccc atcttctctg ggtccctcta  
1801 acatctccca tggctctccc cgcttctcct ggtcactgga gtctctccc catgtacca  
1861 aggaagatgg agctcccca tcccacacgc actgcactgc cattgtcttt tgggtgccat  
1921 ggtcaccaaa caggaagtgg acatttcaag ggaggagtac tgaagagtga cggacttctg  
1981 aggcgtgtttc ctgctgctcc tctgacttgg ggcagcttgg gtcttcttgg gcactctct  
2041 gggaaaaccc agggtagagt tcagcctgtg agggctggga tgggttctgt gggccaaag  
2101 ggcagacctt tctttgggac tgtgtggacc aaggagcttc catctagtga caagtgacc  
2161 ccagctatcg cctcttgcc tcccctgttg ccactttcca ggggtggactc tgtctgttc  
2221 actgcagtat cccaactgca ggtccagtgc aggaataaa tatgtgatg aaaaaacgat  
2281 agcggaatcc tcaaggttt caaggctgtc tcttcaggc agccttccc gaatttcca  
2341 tccctcagtg caggatgggg gctggctctc agctgtctgc cctcagcccc tggccccc  
2401 ggaagcctct tcatgggct gttaggttga cttcagtttt gcctcttga caacaggggg  
2461 tctgtacat ccttgggtga ccaggaaaag ttcaggctat ggggggcaa agggagggt  
2521 gcccttccc caccagtgc cactttatc cacttctcc attaccagt tttggcccac  
2581 agagtgttgg ccccccaaa cctcgacca atatccctc aaacatcaat ctatctctc  
2641 gttaaagaaa aaaaaaatg ggactgggag cagtggctca tgctgtaat cccagcactt  
2701 tgggagggcg aggcaggtac atcacctgag gtcaggagt caagactagc ctggccaaca  
2761 tagtgaaacc ctgtctctac taaaaataca aagattagtc aggtgtgttg gcacatgcct  
2821 gtatcccg ctactgggga ggtgaggca ggagaattgc ttgaacccgg gaagcggagg  
2881 gaggttgcag tgagctgaga tcagctact gcactccagc ctgggtgaca gactaagact  
2941 ccgtctcaaa aaaaaaaaaa aagattcaat gaccctgtt aaagcaggt aaggaagact  
3001 ttgttcaagg ggagtgggac tctctcaatc actgcaggga ctgcagctat gggattttgc  
3061 agtgggggca tttgggctca actatgagta cagcaggggc aagtgggagc tgatagccag  
3121 ggaacagggt tggatatctg cagctggaaa attaccaaga ggaacatca ggggaagggg  
3181 aattctggct aaactgactg ctgggagtgg gttctcggtc atttctaca ctgacctaac  
3241 aggttcata ctggaggcag gccagggtgc tcagacatca ccgggggat ggtggcagat  
3301 gaggaacgtg atcagatata ggaggtgatc agatatggga ggtgatcaga tatggagtgg  
3361 tggggggagg gttgttgcta agctgactta gcagagttct tgttagaac

## (2) INFORMATION FOR SEQ ID NO:182:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1830 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

1 cctgcctgca cggcacagga gagcaactt ctacagacag accaaggctt ccatttgcgtg  
61 ctgacacatg gaactgaggt gaaattgtgc tccatgattt tacagatttc ataacgttta  
121 agagacggga ctcaggtcat caaaatgaaa gccctcatct ttgcagctgc tggcctcctg  
181 cttctgttgc ccactttttg tcagagtggc atggaaaatg atacaaaca cttggcaaa  
241 ccaaccttac ccattaagac cttctgtgga gctccccaa attctttga agagtcccc  
301 ttttctgcct tggaaaggctg gacaggagcc acgattactg taaaaattaa gtgcctgaa  
361 gaaagtgtct cacatctcca tgtgaaaaat gctaccatgg ggtacctgac cagctctta  
421 agtactaaac tgatacctgc catctacctc ctgggtgttg tagttgtgt cccggccaat  
481 gctgtgaccc tgtggatgct tttcttcagg accagatcca tctgtaccac tgtattctac  
541 accaacctgg ccattgcaga tttcttttt tgtgttacat tgcctttta gatagcttat  
601 catctcaatg ggaacaactg ggtattttga gaggtcctgt gccgggccac cacagtcatc  
661 ttctatggca acatgtactg ctccattctg ctccctgctt gcatcagcat caaccgctac  
721 ctggccatcg tccatccttt cacctaccgg ggctgccc agcacaccta tgccttggtg  
781 acatgtggac tgggtgtggc aacagttttc ttatatatgc tgccatttt cactactgag  
841 caggaatatt atcttgttca gccagacatc accacctgcc atgatgttca caacacttgc  
901 gagtccctat ctcccctcca actctattac tcatctcct tggcattctt tggattctta  
961 attccatttg tgccttcat ctactgctat gcagccatca tccggacact taatgcatac  
1021 gatcatagat ggttgtggta tgttaaggcg agtctcctca tcttgtgat tttaccatt  
1081 tgctttgtc caagcaatat tattcttatt attcaccatg ctaactacta ctacaacaac  
1141 actgatggct tatattttat atatctcata gctttgtgcc tgggtagtct taatagtgc  
1201 ttgatccat tctttattt tctcatgtca aaaaccagaa atcactccac tgcctacctt  
1261 acaaatagtg gaaatgatct tagagaacaa ggacagccat cacagagAAC gctgttttc  
1321 aagaacaaca taagcatagt gcaaggagct ccatttccga gctcctaaga aatatgcttc  
1381 aaaggtcaaa cattacaaaa gcattagtag tttgtttgtt tgtttttgag actgagtctc  
1441 actttatcac ccagactggc gtgcagtggc actatcttgg ctcatgcaa cctctgcctc  
1501 ccaggctcag ctcccaagta gctgggatta caccaccatg cccagctact aaaaatactt  
1561 gtatttttag tagagcggg gtttcaccat gttgaccagg ctggcttga actcctgacc  
1621 tcaagtgtac ttcggcctc agcctcccaa agtgctggat tacaggcgtg agccactgag  
1681 ccagccagca ttagtaattt ttaaaaacac tttatcagta ttttaaaat gttaatgcag  
1741 gagaaaagat atcacaactc tatggaaaat gacatttcca tttgccttat tgctacttca  
1801 agctctttta atcaccatct tccctatttc

## (2) INFORMATION FOR SEQ ID NO:183:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1534 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

1 tcactgtgggg gcgactgctc ctgtggcccc tgggtgctggg gttcagcctg tctggcggca  
61 cccagaccccc cagcgtctac gacgagagcg ggagcaccgg aggtggtgat gacagcacgc  
121 cctcaatect gcctgcccc cgcggctacc caggccaagt ctgtgccaat gacagtgaca  
181 ccctggagct cccggacagc tcacgggcac tgcttctggg ctgggtgccc accaggtgg  
241 tgcccgccct ctatgggctg gtccctggtg tggggctgcc ggccaatggg ctggcgctgt  
301 ggggtgctgg cagcgaggca cctcggctgc cctccaccat gctgctgatg aacctcgca  
361 ctgctgacct cctgctggcc ctggcgctgc ccccgcgat cgcctaccac ctgctggcc  
421 agcgtggtgc cttcggggag gccgcctgcc gcctggccac ggccgactc tatggtcaca  
481 tgataggctc agtgtgctg ctggccgcgc tcagcctgga tcgctacctg gccctggtgc  
541 acccgctgag ggcccgccgc ctgctgggcc ggccgctggc ccttgactc tgcattgctg  
601 cttggtctat ggccggccgc ctggcactgc cctgacact gcagcggcag acctccggc  
661 tggcgctcgc cgtacgctg ctctgccatg acgcgtgcc cctggacgca caggcctccc  
721 actggcaacc ggcccttcacc tgcctggcgc tgttgggctg tttcctgccc ctgctggcca  
781 tgctgctgtg ctacggggcc acctgcaca cgctggcggc cagcggccgg cgctacggcc  
841 acgcgtgtag gctgaccgca gtggtgctgg cctccgccgt ggccctcttc gtgccagca  
901 acctgctgct gctgctgcat tactcggacc cgagcccccag cgcctggggc aacctctatg  
961 gtgcctacgt gccagcctg gcgctgagca cctcaacag ctgctggat ccttctcat  
1021 actactacgt gtcggccgag ttcagggaca aggtgctggc agggctcttc caacgtcgc  
1081 cgggggacac cgtggcctcc aaggcctctg cggaaggggg cagccggggc atgggacccc  
1141 actcctcttt gctccagtga cacaagtgg ggaaggctgt actgggtcga acagggtccc  
1201 tccccccact tcacgtcctt cctgggacct cagaatgtga ccttatttgg aaatagggtt  
1261 gttacaactg tctactagcag aggtcacttt ggagaagggt gggccttaca tccagtgtgg  
1321 gtggtgtcct cataagataa ggagaggcca ggccctggtg ctacgcctg taatcccagc  
1381 accttaagag gccaaggcgg atggatcact tgagcccagg agttcaacac cagcctgagc  
1441 aacatggtaa aaccccatct ctacaaaaa tacaaaaatt agctgggctt ggtggtggc  
1501 gcctgtaatc ccagctactc angagactga ggca

## (2) INFORMATION FOR SEQ ID NO:184:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3472 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

cgcacccggg  
301 cccgcaggcc agaataaaaa gcaacaaatg ccaccttaga tccccgtca tttcttctca  
361 ggaaccccaa tgataaatat gaaccatttt gggaggatga ggagaaaaat gaaagtgggt  
421 taactgaata cagattagtc tccatcaata aaagcagtc cttcaaaaa caacttctg  
481 cattcatctc agaagatgcc tccggatatt tgaccagctc ctggctgaca ctcttctgctc  
541 catctgtgta caccggagtg tttgtagtca gcctccact aaacatcatg gccatcggtg  
601 tgttcatcct gaaaatgaag gtcaagaagc cggcggtggt gtacatgctg cacctggcca  
661 cggcagatgt gctgtttgtg tctgtgctcc cctttaagat cagctattac tttccggca  
721 gtgattggca gtttgggtct gaattgtgtc gcttcgtcac tgcagcattt tactgtaaca  
781 tgtacgctc tatcttgctc atgacagtca taagcattga ccggtttctg gctgtggtgt  
841 atcccatgca gtccctctcc tggcgactc tgggaagggc ttccttact tgcctggcca  
901 tctgggcttt ggccatcgca ggggtagtgc ctctcgtcct caaggagcaa accatccagg  
961 tgcccgggct caacatcact acctgtcatg atgtgctcaa tgaaacctg ctgaaaggct  
1021 actatgcta ctacttctca gccttctctg ctgtcttctt tttgtgccc ctgatcatt  
1081 ccacggtctg ttatgtgtct atcattcgat gtcttagctc ttcgcagtt gccaacccga  
1141 gcaagaagtc ccgggctttg ttcctgtcag ctgctgtttt ctgcatcttc atcatttct  
1201 tcggacccac aaacgtctc ctgattgctc attactcatt ccttctcac acttccacca  
1261 cagaggctgc ctactttgcc tacctcctct gtgtctgtgt cagcagcata agctcgtgca  
1321 tcgacccct aatttactat tacgcttct ctgagtgeca gaggtacgtc tacagtatct  
1381 tatgctgcaa agaaagtcc gatcccagca gttataacag cagtgggcag ttgatggcaa  
1441 gtataaatgga tactgtctct agtaacctga ataacagcat atacaaaaag ctgtaactt  
1501 agggaaaggg actgttggga ggttaaaaaa aaaagtttat aaaagtgaat aacctgagga  
1561 ttctattagt cccaccccaa actttattga ttcacctctt aaaacaacag atgtacgact  
1621 tgcatacctg ctttttatgg gagctgtcaa gcatgtattt ttgtcaatta ccagaaagat  
1681 aacaggacga gatgacggtg ttattccaag ggaatattgc caatgctaca gtaataaatg  
1741 aatgtcact ctggtatag ctagggtgaca tatacatact tacatgtgtg tatatgtaga  
1801 tgtatgcaca cacatatatt atttgcagtg cagtatagaa taggcacttt aaacactct  
1861 tccccgcac cccagcaatt atgaaaaata tctctgattc cctgatttaa tatgcaaagt  
1921 ctagggtggg agagtttagc cctgaacatt tcatggtgt catcaacagt gagagactcc  
1981 atagtttggg cttgtaccac ttttgcaaat aagtgtattt tgaaattgtt tgacggcaag

2041 gtttaa ttaagaggta agacttagta ctatctgtgc gttaggtc tagtgttttc  
2101 aatttttaaac atatccaagt ttgaattcct aaaattatgg aaagagatga aaagcctctg  
2161 ttttgatatg ggtagtattt ttacattttt acacactgta cacataagcc aaaactgagc  
2221 taagtccctc tagtgaatgt aggcctggctt tcagagttag ctattccctga gagctgcatg  
2281 tgtccgcccc cgatggagga ctccaggcag cagacacatg ccagggccat gtcagacaca  
2341 gattggccag aaaccttctc gctgagcctc acagcagtga gactggggcc actacatttg  
2401 ctccatctc ctgggattgg ctgtgaactg atcatgttta tgagaaactg gcaaagcaga  
2461 atgtgatatc ctaggaggta atgaccatga aagacttctc taccatctt aaaaacaacg  
2521 aaagaaggca tggacttctg gatgccatc cactgggtgt aaacacatct agtagttgtt  
2581 ctgaaatgtc agttctgata tggaaacacc cattatgctg tgtggccact ccaatagggtg  
2641 ctgagtgtac agagtggaat aagacagaga cctgccctca agagcaaagt agatcatgca  
2701 tagagtgtga tgtatgtgta ataaatatgt ttcacacaaa caaggcctgt cagctaaaga  
2761 agtttgaaaca tttgggttac tatttcttgt ggttataact taatgaaaac aatgcagtac  
2821 aggacatata ttttttaaaa taagtctgat ttaattgggc actatttatt tacaattgtt  
2881 ttgctcaata gattgctcaa atcagggtttt cttttaagaa tcaatcatgt cagctctgtt  
2941 agaaataaca gaagaaaata gaattgacat tgaaatctag gaaaattatt ctataatttc  
3001 catttactta agacttaatg agactttaaa agcatttttt aacctcctaa gtatcaagta  
3061 tagaaaatct tcatggaatt cacaagtaa tttggaaatt aggttgaaac atatctctta  
3121 tcttacgaaa aaatggtagc attttaaaca aaatagaaa tgcaaggca aatgtttatt  
3181 taaaagagca ggccaggcgc ggtggtcac gcctgtaatc ccagcacttt gggaggctga  
3241 ggcggttga tcacgaggtc aggagatcga gaccatctg gctaacacgg tgaaaccgt  
3301 ctctactaaa aatgcaaaaa aaattagccg ggcgtggtg caggcacctg tagtcccagc  
3361 tactcgggag gctgaggcag gagactggcg tgaaccagg aggcggacct tgtagtgcg  
3421 cgagatcgcg ccactgtgct ccagcctggg caacagagca agactccatc tc

## (2) INFORMATION FOR SEQ ID NO:185:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6836 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

1 cctgcctgca cggcacagga gagcaaactt ctacagacag accaaggctt ccatttgctg  
61 ctgacacatg gaactgaggt gaaattgtgc tccatgattt tacagatttc ataacgttta  
121 agagacggga ctgaggtcat caaaatgaaa gccctcatct ttgcagctgc tggcctcctg  
181 cttctgttgc ccactttttg tcagagtggc atggaaaatg atacaaacaa cttggcaaa  
241 ccaaccttac ccattaagac ctttcgtgga gctccccaa attcttttga agagtctccc  
301 ttttctgcct tggaaggctg gacaggagcc acgattactg taaaaattaa gtgccctgaa  
361 gaaagtgcct cacatctcca tgtgaaaaat gctaccatgg ggtacctgac cagctcctta  
421 agtactaaac tgatacctgc catctacctc ctggtgtttg tagttggtgt cccggccaat  
481 gctgtgacct tgtggatgct tttcttcagg accagatcca tctgtaccac tgtattctac  
541 accaacctgg ccattgcaga tttctttttt tgtgttacat tgccctttaa gatagcttat  
601 catctcaatg ggaacaactg ggtatttgga gaggtcctgt gccgggccac cacagtcac  
661 ttctatggca acatgtactg ctccattctg ctccctgect gcatcagcat caaccgctac  
721 ctggccatcg tccatccttt cacctaccgg ggctgccc agcacaccta tgccttgga  
781 acatgtggac tgggtgtggc aacagttttt ttatatatgc tgccattttt caractgaag  
841 caggaatatt atcttgttca gccagacatc accacctgcc atgatgttca caacacttgc  
901 gagtccctcat ctcccttcca actctattac ttcatctcct tggcattctt tggattctta  
961 attccatttg tgcttatcat ctactgctat gcagccatca tccggacact taatgcatac  
1021 gatcatagat ggttgtggtg tgttaaggcg agtctcctca tccctgtgat ttttaccatt  
1081 tgctttgctc caagcaatat tattcttatt attcaccatg ctaactacta ctacaacaac  
1141 actgatggct tatattttat atatctcata gcttgtgccc tgggtagtct taatagttgc  
1201 ttagatccat tccctttatt tctcatgtca aaaaccagaa atcaactccac tgcttacctt  
1261 acaaaatagt gaaatgatct tagagaacaa ggacagccat cacagagaac gtctgttttc  
1321 aagaacaaca taagcatagt gcaaggagct ccatttccga gctcctaaga aatagtcttc  
1381 aaaggctcaaa cattacaaaa gcattagtat tttgtttgtt tgtttttgag actgagctc  
1441 actttatcac ccagactggc gtgcagtggc actatcttgg ctcatgcaa cctctgctc  
1501 ccaggctcagc ctcccaagta gctgggatta caccaccatg cccagctact aaaaatactt  
1561 gtatttttag tagagacggg gtttcacat gttgaccagg ctggtcttga actcctgacc  
1621 tcaagtgate ttccggctc agcctcccaa agtgctggat tacaggcgtg agccactgag  
1681 ccagccagca ttagtaattt ttaaaaacac tttatcagta ttttaaaat gtaatgcag  
1741 gagaaaagat atcacaaact tatggaaaat gacatttcca tttgccttat tgctacttca  
1801 agctctttta atcaccatct tccctatttc  
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3421 cgagatcgcg ccaactgtgt ccagcctggg caacagagca agactccatc tc

351086

**WHAT IS CLAIMED AS NOVEL AND UNOBVIOUS  
IN UNITED STATES LETTERS PATENT IS:**

1. A pharmaceutical composition, comprising a nucleic acid which comprises an oligonucleotide (oligo) consisting of up to about 15% adenosine (A), and which is effective for alleviating or inhibiting bronchoconstriction, allergy(ies) and/or inflammation, the oligo being anti-sense to a target selected from the group consisting of

target genes and their corresponding mRNAs;  
genomic and mRNA flanking regions selected from the group consisting of 3' and 5' intron-exon borders and the juxta-section between coding and non-coding regions; and  
all mRNA segments encoding polypeptides associated with a disease(s) or condition(s) afflicting lung airways;

combinations thereof;  
pharmaceutically acceptable salts thereof; and  
mixtures thereof.

2. The composition of claim 1, wherein the oligo consists of up to about 10% A.

3. The composition of claim 2, wherein the oligo consists of up to about 5% A.

4. The composition of claim 3, wherein the oligo consists of up to about 3% A.

5. The composition of claim 4, wherein the oligo is A-free.

6. The composition of claim 1, wherein the target gene is selected from the group consisting of target genes and mRNAs encoding polypeptides selected from the group consisting of transcription factors, stimulating and activating factors, interleukins, interleukin receptors, chemokines, chemokine receptors, endogenously produced specific and non-specific enzymes, immunoglobulins, antibody receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, adhesion molecules, defensins, growth factors, vasoactive peptides and receptors, and binding proteins; and target genes and mRNAs corresponding to oncogenes, and flanking regions and intron and exon borders.

7. The agent of claim 6, wherein the encoded polypeptides are selected from the group consisting of NfκB Transcription Factor, Interleukin-8 Receptor (IL-8 R), Interleukin 5 Receptor (IL-5 R), Interleukin 4 Receptor (IL-4 R), Interleukin 3 Receptor (IL-3 R), Interleukin-1β (IL-1β), Interleukin 1β Receptor (IL-1β R), Eotaxin, Tryptase, Major Basic Protein, β2-adrenergic Receptor Kinase, Endothelin Receptor A, Endothelin Receptor B, Preproendothelin, Bradykinin B2 Receptor, IgE High Affinity Receptor, Interleukin 1 (IL-1), Interleukin 1 Receptor (IL-1 R), Interleukin 9 (IL-9), Interleukin-9 Receptor (IL-9 R), Interleukin 11 (IL-11), Interleukin-11 Receptor (IL-11 R), Inducible Nitric Oxide Synthase, Cyclooxygenase (COX), Intracellular Adhesion Molecule 1 (ICAM-1) Vascular Cellular Adhesion Molecule (VCAM), Rantes, Endothelial Leukocyte Adhesion Molecule (ELAM-1), Monocyte Activating Factor, Neutrophil Chemotactic Factor, Neutrophil Elastase, Defensin 1, 2 and 3, Muscarinic Acetylcholine Receptors, Platelet Activating Factor, Tumor Necrosis Factor α, 5-lipoxygenase, Phosphodiesterase IV, Substance P, Substance P Receptor, Histamine Receptor, Chymase, CCR-1 CC Chemokine Receptor, CCR-2 CC Chemokine Receptor, CCR-3 CC Chemokine Receptor, CCR-4 CC Chemokine Receptor, CCR-5 CC Chemokine Receptor, Prostanoid Receptors, GATA-3 Transcription Factor, Neutrophil Adherence Receptor, MAP Kinase, Interleukin-9 (IL-9), NFAT Transcription Factors, STAT 4, MIP-1α, MCP-2, MCP-3, MCP-4, Cyclophilins, Phospholipase A2, Basic Fibroblast Growth Factor, Metalloproteinase, CSBP/p38 MAP Kinase, Tryptose Receptor, PDG2, Interleukin-3 (IL-3), Interleukin-1β (IL-1β), Cyclosporin A-Binding Protein, FK5-Binding Protein, α4β1 Selectin, Fibronectin, α4β7 Selectin, Mad CAM-1, LFA-1 (CD11a/CD18), PECAM-1, LFA-1 Selectin, C3bi, PSGL-1, E-Selectin, P-Selectin, CD-34, L-Selectin, p150,95, Mac-1 (CD11b/CD18), Fucosyl transferase, VLA-4, CD-18/CD11a, CD11b/CD18, ICAM2 and ICAM3, C5a, CCR3 (Eotaxin Receptor), CCR1, CCR2, CCR4, CCR5, LTB-4, AP-1 Transcription Factor, Protein kinase C, Cysteinyl Leukotriene Receptor, Tachychinins Receptors (tach R), IκB Kinase 1 & 2, STAT 6, c-mas and NF-Interleukin-6 (NF-IL-6).

8. The composition of claim 1, wherein at least one A is substituted by a universal base selected from the group consisting of heteroaromatic bases which bind to a thymidine base but have antagonist activity and less than about 0.3 of the adenosine base agonist activity at the adenosine A<sub>1</sub>, A<sub>2b</sub> and A<sub>3</sub> receptors, and heteroaromatic bases which have no activity or have an agonist activity at the adenosine A<sub>2a</sub> receptor.

9. The composition of claim 8, wherein all As are substituted by universal bases selected from the group consisting of heteroaromatic bases which bind to a thymidine base but have antagonist activity and less than about 0.3 of the adenosine base agonist activity at the adenosine A<sub>1</sub>, A<sub>2b</sub> and A<sub>3</sub> receptors, and heteroaromatic bases which have no activity or have an agonist activity at the adenosine A<sub>2a</sub> receptor.

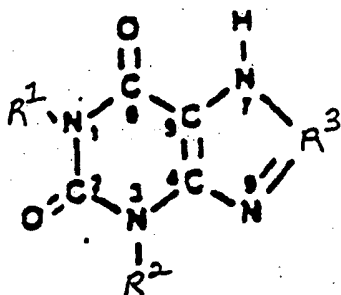
10. The composition of claim 8, wherein the heteroaromatic bases are selected from the group consisting of pyrimidines and purines, which may be substituted by O, halo, NH<sub>2</sub>, SH, SO, SO<sub>2</sub>, SO<sub>3</sub>, COOH and branched and fused primary and secondary amino, alkyl, alkenyl, alkynyl, cycloalkyl, heterocycloalkyl, aryl, heteroaryl, alkoxy, alkenoxy, acyl, cycloacyl, arylacyl, alkynoxy, cycloalkoxy, aroyl, arylthio, arylsulfoxyl,



halocycloalkyl, alkylcycloalkyl, alkenylcycloalkyl, alkynylcycloalkyl, haloaryl, alkylaryl, alkenylaryl, alkynylaryl, arylalkyl, arylalkenyl, alkynyl, arylcycloalkyl, which may be further substituted by O, halo, NH<sub>2</sub>, primary, secondary and tertiary amine, SH, SO, SO<sub>2</sub>, SO<sub>3</sub>, cycloalkyl, heterocycloalkyl, heteroaryl.

11. The composition of claim 10, wherein the pyrimidines and purines are substituted at positions 1, 2, 3, 4, 7 and 8.

12. The composition of claim 11, wherein the pyrimidines and purines are selected from the group consisting of theophylline, caffeine, dyphylline, etophylline, acephylline piperazine, bamifylline, enprofylline and xantine having the chemical formula



wherein R<sup>1</sup> and R<sup>2</sup> are independently H, alkyl, alkenyl or alkynyl and R<sup>3</sup> is H, aryl, dicycloalkyl, dicycloalkenyl, dicycloalkynyl, cycloalkyl, cycloalkenyl, cycloalkynyl, O-cycloalkyl, O-cycloalkenyl, O-cycloalkynyl, NH<sub>2</sub>-alkylamino-ketoxyalkoxy-aryl and mono and dialkylaminoalkyl-N-alkylamino-SO<sub>2</sub> aryl.

13. The composition of claim 12, wherein the universal base is selected from the group consisting of 3-nitropyrrole-2'-deoxynucleoside, 5-nitro-indole, 2-deoxyribosyl-(5-nitroindole), 2-deoxyribofuranosyl-(5-nitroindole), 2'-deoxyinosine, 2'-deoxynebularine, 6H, 8H-3,4-dihydropyrimido [4,5-c] oxazine-7-one or 2-amino-6-methoxyaminopurine.

14. The composition of claim 1, where a methylated cytosine ("C") is substituted for at least one CpG dinucleotide if present in the oligo(s).

15. The composition of claim 1, wherein at least one nucleotide linking residue of the anti-sense oligonucleotide(s) is a residue selected from the group consisting of methylphosphonate, phosphotriester, phosphorothioate, phosphorodithioate, boranophosphate, formacetal, thioformacetal, thioether, carbonate, carbamate, sulfate, sulfonate, sulfamate, sulfonamide, sulfone, sulfite, sulfoxide, sulfide, hydroxylamine, methylene(methylimino), methyleneoxy (methylimino), 2'-O-methyl, phosphoramidate residues and combinations thereof.

16. The agent of claim 15, wherein all nucleotide linking residues are selected from the group consisting of methylphosphonate, phosphotriester, phosphorothioate, phosphorodithioate, boranophosphate, formacetal, thioformacetal, thioether, carbonate, carbamate, sulfate, sulfonate, sulfamate, sulfonamide, sulfone, sulfite, sulfoxide, sulfide, hydroxylamine, methylene(methylimino), methyleneoxy (methylimino), 2'-O-methyl, phosphoramidate residues and combinations thereof.

17. The composition of claim 1, wherein the anti-sense oligonucleotide comprises about 7 to 60 mononucleotides.

18. The composition of claim 1, wherein the anti-sense oligonucleotide comprises fragments 1 to 1670 (SEQ ID NOS: 11 through 1680).

19. The composition of claim 1, wherein the anti-sense oligonucleotide is linked to an agent selected from the group consisting of cell internalized or up-taken agent(s) and cell targeting agents.

20. The composition of claim 19, wherein the cell internalized or up taken agent is selected from the group consisting of transferrin, asialoglycoprotein and streptavidin.

21. The composition of claim 19, wherein the nucleic acid is linked to a vector.

22. The vector of claim 21, which comprises a prokaryotic or eukaryotic vector.

23. The composition of claim 1, wherein the oligo is hybridized to a ribonucleic acid.

24. A cell, comprising the agent of claim 1.

25. The composition of claim 1, further comprising a carrier.

26. The composition of claim 25, wherein the carrier comprises a biologically acceptable carrier.

27. The composition of claim 26, wherein the carrier comprises a pharmaceutically or veterinarily acceptable carrier.

28. The composition of claim 25, wherein the carrier is selected from the group consisting of gaseous, liquid, solid carriers and mixtures thereof.

29. The composition of claim 25, further comprising an agent selected from the group consisting of other therapeutic agents, surfactants, antioxidants, flavoring and coloring agents, fillers, volatile oils, buffering agents, dispersants, RNA inactivating agents, anti-oxidants, flavoring agents, propellants and preservatives.

30. The composition of claim 29, comprising the nucleic acid, a surfactant and a carrier.

31. The composition of claim 29, wherein the surfactant is selected from the group consisting of surfactant protein A, surfactant protein B, surfactant protein C, surfactant protein D and surfactant protein and active fragments thereof, non-dipalmitoyl disaturated phosphatidylcholine, dipalmitylphosphatidylcholine, phosphatidylcholine, phosphatidylglycerol, phosphatidylinositol, phosphatidylethanolamine, phosphatidylserine, phosphatidic acid, ubiquinones, lysophosphatidylethanolamine, lysophosphatidylcholine, palmitoyl-lysophosphatidylcholine, dehydroepiandrosterone, dolichols, sulfatidic acid, glycerol-1-3-phosphate, dihydroxyacetone phosphate, glycerol, glycerol-3-phosphocholine, dihydroxyacetone, palmitate, cytidine diphosphate (CDP) diacylglycerol, CDP choline, choline, choline phosphate, artificial lamellar bodies vehicles for surfactant components, omega-3 fatty acids, polyenic acid, polyenoic acid, lecithin, palmitic acid, non-ionic ethylene and/or propylene oxide block copolymers, polyoxypropylene, polyoxyethylene, poly(vinyl amine) with dextran and/or alkanoyl side chains, Brij 35, Triton X-100, ALEC, Exosurf, Survant and Atovaquone.

32. The composition of claim 31, wherein the RNA inactivating agent comprises an enzyme, preferably a ribozyme.

33. The composition of claim 1, wherein the anti-sense oligonucleotide is present in an amount of about 0.01 to about 99.99 w/w of the composition.

34. The composition of claim 33, wherein the anti-sense oligonucleotide is present in an amount of about 1 to about 40 w/w of the composition.

35. The composition of claim 34, wherein the anti-sense oligonucleotide is present in an amount of about 5 to about 20 w/w of the composition.

36. A formulation, comprising the composition of claim 25, selected from the group consisting of systemic and topical formulations.

37. The formulation of claim 36, selected from the group consisting of oral, intrabuccal, intrapulmonary, rectal, intrauterine, intratumor, intracranial, nasal, intramuscular, subcutaneous, intravascular, intrathecal, inhalable, transdermal, intradermal, intracavitary, implantable, iontophoretic, ocular, vaginal, intraarticular, otical, intravenous, intramuscular, intraglandular, intraorgan, intralymphatic, implantable, slow release and enteric coating formulations.

38. The formulation of claim 37, which is an oral formulation, wherein the carrier is selected from the group consisting of solid and liquid carriers.

39. The oral formulation of claim 38, wherein the liquid carrier is selected from the group consisting of solutions, suspensions, and oil-in-water and water-in-oil emulsions.

40. The oral formulation of claim 38, which is selected from the group consisting of a powder, dragees, tablets, capsules, sprays, aerosols, solutions, suspensions and emulsions.

41. The formulation of claim 36, which is a topical formulation, wherein the carrier is selected from the group consisting of creams, gels, ointments, sprays, aerosols, patches, solutions, suspensions and emulsions.

42. The formulation of claim 36, which is an injectable formulation, wherein the carrier is selected from the group consisting of aqueous and alcoholic solutions and suspensions, oily solutions and suspensions and oil-in-water and water-in-oil emulsions.

43. The formulation of claim 36, which is a rectal formulation in the form of a suppository.

44. The formulation of claim 36, which is a transdermal formulation, wherein the carrier is selected from the group consisting of aqueous and alcoholic solutions, oily solutions and suspensions and oil-in-water and water-in-oil emulsions.

45. The transdermal formulation of claim 36, which is an iontophoretic transdermal formulation, wherein the carrier is selected from the group consisting of aqueous and alcoholic solutions, oily solutions and suspensions and oil-in-water and water-in-oil emulsions, and wherein the formulation further comprises a transdermal transport promoting agent.

46. An implantable capsule or cartridge, comprising the formulation of claim 44.

47. The formulation of claim 36, wherein the carrier is selected from the group consisting of aqueous and alcoholic solutions and suspensions, oily solutions and suspensions and oil-in-water and water-in-oil emulsions.

48. The formulation of claim 36, wherein the carrier comprises a hydrophobic carrier.

49. The formulation of claim 48, wherein the carrier comprises lipid vesicles or particles.

50. The formulation of claim 49, wherein the vesicles comprise liposomes, and the particles comprise microcrystals.

51. The formulation of claim 50, wherein the vesicles comprise liposomes which comprise the anti-sense oligonucleotide.

52. The formulation of claim 49, wherein the vesicles comprise N-(1-[2,3-dioleoyloxy] propyl) - N,N,N-trimethyl-ammonium methylsulfate.

53. The formulation of claim 36, comprising a respirable or inhalable formulation.

54. The respirable or inhalable formulation of claim 53, comprising an aerosol.

55. The formulation of claim 36, in single or multiple unit form.

56. The formulation of claim 36, in bulk.

57. A kit comprising a delivery device; in a separate container, the formulation of claim 36; and instructions for adding a carrier and for use of the formulation.
58. The kit of claim 57, wherein the delivery device comprises a nebulizer which delivers single metered doses of the formulation.
59. The kit of claim 58, wherein the nebulizer comprises an insufflator; and the composition is provided in a pierceable or openable capsule or cartridge.
60. The kit of claim 58, wherein the delivery device comprises a pressurized inhaler; and the composition comprises a suspension, solution or dry formulation of the agent.
61. The kit of claim 57, further comprising, in a separate container, an agent selected from the group consisting of other therapeutic agents, surfactants, anti-oxidants, flavoring agents, fillers, volatile oils, dispersants, antioxidants, propellants, preservatives, buffering agents, RNA inactivating, cell-internalized or up-taken agents and coloring agents.
62. The kit of claim 61, comprising, in separate containers, a nucleic acid, a surfactant and a carrier.
63. The kit of claim 61, wherein the solvent is selected from the group consisting of organic solvents and organic solvents mixed with one or more co-solvents.
64. The kit of claim 57, wherein the composition is provided in a capsule or cartridge.
65. An in vivo method of delivering a nucleic acid comprising an anti-sense oligonucleotide (oligo) to a target polynucleotide associated with a disease(s) or condition(s) afflicting lung airways, comprising administering to a subject the composition of claim 1 comprising an amount of the nucleic acid effective to reach the target polynucleotide.
66. The method of claim 65, wherein the composition is administered into the subject's respiratory system.
67. The method of claim 65, wherein the agent is administered directly into the subject's lung (s).
68. The method of claim 65, wherein the amount of the agent is effective to bind to the nucleic acid.
69. The method of claim 65, wherein the agent is effective to reduce the production or availability, or to increase the degradation, of the target mRNA or to reduce the amount of the target polypeptide present in the lungs.
70. The method of claim 65, wherein the agent is administered as a respirable aerosol.
71. The method of claim 65, wherein the disease or condition is associated with obstruction of the subject's airways.
72. The method of claim 71, wherein the disease or condition is associated with asthma.
73. The method of claim 65, wherein the disease or condition is associated with inflammation.
74. The method of claim 65, wherein the disease or condition is associated with an allergy, and the target is selected from the group consisting of immunoglobulins and antibody receptors, genes and mRNAs encoding them, their genomic and mRNA flanking sequences and exon and intron borders of the gene (s) and mRNA(s).
75. The method of claim 65, wherein the disease or condition is associated with a malignancy or cancer, and the mRNA encodes a target selected from the group consisting of immunoglobulins and antibody receptors, genomic flanking sequences and genes and mRNAs encoding them and oncogenes.
76. The method of claim 65, wherein the composition is administered by a transdermal or systemic route.
77. The method of claim 76, wherein the composition is administered orally, intracavitarily, intranasally, intraanally, intravaginally, intrauterally, intraarticularly, transdermally, intrabucally, intravenously, subcutaneously, intramuscularly, intravascularly, intratumorously, intraglandularly, intraocularly, intracranial, into an organ, intravascularly, intrathecally, intralymphatically, intraotically, by implantation, by inhalation, intradermally, intrapulmonarily, intraotically, by slow release, by sustained release and by a pump.
78. The method of claim 65, wherein the subject is a mammal.
79. The method of claim 78, wherein the mammal is selected from the group consisting of humans and animals.
80. The method of claim 79, wherein the mammal is a human.
81. The method of claim 79, wherein the subject is an animal.
82. The method of claim 65, wherein the anti-sense oligonucleotide is administered in amount of about 0.005 to about 150 mg/kg body weight.
83. The method of claim 82, wherein the anti-sense oligonucleotide is administered in an amount of about 0.01 to about 75 mg/kg body weight.

84. The method of claim 83, wherein the anti-sense ligonucleotide is administered in an amount of about 1 to 50 mg/kg body weight.

85. The method of claim 65, which is a prophylactic method.

86. The method of claim 65, which is a therapeutic method.

87. The method of claim 65, wherein the oligo is obtained by

(a) selecting fragments of a target nucleic acid having at least 4 contiguous nucleic acids selected from the group consisting of G and C;

(b) obtaining a first oligonucleotide 4 to 60 nucleotides long which comprises the selected fragment and has a C and G nucleic acid content of up to and including about 15%; and

(c) obtaining a second oligonucleotide 4 to 60 nucleotides long comprising a sequence which is anti-sense to the selected fragment, the second oligonucleotide having an A base content of up to and including about 15%.

88. The method of claim 61, wherein the oligo consists of up to about 10% A.

89. The method of claim 88, wherein the oligo consists of up to about 5% A.

90. The method of claim 88, wherein the oligo consists of up to about 3% A.

91. The method of claim 92, wherein the oligo is A-free.

92. The method of claim 65, wherein the target is selected from the group consisting of genes and mRNAs encoding polypeptides selected from the group consisting of transcription factors, stimulating and activating factors, interleukins, interleukin receptors, chemokines, chemokine receptors, endogenously produced specific and non-specific enzymes, immunoglobulins, antibody receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, adhesion molecules, defensins, growth factors, vasoactive peptides, peptide receptors and binding proteins; and

genes and mRNAs corresponding to oncogenes.

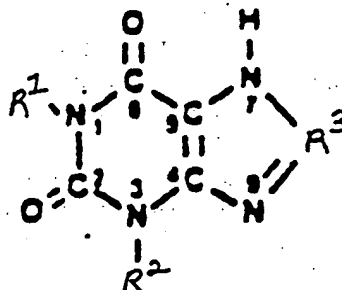
93. The method of claim 65, wherein at least one A is substituted by a universal base selected from the group consisting of heteroaromatic bases which bind to a thymidine base but have antagonist activity and less than about 0.3 of the adenosine base agonist activity at the adenosine A<sub>1</sub>, A<sub>2b</sub> and A<sub>3</sub> receptors, and heteroaromatic bases which have no activity or have an agonist activity at the adenosine A<sub>2a</sub> receptor.

94. The method of claim 93, wherein all As are substituted by universal bases selected from the group consisting of heteroaromatic bases which bind to a thymidine base but have antagonist activity and less than about 0.3 of the adenosine base agonist activity at the adenosine A<sub>1</sub>, A<sub>2b</sub> and A<sub>3</sub> receptors, and heteroaromatic bases which have no activity or have an agonist activity at the adenosine A<sub>2a</sub> receptor.

95. The method of claim 95, wherein the heteroaromatic bases are selected from the group consisting of pyrimidines and purines, which may be substituted by O, halo, NH<sub>2</sub>, SH, SO, SO<sub>2</sub>, SO<sub>3</sub>, COOH and branched and fused primary and secondary amino, alkyl, alkenyl, alkynyl, cycloalkyl, heterocycloalkyl, aryl, heteroaryl, alkoxy, alkenoxy, acyl, cycloacyl, arylacyl, alkynoxy, cycloalkoxy, aroyl, arylthio, arylsulfoxyl, halocycloalkyl, alkylcycloalkyl, alkenylcycloalkyl, alkynylcycloalkyl, haloaryl, alkylaryl, alkenylaryl, alkynylaryl, arylalkyl, arylalkenyl, arylalkynyl, arylcycloalkyl, which may be further substituted by O, halo, NH<sub>2</sub>, primary, secondary and tertiary amine, SH, SO, SO<sub>2</sub>, SO<sub>3</sub>, cycloalkyl, heterocycloalkyl and heteroaryl.

96. The method of claim 95, wherein the pyrimidines and purines are substituted at positions 1, 2, 3, 4, 7 and 8.

97. The method of claim 96, wherein the pyrimidines and purines are selected from the group consisting of theophylline, caffeine, dyphylline, etophylline, acephylline piperazine, bamifylline, enprofylline and xantine having the chemical formula



wherein R<sup>1</sup> and R<sup>2</sup> are independently H, alkyl, alkenyl or alkynyl and R<sup>3</sup> is H, aryl, dicycloalkyl, dicycloalkenyl, dicycloalkynyl, cycloalkyl, cycloalkenyl, cycloalkynyl, O-cycloalkyl, O-cycloalkenyl, O-cycloalkynyl, NH<sub>2</sub>-alkylamino-ketoxyalkoxy-aryl and mono and dialkylaminoalkyl-N-alkylamino-SO<sub>2</sub> aryl.

98. The method of claim 97, wherein the universal base is selected from the group consisting of 3-nitropyrrole-2'-deoxynucleoside, 5-nitro-indole, 2-deoxyribosyl-(5-nitroindole), 2-deoxyribofuranosyl-(5-nitroindole), 2'-deoxyinosine, 2'-deoxynebularine, 6H, 8H-3,4-dihydropyrimido [4,5-c] oxazine-7-one or 2-amino-6-methoxaminopurine.

99. The method of claim 65, further comprising methylating at least one cytosine (mC) if a CpG dinucleotide is present in the oligo(s).

100. The method of claim 65, further comprising substituting at least one nucleotide linking residue of the anti-sense oligonucleotide(s) with a residue selected from the group consisting of methylphosphonate, phosphotriester, phosphorothioate, phosphorodithioate, boranophosphate, formacetal, thioformacetal, thioether, carbonate, carbamate, sulfate, sulfonate, sulfamate, sulfonamide, sulfone, sulfite, sulfoxide, sulfide, hydroxylamine, methylene(methylimino), methyleneoxy (methylimino), 2'-O-methyl, phosphoramidate residues, and combinations thereof.

101. The method of claim 100, wherein all nucleotide linking residues of the oligo are substituted.

102. The method of claim 65, further comprising linking the anti-sense oligonucleotide to an agent selected from the group consisting of cell internalized and up-taken agent(s) and cell targeting agents.

103. The method of claim 102, wherein the cell internalized or up taken agent is selected from the group consisting of transferrin, asialoglycoprotein, and streptavidin.

104. The method of claim 102, wherein the cell targeting agent is a vector.

105. The method of claim 104, wherein the vector to which the agent is operatively linked is a prokaryotic or eukaryotic vector.

106. A method of identifying segments in a target polynucleotide suitable for constructing oligonucleotides which are anti-sense to the target polynucleotide and have an adenosine (A) content of up to and including about 15% of all nucleotides, comprising

(a) selecting fragments of a target polynucleotide acid having at least 4 contiguous nucleic acids selected from the group consisting of G and C; and

(a) obtaining a first oligonucleotide 4 to 60 nucleotides long which comprises the selected fragment and has a C and G content of up to and including about 15%.

107. A method of obtaining oligonucleotides which are anti-sense to a target polynucleotide and have an adenosine content of 0 to up to and including about 15%, comprising conducting the method of claim 106; wherein the first oligonucleotide comprises a sequence which is anti-sense to the selected fragment and has an A content of up to and including about 15%.

108. The method of claim 107, further comprising, when the anti-sense fragment comprises at least one A, substituting at least one A with a universal base selected from the group consisting of

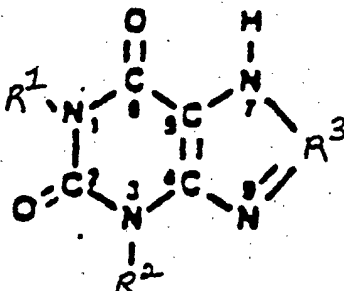
heteroaromatic bases which bind to thymidine (T) but have less than about 0.3 of A's adenosine A<sub>1</sub>, A<sub>2b</sub> and A<sub>3</sub> receptor agonist activity; and

heteroaromatic bases which have no activity or have adenosine A<sub>2a</sub> receptor agonist activity.

109. The method of claim 108, wherein the heteroaromatic bases are selected from the group consisting of pyrimidines and purines, which may be substituted by O, halo, NH<sub>2</sub>, SH, SO, SO<sub>2</sub>, SO<sub>3</sub>, COOH and branched and fused primary and secondary amino, alkyl, alkenyl, alkynyl, cycloalkyl, heterocycloalkyl, aryl, heteroaryl, alkoxy, alkenoxy, acyl, cycloacyl, arylacyl, alkynoxy, cycloalkoxy, aroyl, arylthio, arylsulfoxyl, halocycloalkyl, alkylcycloalkyl, alkenylcycloalkyl, alkynylcycloalkyl, haloaryl, alkylaryl, alkenylaryl, alkynylaryl, arylalkyl, arylalkenyl, arylalkynyl, arylcycloalkyl, which may be further substituted by O, halo, NH<sub>2</sub>, primary, secondary and tertiary amine, SH, SO, SO<sub>2</sub>, SO<sub>3</sub>, cycloalkyl, heterocycloalkyl and heteroaryl.

110. The method of claim 109, wherein the pyrimidines and purines are substituted at positions 1, 2, 3, 4, 7 and 8.

111. The method of claim 109, wherein the pyrimidines and purines are selected from the group consisting of theophylline, caffeine, dyphylline, etophylline, acephylline piperazine, bamifylline, enprofylline and xantine having the chemical formula



wherein R<sup>1</sup> and R<sup>2</sup> are independently H, alkyl, alkenyl or alkynyl and R<sup>3</sup> is H, aryl, dicycloalkyl, dicycloalkenyl, dicycloalkynyl, cycloalkyl, cycloalkenyl, cycloalkynyl, O-cycloalkyl, O-cycloalkenyl, O-cycloalkynyl, NH<sub>2</sub>-alkylamino-ketoxyalkoxy-aryl and mono and dialkylaminoalkyl-N-alkylamino-SO<sub>2</sub> aryl.

112. The method of claim 108, wherein the universal base is selected from the group consisting of 3-nitropyrrole-2'-deoxynucleoside, 5-nitro-indole, 2-deoxyribosyl-(5-nitroindole), 2-deoxyribofuranosyl-(5-nitroindole), 2'-deoxyinosine, 2'-deoxynebularine, 6H, 8H-3,4-dihydropyrimido [4,5-c] oxazine-7-one or 2-amino-6-methoxyaminopurine.

113. A method of treating a disease or condition associated with a target selected from the group consisting of proteins, gene (s) and their corresponding mRNA(s) encoding the proteins, the genes and mRNA flanking regions and their intron and exon borders, associated with a disease or condition afflicting lung airways, comprising administering to a subject afflicted with the disease or condition the composition of claim 1 comprising an anti-bronchoconstriction, anti-allergic and/or anti-inflammatory effective amount of the nucleic acid.

114. The method of claim 113, wherein the amount of nucleic acid administered is effective to reduce the production or availability, or to increase the degradation, of the mRNA, or to reduce the amount of the polypeptide present in the lungs.

115. The method of claim 113, wherein the nucleic acid is administered directly to the lung (s) of the subject.

116. The method of claim 113, wherein the nucleic acid is administered as a respirable aerosol.

117. The method of claim 113, wherein the disease or condition is a disease or condition afflicting the lung (s).

118. The method of claim 117, wherein the disease or condition is associated with obstruction of the subject's airways.

119. The method of claim 117, wherein the disease or condition is associated with asthma.

120. The method of claim 117, wherein the disease or condition is associated with inflammation.

121. The method of claim 113, wherein the disease or condition is associated with allergy (ies), and the target is selected from the group consisting of immunoglobulins and antibody receptors, gene(s) and corresponding mRNA(s) encoding them, the genes and mRNA flanking regions and intron and exon borders.

122. The method of claim 113, wherein the disease or condition is associated with a malignancy or cancer; and the target is selected from the group consisting of immunoglobulins and antibody receptors, gene(s) and mRNA(s) encoding them, gene(s) and mRNA(s) associated with oncogenes, genomic and mRNA flanking regions and exon and intron borders.

123. The method of claim 113, wherein the composition is administered by a topical or systemic route.

124. The method of claim 123, wherein the composition is administered orally, intracavitarily, intranasally, intraanally, intravaginally, intrauterally, intraarticularly, intraotically, intralymphatically, transdermally, intrabucally, intravenously, subcutaneously, intramuscularly, intratumorously, intraglandularly, intraocularly, intracranial, into an organ, intravascularly, intrathecally, by implantation, by inhalation, intradermally, intrapulmonarily, into the ear, by slow release, by sustained release and by a pump.

125. The method of claim 124, wherein the subject is a mammal.

126. The method of claim 125, wherein the mammals are selected from the group consisting of humans and animals.

127. The method of claim 113, wherein the anti-sense oligonucleotide is administered in amount of about 0.005 to about 150 mg/kg body weight.

128. The method of claim 127, wherein the anti-sense oligonucleotide is administered in an amount of about 0.01 to about 75 mg/kg body weight.

129. The method of claim 130, wherein the anti-sense oligonucleotide is administered in an amount of about 1 to about 50 mg/kg body weight.

130. The method of claim 113, which is a prophylactic method.

131. The method of claim 113, which is a therapeutic method.

132. A method of producing anti-sense oligonucleotide(s) (oligos) consisting of up to and including about 15% adenosine (A), comprising

selecting a target from the group consisting of polypeptides associated with a disease(s) and/or condition(s) afflicting lung airways, genes and RNAs encoding them, the genomic and mRNA flanking regions and the gene(s) and mRNA(s) intron and exon borders;

obtaining the sequence of a mRNA(s) selected from the group consisting of mRNAs corresponding to the target gene(s) and mRNAs encoding the target polypeptide(s), genomic and mRNA flanking regions and the genes and mRNAs intron and exon borders;

selecting at least one segment of the mRNA(s);

synthesizing one or more oligo anti-sense to the selected mRNA segment(s); and

substituting, if necessary, a universal base(s) for one or more A(s) to reduce the content of A present in the oligo to up to about 15% of all nucleotides.

133. The method of claim 132, wherein the universal base is selected from the group consisting of heteroaromatic bases which bind to a thymidine base but have antagonist activity and less than about 0.3 of the adenosine base agonist activity at the adenosine A<sub>1</sub>, A<sub>2b</sub> and A<sub>3</sub> receptors, and heteroaromatic bases which have no activity or have an agonist activity at the adenosine A<sub>2a</sub> receptor.

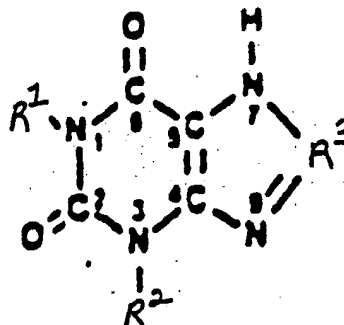
134. The method of claim 132, wherein all As are substituted with universal bases selected from the group consisting of heteroaromatic bases which bind to a thymidine base but have antagonist activity and less than

about 0.3 of the adenosine agonist activity at the adenosine A<sub>1</sub>, A<sub>2b</sub> and A<sub>3</sub> receptors, and heteroaromatic bases which have no activity or have an agonist activity at the adenosine A<sub>2b</sub> receptor.

135. The method of claim 133, wherein the heteroaromatic bases are selected from the group consisting of pyrimidines and purines, which may be substituted by O, halo, NH<sub>2</sub>, SH, SO, SO<sub>2</sub>, SO<sub>3</sub>, COOH and branched and fused primary and secondary amino, alkyl, alkenyl, alkynyl, cycloalkyl, heterocycloalkyl, aryl, heteroaryl, alkoxy, alkenoxy, acyl, cycloacyl, arylacyl, alkynoxy, cycloalkoxy, aroyl, arylthio, arylsulfoxyl, halocycloalkyl, alkylcycloalkyl, alkenylcycloalkyl, alkynylcycloalkyl, haloaryl, alkylaryl, alkenylaryl, alkynylaryl, arylalkyl, arylalkenyl, arylalkynyl, arylcycloalkyl, which may be further substituted by O, halo, NH<sub>2</sub>, primary, secondary and tertiary amine, SH, SO, SO<sub>2</sub>, SO<sub>3</sub>, cycloalkyl, heterocycloalkyl and heteroaryl.

136. The method of claim 135, wherein the pyrimidines and purines are substituted at positions 1, 2, 3, 4, 7 and 8.

137. The method of claim 135, wherein the pyrimidines and purines are selected from the group consisting of theophylline, caffeine, dyphylline, etophylline, acephylline piperazine, bamifylline, enprofylline and xantine having the chemical formula



wherein R<sup>1</sup> and R<sup>2</sup> are independently H, alkyl, alkenyl or alkynyl and R<sup>3</sup> is H, aryl, dicycloalkyl, dicycloalkenyl, dicycloalkynyl, cycloalkyl, cycloalkenyl, cycloalkynyl, O-cycloalkyl, O-cycloalkenyl, O-cycloalkynyl, NH<sub>2</sub>-alkylamino-ketoxyalkyloxy-aryl and mono and dialkylaminoalkyl-N-alkylamino-SO<sub>2</sub> aryl.

138. The method of claim 135, wherein the universal base is selected from the group consisting of 3-nitropyrrole-2'-deoxynucleoside, 5-nitro-indole, 2-deoxyribosyl-(5-nitroindole), 2-deoxyribofuranosyl-(5-nitroindole), 2'-deoxyinosine, 2'-deoxynebularine, 6H, 8H-3,4-dihydropyrimido [4,5-c] oxazine-7-one or 2-amino-6-methoxyaminopurine.

139. The method of claim 132, wherein the proportion of A in the oligo is reduced to up to about 10%.

140. The method of claim 139, wherein the proportion of A in the oligo is reduced to up to about 5%.

141. The method of claim 140, wherein the proportion of A in the oligo is reduced to up to about 3%.

142. The method of claim 141, wherein the proportion of A in the oligo is reduced to about 0.

143. The method of claim 139, wherein the selected segment contains less than about 15% T.

144. The method of claim 132, further comprising substituting a methylated cytosine for cytosine in at least one CpG dinucleotide present in the anti-sense oligo(s).

145. The method of claim 132, wherein the anti-sense oligo(s) are about 7 to about 60 nucleotides long.

146. The method of claim 132, wherein the target is selected from the group consisting of transcription factors, stimulating and activating factors, interleukins, interleukin receptors, chemokines, chemokine receptors, endogenously produced specific and non-specific enzymes, immunoglobulins, antibody receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, adhesion molecules, selectins, defensins, growth factors, vasoactive peptides, vasoactive peptide receptors, and binding proteins and oncogenes.

147. The method of claim 146, wherein the target genes are selected from the group consisting of oncogenes.

148. An anti-sense oligonucleotide produced by the method of claim 132.

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